“Utilizing Wildlife Health to Conserve Biodiversity in the Appalachians and Beyond."

The 62nd International Conference of the Wildlife Disease Association

July 27- August 2, 2013
Knoxville, Tennessee



WELCOME!

Welcome to Knoxville, Tennessee and the 62nd International conference of the Wildlife Disease Association, the Second International Symposium on Ranaviruses, and the 2013 Annual Meeting of the American Association of Wildlife Veterinarians. We are excited that you are here and hope that you will take time to enjoy our wonderful city and explore the surrounding attractions such as the Great Smoky Mountain National Park. As with previous conferences, much planning and effort has gone into making this an enjoyable and rewarding experience for the attendees. To facilitate this, we purposely implanted a day at mid-conference to allow for sharing scientific knowledge in a field setting (i.e., Ranavirus sampling in the Smokies or sampling box turtles using dogs), just plain fun in the sun (rafting, hiking), or pure relaxation. The theme for this year's conference is "Utilizing Wildlife Health to Conserve Biodiversity in the Appalachians and Beyond." We hope you leave here with an appreciation of the wealth of biodiversity in this region of the world, and most importantly, we hope that the field events allow you to witness that biodiversity first-hand.

We are especially grateful to the University of Tennessee Institute of Agriculture, specifically the Department of Forestry, Wildlife and Fisheries and the College of Veterinary Medicine, for in-kind and financial support for this event. We are indebted to the professionals and students who worked diligently to plan and prepare for this conference. It was especially heart-warming to work with the students. They displayed much enthusiasm and drive to make this conference a success. It leaves one feeling that the future of our profession will definitely be in good hands! We also extend sincere appreciation to the sponsors who provided funds to help defray conference costs and keep registration fees down.

The conference will begin with a plenary session and the keynote address from Jonathan Gassett on 'Navigating the wildlife disease minefield: merging science, policy, and politics to protect our wildlife resources.' For this plenary session, we strove to encompass talks that highlighted key topics within the Appalachian region as well as globally. Thus, topics include white-nose syndrome in bats, emerging threats to herpetofauna, the latest on hemorrhagic disease and our elusive decline of honey bees. The plenary session will also include a synopsis of The Second International Symposium on Ranaviruses, which will have just concluded. In all, the conference includes a full day of student presentations and 11 themed sessions (conference theme; bats and emerging diseases; mammalian diseases; amphibian, reptile and aquatic health; avian diseases; avian influenza and waterfowl diseases; one health; tools and techniques; cervid diseases; linking disease ecology with wildlife health; AAWV-WVS: raising the bar for animal care in wildlife capture and field anesthesia). There will be 117 oral presentations and 65 poster presentations delivered by researchers, biologists, veterinarians and students.

We hope you enjoy the conference and look forward to interacting with you!

Sincerely,
Your local host committee: Deb Miller, Rick Gerhold, Ed Ramsay, Marcy Souza, Lisa Muller, Shige Eda, Matt Gray, Lauren Maestas, Sara Willard-Eroh, Jill Wilson

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MANY THANKS TO OUR UNIVERSITY OF TENNESSEE STUDENT VOLUNTEERS

Lauren Maestas

Sarah Willard-Eroh

Jill Wilson

Jose Grenet

Ashley Schenk

Lauren Henderson

Caroline Brown

Carrie Dobey

Louden Wright

Caroline Grunenwald

Kate Purple

Michelle Gates

James Gaddis

Justin Droke

Patrick Reilly

Jordan Chaney

Kevin Hamed

Mabre Brand

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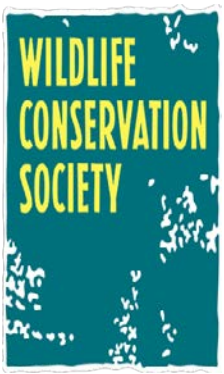
Many thanks to our sponsors:

























2013 INTERNATIONAL WILDLIFE DISEASE ASSOCIATION CONFERENCE
SCHEDULE OF EVENTS

SATURDAY, JULY 27, 2013

1:00	STUDENT WORKSHOP IN THE SMOKIES; RETURN BY 5PM SUNDAY THE 28TH	MEET IN HOTEL LOBBY
8:00-5:00	REGISTRATION	PARLOR 1
8:00-5:00	LOADING OF PRESENTATIONS	PARLOR 3

SUNDAY, JULY 28, 2013

8:00-5:00	REGISTRATION	PARLOR 1
8:00-5:00	LOADING OF PRESENTATIONS	PARLOR 3
8:00-12:00	EDITORIAL BOARD MEETING	CRYSTAL ROOM
8:00-5:00	ACZM ULTRA SHORT COURSE	PARLOR 8
9:00-5:00	WNS WORKSHOP	PARASITOLOGY LAB-UTCVM
9:30-1:30	STUDENT WORKSHOP: INTRODUCTION TO POPULATION WILDLIFE DISEASE MODELING	MEET IN HOTEL LOBBY
12:00-1:00	EDITORIAL BOARD AND WDA COUNCIL LUNCH	CRYSTAL ROOM
1:00-5:00	WDA COUNCIL MEETING	CRYSTAL ROOM
6:30-10:00	ICE BREAKERS TROLLEY STARTS LEAVING FROM LOBBY AT 6:00PM	BARLEY'S TAPROOM

MONDAY, JULY 29, 2013

	PLENARY (RICK GERHOLD)	
8:00-5:00	REGISTRATION	PARLOR 1
8:00-5:00	LOADING OF PRESENTATIONS	PARLOR 3
8:00-8:15	**UT SYSTEMS PRESIDENT JOE DIPIETRO:** WELCOMING REMARKS	GRAND PAVILION BALLROOM
8:15-8:45	**1. KEYNOTE SPEAKER JONATHAN GASSETT:** NAVIGATING THE WILDLIFE DISEASE MINEFIELD: MERGING SCIENCE, POLICY, AND POLITICS TO PROTECT OUR WILDLIFE RESOURCES	GRAND PAVILION BALLROOM
8:45-9:15	**2. GARY MCCRACKEN:** WHITE-NOSE SYNDROME IN BATS	GRAND PAVILION BALLROOM
9:15-9:45	**3. GREGORY CHINCHAR:** SUMMARY OF RANAVIRUS SYMPOSIUM	GRAND PAVILION BALLROOM
9:45-10:15	**4.. DAVID GREEN**: EMERGING AND RE-EMERGING LETHAL INFECTIOUS DISEASES OF WILD AMPHIBIANS AND REPTILES IN SOUTHEASTERN USA	GRAND PAVILION BALLROOM
10:15-10:45	BREAK	
10:45-11:15	**5. DAVE STALLKNECHT:** HEMORRHAGIC DISEASE AND THE MANY MEANINGS OF NO-SEE-UMS	GRAND PAVILION BALLROOM
11:15-11:45	**6. PETER DASZAK**: HONEY BEE DECLINE	GRAND PAVILION BALLROOM
11:45-12:00	**QUESTIONS AND DISCUSSION FOR PLENARY SPEAKERS**	GRAND PAVILION BALLROOM
12:00-1:30	WDA BUSINESS LUNCH	GRAND PAVILION BALLROOM

UTILIZING WILDLIFE HEALTH TO CONSERVE BIODIVERSITY IN THE APPALACHIANS AND BEYOND (ED RAMSAY)		
1:30-1:45	**7. RENE SALINAS:** USING AN INDIVIDUAL-BASED MODEL TO STUDY THE SPREAD AND CONTROL OF PSEUDO-RABIES VIRUS IN FERAL HOGS IN GREAT SMOKY MOUNTAINS NATIONAL PARK	GRAND PAVILION BALLROOM
1:45-2:00	**8. ASHLEY SCHENK:** CAUSES OF MORBIDITY AND MORTALITY OF WILDLIFE SPECIES PRESENTED TO A WILDLIFE CLINIC IN EAST TENNESSEE, USA, 2000–2011	GRAND PAVILION BALLROOM
2:00-2:15	**9. RICK GERHOLD**: DETECTION AND EPIDEMIOLOGY OF *TRICHOMONAS GALLINAE* IN PEREGRINE FALCON NESTLINGS IN KENTUCKY	GRAND PAVILION BALLROOM
2:15-2:30	**10. SARA SCHWEITZER:** UNUSUAL WINTER MORTALITY EVENTS IN MULTIPLE ATLANTIC SEABIRD SPECIES	GRAND PAVILION BALLROOM
2:30-2:45	**11. REBECCA HARDMAN:** PREVALENCE OF RANAVIRUS AND BD IN HELLBENDER POPULATIONS IN TENNESSEE AND ARKANSAS	GRAND PAVILION BALLROOM
2:45-3:00	**12. BRANDON MUNK:** INFECTIOUS CAUSES OF DERMATOLOGIC DISEASE IN FREE-RANGING WHITE-TAILED DEER (*ODOCOILEUS VIRGINIANUS*) FROM THE SOUTHEASTERN UNITED STATES	GRAND PAVILION BALLROOM
3:00-3:30	**BREAK**	
BATS AND EMERGING DISEASES (CHARLES RUPPRECHT)		
3:30-3:45	**13. CHARLES RUPPRECHT:** THE UNDISCOVERED COUNTRY: BATS, EMERGING INFECTIOUS DISEASES, MANAGEMENT STRATEGIES, AND CONSERVATION	GRAND PAVILION BALLROOM
3:45-4:00	**14. IVAN KUZMIN:** BAT RABIES: AN ANCIENT DISEASE WITH MANY UNKNOWNS	GRAND PAVILION BALLROOM
4:00-4:15	**15. IVAN KUZMIN:** SPILL-OVER INFECTIONS AND HOST SHIFTS OF BAT RABIES VIRUSES TO CARNIVORES: RECENT EXAMPLES FROM NORTH AMERICA	GRAND PAVILION BALLROOM
4:15-4:30	**16. MELINDA ROSTAL:** USAID PREDICT WILDLIFE SURVEILLANCE IN MEXICO	GRAND PAVILION BALLROOM
4:30-4:45	**17. M. KEVIN KEEL:** A TISSUE EXPLANT MODEL TO INVESTIGATE THE PATHOGENESIS OF WHITE-NOSE SYNDROME OF BATS	GRAND PAVILION BALLROOM
4:45-5:00	**18. ALISON ROBBIN**S: INVESTIGATING THE USE OF MUNITIONS BUNKERS AS ARTIFICIAL BAT HIBERNACULA	GRAND PAVILION BALLROOM
5:00-6:30	AAWV BUSINESS MEETING	GRAND PAVILION BALLROOM
6:30	**STUDENT & FACULTY MIXER**	TENNESSEE BALLROOM

TUESDAY, JULY 30, 2013

TERRY AMUNDSON STUDENT AWARD COMPETITION (EMI SAITO)		
8:00-5:00	REGISTRATION	PARLOR 1
8:00-5:00	LOADING OF PRESENTATIONS	PARLOR 3
8:00-8:15	**EMI SAITO:** OPENING REMARKS AND INTRODUCTION	GRAND PAVILION BALLROOM
8:15-8:45	**19. GRADUATE RESEARCH RECOGNITION AWARD**: **DE WET:** A SYSTEMATIC HEALTH ASSESSMENT OF THE INDIAN OCEAN BOTTLENOSE DOLPHIN (*TURSIOPS ADUNCUS*) AND THE INDO-PACIFIC HUMPBACK DOLPHIN (*SOUSA CHINENSIS*) INCIDENTALLY CAUGHT IN SHARK NETS OFF THE KWAZULU-NATAL COAST, SOUTH AFRICA	GRAND PAVILION BALLROOM
8:45-9:00	**20. LETICIA GUTIERREZ JIMENEZ:** TROPHIC COMPLEXITY: DOES IT PROTECT US FROM EMERGING INFECTIOUS DISEASES?	GRAND PAVILION BALLROOM
9:00-9:15	**21. MARIANNE PARENT:** CORRELATING ANTHROPOGENIC CAUSES OF WILDLIFE MORTALITY WITH HUMAN POPULATION DENSITY ESTIMATED BY NIGHT-LIGHT RADIANCE IN THE CANADIAN MARITIMES	GRAND PAVILION BALLROOM
9:15-9:30	**22. N. JANE HARMS:** CARRY-OVER EFFECTS OF ENVIRONMENTAL CONDITIONS AND STRESS DURING PREVIOUS MOULT ON REPRODUCTIVE SUCCESS IN NORTHERN COMMON EIDERS FACING ANNUAL AVIAN CHOLERA OUTBREAKS	GRAND PAVILION BALLROOM
9:30-9:45	**23. LIZABETH GLEIM:** THE EFFECTS OF LONG-TERM PRESCRIBED BURNING ON TICK-BORNE PATHOGEN PREVALENCE AND DISEASE RISK IN SOUTHWEST GEORGIA	GRAND PAVILION BALLROOM
9:45-10:00	**24. ZAIDA RENTERIA-SOLIS:** DISEASES IN INVASIVE SPECIES: INVESTIGATIONS IN FREE-RANGING RACCOONS *(PROCYON LOTOR*) IN GERMANY	GRAND PAVILION BALLROOM
10:00-10:45	**BREAK/ STUDENT POSTER SESSION**	**TENNESSEE BALLROOM**
10:45-11:00	**25. NADINE VOGT:** AN INVESTIGATION OF HATCH-YEAR MORTALITY IN AN ONTARIO CAPTIVE BREEDING PROGRAM FOR THE ENDANGERED EASTERN LOGGERHEAD SHRIKE (*LANIUS LUDOVICIANUS MIGRANS*), 2006-2011	GRAND PAVILION BALLROOM
11:00-11:15	**26. KENDALL SIMON:** CAUSE OF DEATH AND TRENDS OF MORTALITY FOR BALD EAGLES (*HALIAEETUS LEUCOCEPHALUS*) IN MICHIGAN OVER A 25 YEAR PERIOD	GRAND PAVILION BALLROOM
11:15-11:30	**27. PEDRO JIMENEZ-BLUHM:** IDENTIFICATION AND CHARACTERIZATION OF AVIAN INFLUENZA ISOLATED IN THE CENTRAL REGION OF CHILE	GRAND PAVILION BALLROOM
11:30-11:45	**28. RODOLFO NALLAR:** DEMOGRAPHIC AND SPATIOTEMPORAL PATTERNS OF AVIAN INFLUENZA VIRUS INFECTION AT THE CONTINENTAL SCALE, AND IN RELATION TO ANNUAL LIFE CYCLE OF A MIGRATORY HOST	GRAND PAVILION BALLROOM
11:45-12:00	**29. WHITNEY KISTLER:** CANADA GEESE (*BRANTA CANADENSIS*) AND INFLUENZA A VIRUSES: WHAT CAN WE LEARN?	GRAND PAVILION BALLROOM
12:00-1:30	**LUNCH ON YOUR OWN**	

TERRY AMUNDSON STUDENT AWARD COMPETITION (EMI SAITO)		
1:30-1:45	**30. CLAUDIA NIEMEYER:** A NOVEL AVIPOXVIRUS ASSOCIATED TO CUTANEOUS AND DIFTERIC DISEASE IN MAGELLANIC PENGUINS (*SPHENISCUS MAGELLANICUS*) IN BRAZIL	GRAND PAVILION BALLROOM
1:45-2:00	**31. BEN STADING:** ASSESSMENT OF RECOMBINANT POXVIRUSES AS VACCINE VECTORS FOR BATS THROUGH *IN VIVO* IMAGING	GRAND PAVILION BALLROOM
2:00-2:15	**32. MICHELLE VERANT:** ASSESSMENT OF PHYSIOLOGICAL EFFECTS OF WHITE-NOSE SYNDROME IN BATS USING DOUBLY LABELED WATER AND CLINICAL CHEMISTRY	GRAND PAVILION BALLROOM
2:15-2:30	**33. ALBERT MERCURIO:** AN EXPERIMENTAL TRIAL INDUCES AVIAN VACUOLAR MYELINOPATHY IN PAINTED TURTLES (*CHRYSEMYS PICTA*)	GRAND PAVILION BALLROOM
2:30-2:45	**34. JESSICA GONYNOR-MCGUIRE:** EFFECTS OF UPPER RESPIRATORY TRACT DISEASE ON MOVEMENT AND BEHAVIOR OF GOPHER TORTOISES (*GOPHERUS POLYPHEMUS*)	GRAND PAVILION BALLROOM
2:45-3:30	**BREAK/ STUDENT POSTER SESSION**	**TENNESSEE BALLROOM**
TERRY AMUNDSON STUDENT AWARD COMPETITION (EMI SAITO)		
3:30-3:45	**35. A. CHRISTY WYCKOFF:** BIOASSAY DETECTION OF CHRONIC WASTING DISEASE PRIONS IN SOIL	GRAND PAVILION BALLROOM
3:45-4:00	**36. BRANDI COX:** ROLE OF THE HYPERMUCOID PHENOTYPE IN THE RESISTANCE OF *KLEBSIELLA PNEUMONIAE* TO OXIDATIVE AND SERUM KILLING IN NON-HUMAN PRIMATES	GRAND PAVILION BALLROOM
4:00-4:15	**37. BARBARA SHOCK:** ECTOPARASITES AND THEIR RELATIONSHIP TO THE NOVEL BABESIA DETECTED IN THE ENDANGERED FLORIDA PUMA *(PUMA CONCOLOR CORYI*)	GRAND PAVILION BALLROOM
4:15-4:30	**38. CAROLINE GRUNENWALD:** SURVEILLANCE OF FILARIAL NEMATODES IN FREE RANGING MOOSE FROM MINNESOTA	GRAND PAVILION BALLROOM
4:30-4:45	**39. JANNA SCHURER:** *ECHINOCOCCUS MULTILOCULARIS* AND *E. CANADENSIS* IN WOLVES FROM WESTERN CANADA	GRAND PAVILION BALLROOM
4:45-5:00	**40. SPENCER KEHOE:** *BARTONELLA* INFECTION PREVALENCE IN CARDIAC VALVES OF COYOTES, A NATURAL RESERVOIR IN CALIFORNIA	GRAND PAVILION BALLROOM
5:00-6:00	WVS BUSINESS MEETING	BALLROOM
6:00-10:00	**AUCTION AT IJAMS NATURE CENTER --BUSES START LEAVING HOTEL AT 5:00** **DINNER STARTS AT 6:30**	IJAMS NATURE CENTER 2915 Island Home Ave, Knoxville, TN 37920

WEDNESDAY, JULY 31, 2013

MAMMALIAN DISEASES (KEVIN KEEL)		
8:00-5:00	REGISTRATION	PARLOR 1
8:00-5:00	LOADING OF PRESENTATIONS	PARLOR 3
8:00-8;15	**41. MARIA SPRIGGS:** 25 YEARS POST REINTRODUCTION: SEROSURVEY OF SELECT PATHOGENS IN A POPULATION OF AMERICAN MARTEN IN MICHIGAN	GRAND PAVILION BALLROOM
8:15-8:30	**42. MARK DREW:** CONTACT BETWEEN BIGHORN SHEEP AND DOMESTIC LIVESTOCK	GRAND PAVILION BALLROOM
8:30-8:45	**43. DENIS MCALOOSE:** CANINE DISTEMPER VIRUS: AN EMERGING DISEASE IN WILD ENDANGERED AMUR TIGERS *(PANTHERA TIGRIS ALTAICA*)	GRAND PAVILION BALLROOM
8:45-9:00	**44. ANNE JUSTICE-ALLEN:** BLUETONGUE VIRUS 10 AND 11 INFECTION IN TWO DESERT BIGHORN SHEEP	GRAND PAVILION BALLROOM
9:00-9:15	**45. CHERYL SANGSTER:** OUTBREAK OF MYCOBACTERIAL DERMATITIS AND CELLULITIS IN FOUR TASMANIAN DEVILS (*SARCOPHILUS HARRISII*)	GRAND PAVILION BALLROOM
9:15-9:30	**46. MARIA-PIERRE RYSER-DEGIORGIS:** HEALTH SURVEILLANCE AS AN IMPORTANT TOOL IN WILDLIFE CONSERVATION: EXPERIENCES WITH THE EURASIAN LYNX	GRAND PAVILION BALLROOM
9:30-9:45	**47. MAUD LELU:** IMPACTS OF HOST DENSITIES ON THE EVOLUTION OF *TOXOPLASMA GONDII* TRANSMISSION ROUTES	GRAND PAVILION BALLROOM
9:45-10:00	**48. DAVID PEACOCK:** CAN NEW AND TRANSLOCATED SPECIES OF *EIMERIA* ASSIST IN THE MANAGEMENT OF AUSTRALIA'S PEST EUROPEAN RABBIT (*ORYCTOLAGUS CUNICULUS CUNICULUS)* POPULATION?	GRAND PAVILION BALLROOM
10:00-10:15	**49. SUZANNE LENHART:** CONTROL APPLICATIONS IN WILDLIFE DISEASE MODELS	GRAND PAVILION BALLROOM
	END OF PRESENTATIONS FOR THE DAY	
	FIELD TRIPS AND WORKSHOPS	
1:00-4:00	**HERPTILE NECROPSY WORKSHOP**	PARLOR 6
	LUNCH AND DINNER ON YOUR OWN	

THURSDAY, AUGUST 1, 2013

	AMPHIBIAN, REPTILE, & AQUATIC HEALTH (DEB MILLER) MEDALLION ROOM	**AVIAN DISEASES** (ROGER APPLEGATE) CARRIAGE/CRYSTAL ROOM
8:00-5:00	REGISTRATION	PARLOR 1
8:00-5:00	LOADING OF PRESENTATIONS	PARLOR 3
8:00-8:15	**50. ANNE BALLMAN**: ROAD PROJECTS, TURTLE RELOCATION AND RANAVIRUS: LESSONS FOR US ALL	**63. YVETTE GIRARD:** EPIDEMIC MORTALITY DUE TO TRICHOMONOSIS IN A DECLINING BAND-TAILED PIGEON POPULATION
8:15-8:30	**51. MAUREEN MURRAY:** FUNGAL DERMATITIS IN TWO FREE-LIVING SNAKES ASSOCIATED WITH *CHRYSOSPORIUM OPHIODIICOLA* AND *ACREMONIUM (SAROCLADIUM) STRICTUM*	**64. CHARLES VAN RIPER III:** THE DISTRIBUTION AND EXTENT OF HEAVY METAL ACCUMULATION AND BLOOD PARASITES IN SONG SPARROWS OF ARIZONA'S UPPER SANTA CRUZ RIVER WATERSHED
8:30-8:45	**52. JULIA EARL:** CAPABILITY OF RANAVIRUS TO CAUSE EXTINCTION IN LOCAL POPULATIONS OF WOOD FROGS	**65. ANNE JUSTICE-ALLEN:** BALD EAGLE NESTLING MORTALITY DUE TO PARASITISM BY TICKS AND SUCCESSFUL MANAGEMENT WITH NEST REPLACEMENT
8:45-9:00	**53. RACHEL MARSCHANG:** LIME DISINFECTION OF FISH PONDS: EFFECTS ON VIRUSES AND ON INVERTEBRATE COMMUNITIES	**66. JUSTIN BROWN:** IDENTIFICATION OF LYMPHOPROLIFERATIVE DISEASE VIRUS IN WILD TURKEYS (*MELEAGRIS GALLOPAVO*) IN NORTH AMERICA
9:00-9:15	**54. THIERRY WORK:** CORAL DISEASE-WHERE ARE THE WILDLIFE HEALTH EXPERTS?	**67. NINA SCHOCH:** COMMON LOON HEALTH ASSESSMENTS IN NEW YORK'S ADIRONDACK PARK, 2003-2012
9:15-9:30	**55. STACEY LANCE:** PREVALENCE OF TWO AMPHIBIAN DISEASES, RANAVIRUS AND CHYTRIDIOMYCOSIS, IN CONTAMINATED AND UNCONTAMINATED SITES ON THE SAVANNAH RIVER SITE	**68. JAMIE PHILLIPS:** WEST NILE VIRUS IN GEORGIA; A TEN-YEAR STUDY
9:30-9:45	**56. WILLIAM SUTTON:** TRENDS IN RANAVIRUS PREVALENCE AMONG PLETHODONTID SALAMANDERS IN THE GREAT SMOKY MOUNTAINS NATIONAL PARK	**69. LUIS CRUZ-MARTINEZ:** NESTLING TREE SWALLOWS EXPOSED TO OIL SANDS-RELATED EMISSIONS: ASSESSMENT OF BIOLOGICAL EFFECTS
9:45-10:00	**57. AMANDA DUFFUS:** RANAVIRAL DISEASE IN THE UK – COMMON FROGS AND COMMON TOADS ARE NOT CREATED EQUAL: EXPERIMENTAL ASSESSMENT OF VIRULENCE AND HOST SPECIFICITY OF UK RANAVIRUS ISOLATES IN *RANA TEMPORARIA* AND *BUFO BUFO* TADPOLES	**70. MICHAEL SAMUEL:** THE PERPLEXING PROBLEM OF AVIAN POX IN HAWAIIAN FOREST BIRDS
10:00-10:45	**BREAK/ GENERAL POSTER SESSION (TENNESSEE BALLROOM)**	

	AMPHIBIAN, REPTILE, & AQUATIC HEALTH (DEB MILLER) MEDALLION ROOM	**AVIAN INFLUENZA AND WATERFOWL DISEASES** (JUSTIN BROWN) CARRIAGE/CRYSTAL ROOM
10:45-11:00	**58. TERRY NORTON:** HEALTH ASSESSMENT OF EASTERN INDIGO SNAKES (*DRYMARCHON COUPERI*) IN GEORGIA	**71. SARAH OLSON:** SURVEILLANCE GAPS AND BIODIVERSITY OF INFLUENZA A SUBTYPES IN WILD BIRDS
11:00-11:15	**59. TERRY NORTON:** PAIN MANAGEMENT STRATEGIES IN CHELONIANS AND PHARMACOKINETICS OF TRAMADOL AND O-DESMETHYLTRAMADOL IN THE LOGGERHEAD SEA TURTLE (*CARETTA CARETTA*)	**72. MARCELA UHART:** EVIDENCE FOR NEGATIVE IMPACT OF LEAD EXPOSURE ON GENERIC INDICES OF HEALTH IN FREE-RANGING DUCKS
11:15-11:30	**60. SONIA HERNANDEZ:** SOUTHEASTERN WILD TURTLES ARE RESERVOIRS OF *SALMONELLA* SPP BUT DO NOT SHED AFTER BEING STRESSED	**73. BARBARA BODENSTEIN:** PATHOLOGY OF DISEASE CAUSED BY WELLFLEET BAY VIRUS, AN EMERGING PATHOGEN OF COMMON EIDERS (*SOMATERIA MOLLISSIMA*)
11:30-11:45	**61. ESTEBAN SOTO:** PHENOTYPIC AND GENOTYPIC HOMOGENEITY AMONGST *STREPTOCOCCUS INIAE* ISOLATES RECOVERED DURING CARIBBEAN REEF FISH OUTBREAKS	**74. DAVID STALLKNECHT:** NEUTRALIZING ANTIBODIES TO INFLUENZA A VIRUSES IN STAGING MALLARDS
11:45-12:00	**62. JOHN ROBERTS:** STUNTING AND MORTALITY OF CAPTIVE RAISED LOWLAND LEOPARD FROG (*LITHOBATES YAVAPAIENSIS*) TADPOLES AND RECENT METAMOPHS ORIGINATING FROM WILD COLLECTED EGG MASSES	**75. M. JOE SLUSHER:** THE ROLE OF PASSERINES AND OTHER TERRESTRIAL BIRDS IN AVIAN INFLUENZA VIRUS EPIDEMIOLOGY
12:00-1:30	**LUNCH ON YOUR OWN**	
	ONE HEALTH (MARCY SOUZA) MEDALLION ROOM	**TOOLS & TECHNIQUES** (MARK DREW) CARRIAGE/CRYSTAL ROOM
1:30-1:45	**76. KRISTA JONES:** *TOXOPLASMA GONDII* IN SCANDINAVIAN BROWN BEARS	**88. BECKI LAWSON:** CITIZEN SCIENCE AS A TOOL FOR WILDLIFE DISEASE SURVEILLANCE: THE EVOLUTION OF THE GARDEN WILDLIFE HEALTH PROJECT IN GREAT BRITAIN
1:45-2:00	**77. CHERYL SANGSTER:** STUDY OF PATHOLOGY IN BRUSHTAIL POSSUMS (*TRICHOSURUS VULPECULA*) IN AN URBAN AUSTRALIAN SETTING	**89. ERIK AGREN:** NATIONAL ECHINOCOCCUS SURVEILLANCE USING A NOVEL PCR TEST FOR FOX FECAL SAMPLES
2:00-2:15	**78. DAWN ROELLIG:** INVESTIGATION OF *GIARDIA DUODENALIS* INFECTION IN A LABORATORY COLONY OF PRAIRIE DOGS, *CYNOMYS LUDOVISIANUS*	**90. JENNY POWERS:** EFFECTS OF GONADOTROPIN-RELEASING HORMONE VACCINATION (GONACON-B) ON FERTILITY IN FREE-RANGING FEMALE ROCKY MOUNTAIN ELK (*CERVUS ELAPHUS NELSONI*)
2:15-2:30	**79. ELIZABETH FALENDYSZ:** EVALUATION OF THE GAMBIAN POUCHED RAT (*CRICETOMYS GAMBIANUS*) AS A POTENTIAL MONKEYPOX RESERVOIR USING BIOLUMINESCENT IMAGING	**91. JORDONA KIRBY:** PARADIGM SHIFT IN WILDLIFE RABIES SURVEILLANCE TO SUPPORT ORAL RABIES VACCINATION

	ONE HEALTH (MARCY SOUZA) MEDALLION ROOM	**TOOLS & TECHNIQUES** (MARK DREW) CARRIAGE/CRYSTAL ROOM
2:30-2:45	**80. ANGELA BOSCO-LAUTH:** INITIAL ECOLOGICAL INVESTIGATIONS OF HEARTLAND VIRUS IN AREAS ADJACENT TO HUMAN CASE SITES	**92. TAMMIE O'ROURKE:** CHALLENGES OF DEVELOPING A GLOBAL WILDLIFE HEALTH INFORMATION MANAGEMENT SYSTEM PART I: LESSONS LEARNED FROM A DATA ANALYSTS' PERSPECTIVE
2:45-3:00	**81. KIMBERLEE BECKMEN:** ENHANCED RABIES SURVEILLANCE IN ALASKAN WILDLIFE: DETECTION OF NEW HOST RANGE AND RISKS TO TRAPPERS	**93. DAMIEN JOLY:** CHALLENGES OF DEVELOPING A GLOBAL WILDLIFE HEALTH INFORMATION MANAGEMENT SYSTEM PART II: LESSONS LEARNED FROM A WILDLIFE EPIDEMIOLOGIST'S PERSPECTIVE
3:00-3:30	**BREAK/ GENERAL POSTER SESSION (TENNESSEE BALLROOM)**	
	ONE HEALTH (MARCY SOUZA) MEDALLION ROOM	**CERVID DISEASES** (LISA MULLER) CARRIAGE/CRYSTAL ROOM
3:30-3:45	**82. SASCHA KNAUF:** ARE AFRICAN NONHUMAN PRIMATES A RESERVOIR FOR HUMAN YAWS INFECTION?	**94. DAVID EDMUNDS:** WHITE-TAILED DEER DEMOGRAPHY IN A HIGH PREVALENCE CWD ENDEMIC AREA OF WYOMING
3:45-4:00	**83. KENNETH CAMERON:** FECAL VIRAL DIVERSITY AS AN INDICATOR OF HEALTH IN FREE-RANGING GREAT APES IN THE SANGHA REGION OF THE REPUBLIC OF CONGO	**95. KAREN FOX:** CACTUS BUCKS, TESTICULAR LESIONS, AND EPIZOOTIC HEMORRHAGIC DISEASE IN COLORADO MULE DEER
4:00-4:15	**84. LAUREN MAESTAS:** *BORRELIA* INFECTIONS IN IXODES SPECIES TICKS (ACARI: IXODIDAE) ALONG LATIDUDINAL GRADIENTS IN THE SOUTHEASTERN COASTAL UNITED STATES	**96. TODD SHURY:** DIFFERENTIAL MORTALITY AND CLINICAL PATHOLOGY OF SEMI FREE-RANGING MOOSE ASSOCIATED WITH *FASCIOLOIDES MAGNA* IN ELK ISLAND NATIONAL PARK, ALBERTA
4:15-4:30	**85. RYAN MILLER:** DISEASES AT THE LIVESTOCK–WILDLIFE INTERFACE IN THE UNITED STATES: STATUS, CHALLENGES, AND OPPORTUNITIES	**97. MARGARET WILD:** PREVALENCE AND EFFECTS OF CHRONIC WASTING DISEASE IN ELK FROM ROCKY MOUNTAIN NATIONAL PARK
4:30-4:45	**86. STEVEN SWEENEY:** A BIOECONOMIC DECISION MODEL FOR DISEASE MITIGATION AT THE WILDLIFE-LIVESTOCK INTERFACE	**98. KRYSTEN SCHULER:** FIELD SURVEY OF RISK FACTORS FOR CHRONIC WASTING DISEASE SURVEILLANCE
4:45-5:00	**87. COLIN GILLIN:** PROPOSAL TO CREATE A US NATIONAL FISH AND WILDLIFE HEALTH NETWORK	**99. MARGO PYBUS:** IMPROVING HUNTER HARVEST AS A TOOL FOR CWD MANAGEMENT
5:00-6:00	**WDA BUSINESS MEETING IN CRYSTAL ROOM**	
6:00-7:00	**SOCIAL HOUR IN TENNESSEE BALLROOM**	
7:00-10:00	**WDA AWARDS BANQUET FOLLOWED BY DANCING IN MEDALLION /CARRIAGE ROOMS**	

FRIDAY, AUGUST 2, 2013

LINKING DISEASE ECOLOGY WITH WILDLIFE HEALTH (MICHAEL YABSLEY & SONIA HERNANDEZ)		
8:00-8:15	**100. TERRA KELLY:** THREATS TO THE SURVIVAL OF CALIFORNIA CONDORS: IMPACTS OF HUMAN DISTURBANCE ON A CRITICALLY ENDANGERED SCAVENGER	MEDALLION ROOM
8:15-8:30	**101. CHRISTIAN GORTAZAR:** WHICH FACTORS DRIVE TUBERCULOSIS TRANSMISSION? IDENTIFYING SUPER-SHEDDERS IN WILD BOAR POPULATIONS	MEDALLION ROOM
8:30-8:45	**102. GALAXIA CORTES-HINOJOSA:** PHYLOGENETIC ANALYSIS, AND QUANTITATIVE PCR SURVEILLANCE OF A NOVEL HERPESVIRUS OF NORTHERN FUR SEALS (*CALLORHINUS URSINUS*) RELATED TO THE CARCINOMA-ASSOCIATED OTARINE HV1	MEDALLION ROOM
8:45-9:00	**103. JOAQUIN VICENTE:** HOST UNGULATE RICHNESS INCREASES TUBERCULOSIS RISK IN SOUTH SPAIN	MEDALLION ROOM
9:00-9:15	**104. MARTIN GILBERT:** SIMULATING THE POPULATION IMPACT OF CANINE DISTEMPER VIRUS ON AMUR TIGERS (*PANTHERA TIGRIS ALTAICA*) IN RUSSIA	MEDALLION ROOM
9:15-9:30	**105. SARAH OLSON:** DEAD OR ALIVE: ANIMAL SAMPLING DURING EBOLA HEMORRHAGIC FEVER OUTBREAKS IN HUMANS	MEDALLION ROOM
9:30-9:45	**106. KRISTY SEGAL:** LACK OF *BATROCHOCHYTRIUM DENDROBATIDIS* AND RANAVIRUS INFECTIONS IN CANE TOADS (*RHINELLA MARINA*) FROM GUANACASTE COSTA RICA	MEDALLION ROOM
9:45-10:00	**107. CARL-GUSTAF THULIN:** ZOONOSIS AND SOCIETAL PERCEPTION OF WILDLIFE – A SWEDISH PERSPECTIVE	MEDALLION ROOM
END OF SESSION		

FRIDAY, AUGUST 2, 2013

AAWV-WVS: RAISING THE BAR FOR ANIMAL CARE IN WILDLIFE CAPTURE AND FIELD ANESTHESIA (MARGARET WILD & JON ARNEMO)		
8:00-8:05	**JON ARNEMO AND MARGARET WILD:** INTRODUCTION OF THE WILDLIFE VETERINARY SECTION	CARRIAGE/CRYSTAL ROOM
8:05-8:30	**108. MARC CATTET:** LONG-TERM EFFECTS OF CAPTURE AND HANDLING: AN ISSUE FOR WILDLIFE RESEARCH, MANAGEMENT AND CONSERVATION THAT SHOULD NOT BE IGNORED	CARRIAGE/CRYSTAL ROOM
8:30-8:55	**109. BILL LANCE:** STRESS AND PAIN MANAGEMENT IN WILDLIFE-THE NEW FRONTIER FOR WILDLIFE PROFESSIONALS	CARRIAGE/CRYSTAL ROOM
8:55-9:20	**110. PERI WOLFF AND MARK DREW:** COMPARISON OF NET-GUNNING AND FIELD ANESTHESIA	CARRIAGE/CRYSTAL ROOM
9:20-9:45	**111. JON ARNEMO:** CAPTURE-RELATED MORTALITIES IN BROWN BEARS (*URSUS ARCTOS*) IN SCANDINAVIA 1984-2013: A REVIEW OF 1,824 CAPTURES	CARRIAGE/CRYSTAL ROOM
9:45-10:00	**112. KIMBERLEE BECKMEN:** TASER ELECTRONIC CONTROL DEVICE USE FOR WILDLIFE MANAGEMENT	CARRIAGE/CRYSTAL ROOM
10:00-10:30	Break	
10:30-10:45	**113. MARK DREW**- WILDLIFE EUTHANASIA	CARRIAGE/CRYSTAL ROOM
10:45-11:00	**114. ALINA EVANS:** NEW DEVELOPMENTS IN BIO-LOGGING TECHNIQUES: PHYSIOLOGICAL SENSORS WITH A MORTALITY ALERT	CARRIAGE/CRYSTAL ROOM
11:00-11:15	**115. CHRISTOPHER WHITTIER:** APPLIED VETERINARY MEDICINE AS A CONSERVATION TOOL FOR WESTERN LOWLAND GORILLAS (*GORILLA GORILLA*)	CARRIAGE/CRYSTAL ROOM
11:15-11:30	**116. MARIANNE LIAN:** PHYSIOLOGICAL EVALUATION OF MEDETOMIDINE-KETAMINE ANESTHESIA IN FREE-RANGING SVALBARD (*RANGIFER TARANDUS PLATYRHYNCHUS*) AND WILD NORWEGIAN REINDEER (*R. T. TARANDUS*)	CARRIAGE/CRYSTAL ROOM
SESSION AND CONFERENCE ADJOURNS –SAFE TRAVELS		

Student Posters

SP1. **IRENE BUENO PADILLA** PILOTING A TOOL FOR ASSESSING PUBLIC HEALTH RISKS FROM THE IMPORTATION OF WILDLIFE INTO THE UNITED STATES: THE CASE OF RODENT IMPORTATION FROM LATIN AMERICA

SP2. **IRENE BUENO PADILLA** SOCIO-ECONOMIC AND POLITICAL ASPECTS OF SPENT LEAD AMMUNITION

SP3. **CLAUDIA NIEMEYER** WEIGHTS, HEMATOLOGY AND PLASMATIC CHEMISTRY OF 33 FREE-RANGING *PHAETON* TROPICAL SEABIRDS

SP4. **JESSE MICHAEL THOMAS** SURVEILLANCE FOR LYMPHOPROLIFERATIVE DISEASE VIRUS IN HUNTER-KILLED WILD TURKEYS (*MELEAGRIS GALLOPAVO*)

SP5. **WHITNEY M. KISTLER** MORPHOLOGICAL AND MOLECULAR CHARACTERIZATION OF HEMATOZOAN PARASITES OF AMERICAN BLACK DUCKS (*ANAS RUBRIPES*) IN THE EASTERN UNITED STATES.

SP6. **MORGAN JOSEPH SLUSHER** THE ROLE OF PASSERINES AND OTHER TERRESTRIAL BIRDS IN AVIAN INFLUENZA VIRUS EPIDEMIOLOGY

SP7. **EMILY CORNELIUS** HEMOPARASITE INFECTION AFFECTS WHITE BLOOD CELL PROFILES IN SONGBIRDS DURING FALL MIGRATION

SP8. **ANDREW OLSEN** *OXYSPIRURA PETROWI* IN QUAIL FROM SOUTH TEXAS AND THE ROLLING PLAINS

SP9. **CLAUD GANSER** BIOGEOGRAPHY OF TRANSMISSION DYNAMICS FOR A VECTOR-BORNE PATHOGEN RECENTLY FOUND IN ARCTIC-BREEDING SHOREBIRDS

SP10. **NARELLE A. DYBING** FERAL PERIL ON TROPICAL CHRISTMAS ISLAND

SP11. **BARBARA C. SHOCK** UTILITY OF TESTING BLOOD-FED AND QUESTING TICKS FOR PIROPLASMS FOR IDENTIFICATION OF NOVEL VERTEBRATE HOSTS OR VECTORS

SP12. **ELIZABETH R. GLEIM** IMPACTS OF LONG-TERM PRESCRIBED BURNING ON TICK POPULATION DYNAMICS IN SOUTHWEST GEORGIA

SP13. **LUCAS KIRSCHMAN** THE EFFECTS OF ENVIRONMENTAL STRESSORS ON DISEASE DYNAMICS IN AMPHIBIANS

SP14. **SHANE M. HANLON** THE MITIGATION OF AGRICULTURAL PESTICIDES BY AN AMPHIBIAN PATHOGEN IN AQUATIC COMMUNITIES

SP15. **KRISTEN L HUGHES** A COMPARISON OF SPATIAL DISTRIBUTION MODELING METHODS FOR THE AFRICAN BUFFALO (*SYNCERUS CAFER*) POPULATION IN THE KRUGER NATIONAL PARK

SP16. **JESSICA L. GONYNOR-MCGUIRE** SURVEILLANCE FOR UPPER RESPIRATORY TRACT DISEASE AND *MYCOPLASMA* IN FREE-RANGING GOPHER TORTOISES IN GEORGIA

SP17. **ANNIE PAGE-KARJIAN** INVESTIGATING CHELONID FIBROPAPILLOMA-ASSOCIATED HERPESVIRUS IN SYMPTOMATIC AND ASYMPTOMATIC REHABILITATING SEA TURTLES

SP18. **SARAH M. COKER** EFFECTS OF BASKING BEHAVIOR ON PREVALENCE AND PARASITEMIA LEVELS OF HAEMOGREGARINES IN FRESHWATER TURTLES

SP19. **BRIANNA M. WILLIAMS** PREVALENCE AND DIVERSITY OF *BABESIA*, *HEPATOZOON*, *EHRLICHIA*, AND *BARTONELLA* IN WILD AND DOMESTIC CARNIVORES FROM ZAMBIA, AFRICA

SP20. **MICHELLE GATES** PARASITOLOGY, VIROLOGY AND SEROLOGY FINDINGS IN FREE RANGING COYOTES FROM NORTH GEORGIA

SP21. **SARAD PAUDEL** CHARACTERIZATION OF *MYCOBACTERIUM TUBERCULOSIS* ISOLATES FROM CAPTIVE ELEPHANTS OF NEPAL

SP22. **MAURICIO SEGUEL** HOOKWORM DISEASE IN SOUTH AMERICAN FUR SEAL (*ARCTOPHOCA AUSTRALIS*) PUPS AT GUAFO ISLAND, CHILE

SP23. **AMY LYNN WILLIAMS** UNDERSTANDING HOW TABANIDS INFLUENCE THE PREVALENCE OF *ELAEOPHORA SCHNEIDERI* IN MOOSE POPULATIONS AROUND WYOMING, USA

SP24. **LAURA BAQUEDANO SANTANA** ECHINOCOCCOSIS IN *AGOUTI PACA* IN THE PERUVIAN AMAZON

SP25. **KRISTIN J. BONDO** THE POTENTIAL OF RACCOONS TO BIOLOGICALLY AND MECHANICALLY TRANSMIT *SALMONELLA*

General poster session

P1. **MARCO A. ENCISO** MORTALITY IN *TELMATOBIUS MARMORATUS* FROGS AFFECTED BY *BATRACHOCHYTRIUM DENDROBATIDIS* AND MYXOSPORIDIA INFECTION

P2. **ALAN FEDYNICH** SURVEY FOR *OXYSPIRURA PETROWI* IN NORTHERN BOBWHITES FROM THE ROLLING PLAINS ECOREGION OF TEXAS AND WESTERN OKLAHOMA

P3. **CINDY P. DRISCOLL** CHESAPEAKE BAY 2012 AVIAN BOTULISM AND HARMFUL ALGAL BLOOM MORBIDITY AND MORTALITY EVENT

P4. **JENNIFER R. BALLARD** SEROPREVALENCE OF TWO ORTHOMYXOVIRUSES IN COMMON EIDERS

P5. **JUSTIN DAVID BROWN** INVESTIGATING THE POTENTIAL ROLE OF WILD BIRDS IN THE 2009 AND 2011 INTRODUCTIONS OF H7N9 INFLUENZA A VIRUS INTO DOMESTIC POULTRY IN THE UNITED STATES OF AMERICA

P6. **KELLY DEBAENE** A MODEL OF AN AVIAN-HUMAN INFLUENZA OUTBREAK AT LINCOLN PARK ZOO, CHICAGO

P7. **REBECCA L. POULSON** ENVIRONMENTAL STABILITY OF SWINE AND PANDEMIC INFLUENZA VIRUSES IN WATER

P8. **SARAH HELEN OLSON** NOVEL H7N9 AVIAN INFLUENZA IN ASIA AND THE POTENTIAL ROLE OF WILD BIRDS

P9. **PAULINE NOL** DETERMINATION OF TISSUE PERSISTENCE OF *MYCOBACTERIUM BOVIS* BCG IN TEXAS-ORIGIN FERAL SWINE ORALLY VACCINATED WITH *MYCOBACTERIUM BOVIS* BCG

P10. **ANNE B. LICHTENWALNER** PARASITES IN MAINE MOOSE 2010-13: COLLABORATIVE STUDIES

P11. **IAN H. PLUMMER** DETECTION OF CHRONIC WASTING DISEASE PRIONS FROM ENVIRONMENTAL SOURCES BY PROTEIN MISFOLDING CYCLIC AMPLIFICATION

P12. **JOE CORN** POTENTIAL CONTAMINATION OF ENDANGERED FLORIDA KEY DEER HABITAT WITH *MYCOBACTERIUM AVIUM* SUBSPECIES *PARATUBERCULOSIS*

P13. **N. JANE HARMS** TRANSECT SAMPLING METHOD FOR DETECTING WINTER TICKS ON ELK HIDES IN YUKON, CANADA

P14. **ANDREA L MILLER** PHYSIOLOGIC EFFECTS OF HUMAN ENCOUNTERS AND HUNTING ON THE SCANDINAVIAN BROWN BEAR (*URSUS ARCTOS*)

P15. **DAVID PEACOCK** SEEKING ADDITIONAL BIOLOGICAL CONTROL AGENTS TO AUGMENT RABBIT HAEMORRHAGIC DISEASE (RHD) AND MYXOMATOSIS: MANAGING AUSTRALIA'S RECOVERING PEST RABBIT POPULATION

P16. **FELICIA NUTTER** EVALUATING MANAGEMENT ALTERNATIVES FOR FREE-ROAMING CAT POPULATIONS ACROSS A RANGE OF LANDSCAPES: AN INDIVIDUAL-BASED, DEMOGRAPHIC SIMULATING MODELING APPROACH

P17. **AUBREY TAUER** WILDLIFE DISEASE AND ECOSYSTEM HEALTH IN NICARAGUA AND EL SALVADOR

P18. **WALTER O. COTTRELL** A WEB BASED PHARMACEUTICAL MANAGEMENT SYSTEM

P19. **DANNA M. SCHOCK** USING THE HEALTH OF AMPHIBIAN POPULATIONS TO EVALUATE ECOSYSTEM HEALTH IN THE OIL SANDS REGION OF CANADA

P20. **DAVID H. LEY** MULTIPLE HOST TRANSFERS BUT ONLY ONE SUCCESSFUL LINEAGE OF *MYCOPLASMA GALLISEPTICUM* IN HOUSE FINCHES

P21. **GOTTELAND CÉCILE** FOR A BETTER UNDESTANDING OF THE ENVIRONMENTAL CONTAMINATION BY *TOXOPLASMA GONDII* IN RURAL AREA: SPATIAL ANALYSIS OF HOST INFECTION AND SOIL CONTAMINATION.

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P22. **JOSE ANGEL BARASONA** SPATIAL RISK FOR TUBERCULOSIS IN RELATION TO DOMESTIC AND WILD UNGULATE DISTRIBUTION ASSESSED BY UNMANNED AERIAL SYSTEMS

P23. **MARÍA J. FORZÁN** MALFORMATIONS FOUND IN WOOD FROGS, *LITHOBATES SYLVATICUS*, FROM NORTHEAST ALBERTA AND THE NORTHWEST TERRITORIES, CANADA

P24. **SCOTT E. HENKE** VIABILITY OF *BAYLISASCARIS PROCYONIS* EGGS EXPOSED TO FLUCTUATING TEMPERATURES AT RACCOON LATRINE SITES

P25. **TORSTEN MÖRNER** THIAMINE DEFICIENCY AFFECTING WILDLIFE HEALTH IN THE BALTIC SEA AREA

P26. **KAREN A. FOX** BIGHORN SHEEP SINUS TUMORS ARE ASSOCIATED WITH COINFECTIONS BY PNEUMONIA-CAUSING BACTERIAL AGENTS IN THE UPPER RESPIRATORY TRACT

P27**. MADHU NEPAL** PREVALENCE OF ENDOPARASITES RELATED TO DIFFERENT FEEDING SITES OF RODENT IN KIRTIPUR, NEPAL

P28. **SYLVIA FERGUSON** HYDROCEPHALUS IN FOUR BEARS

P29. **ALY CHAPMAN** TRANSMISSION OF *TOXOPLASMA GONDII* IN WILDLIFE IN THE SOUTHEASTERN US

P30. **ERIN EDWARDS** PREVALENCE OF SEXUALLY TRANSMITTED DISEASES IN TWO WILD CHIMPANZEE POPULATIONS

P31. **GABRIELLE ROBINSON** INVESTIGATING THE EFFECTS OF MERCURY AND PCB EXPOSURE ON HEALTH AND REPRODUCTION OF A PISCIVOROUS BIRD

P32. **MAUREEN MURRAY** RODENTICIDES IN BIRDS OF PREY IN MASSACHUSETTS, USA: A COMPARISON OF DATA BEFORE AND AFTER EPA RISK MITIGATION ACTION

P33. **PETER VAN TULDEN** OCCURRENCE OF EXTENDED-SPECTRUM B-LACTAMASE PRODUCING E. COLI IN WILD BIRDS FROM THE NETHERLANDS

P34. **PETER VAN TULDEN** *CHLAMYDIA PSITTACI* IN WILD BIRDS IN THE NETHERLANDS

P35. **VALERIE I SHEARN-BOCHSLER** PARALYTIC SHELLFISH POISONING IN KITTLITZ'S MURRELET NESTLINGS

P36. **MICHAEL J. YABSLEY** ASSOCIATION OF HAEMOGREGARINES INFECTION OF GOPHER TORTOISES (*GOPHERUS POLYPHEMUS*) WITH THE GOPHER TORTOISE TICK (*AMBLYOMMA TUBERCULATUM*)

P37. **MARGO J PYBUS** TIME … AND CWD … MARCHES ON

P38**. CARY D. CHEVALIER_**BLOOD SERUM CHEMISTRY AND HEMATOLOGY IN FIELD-FRESH RACCOONS (*PROCYON LOTOR*) IN NORTHWEST MISSOURI DURING SUMMER.

P39. **DOLORES GAVIER-WIDÉN** DETECTION OF MECC-POSITIVE METHICILLIN-RESISTANT *STAPHYLOCOCCUS AUREUS* (MRSA) (CC130-MRSA-XI) IN DISEASED EUROPEAN HEDGEHOGS (*ERINACEUS EUROPAEUS*) IN SWEDEN

P40. **CRISTINA M HANSEN** DEVELOPMENT AND IMPLEMENTATION OF A BROAD-BASED PCR SURVEILLANCE METHOD FOR BACTERIAL DNA IN ALASKAN WILDLIFE TISSUES

CONTINUATING EDUCATION

Continuing education for this conference was set up by the American Association of Wildlife Veterinarians through the American College of Zoological Medicine. CE forms can be acquired at the conference registration desk.

This Program and Abstracts booklet is available by internet download to all WDA Conference attendees at http://fwf.ag.utk.edu/WDA2013/programs.html The Wildlife Disease Association does not regard this Conference Program and Abstracts booklet as a publication and is only used as an information and reference guide for conference participants. Abstracts included in this program should not be cited in any scientific literature or peer-reviewed publications.

This conference is officially referred to as the Annual International Conference of the Wildlife Disease Association.

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UPCOMING WDA MEETINGS AND CONFERENCES

Annual International: **Holiday Inn, Hosted by University of Tennessee, Knoxville, TN, USA,** *July 28-August 2, 2013*

Latin American Section: **Hosted by School of Veterinary Medicine, University of São Paulo, in São Paulo, Brazil,** *September 19-22, 2013*

Australasian Section: **Hosted by WDA-A at Grampians National Park, Victoria, Australia,** *September 23-28, 2013*

Annual International: **Tenaya Resort, Hosted by New Mexico Game and Fish, Albuquerque, New Mexico, USA,** *Summer 2014*

European Section: **Glasgow, Scotland,** *September 2014*

Australasian Section: **New Zealand, location TBD, Hosted by Australasian Section,** *Midyear 2015*

Annual International and WDA-A: **Darwin, Australia, location TBD, Hosted by Australasian Section,** *Midyear 2015*

Annual International: **Ithaca, New York, Hosted by Cornell University,** *Summer 2016*

1. NAVIGATING THE WILDLIFE DISEASE MINEFIELD: MERGING SCIENCE, POLICY, AND POLITICS TO PROTECT OUR WILDLIFE RESOURCES

Jonathan W Gassett, Kentucky Department of Fish and Wildlife Resources, Frankfort, Kentucky, USA

Currently, one of the greatest challenges facing state fish and wildlife agencies is the management and control of wildlife disease. An estimated 75% of emerging infectious diseases are zoonotic, with many having their origins in wildlife. Infectious pathogens of wildlife not only present a threat to human health and agriculture production, but also free-ranging populations and wildlife-based economies. Many of the disease threats today are associated with highly artificial situations that increase the risk for introduction, establishment, and dissemination of pathogens. Although the mechanisms of introduction for many of these pathogens are unknown, significant changes in the environment and human behavior can facilitate their dissemination. Legitimate wildlife restoration activities as well as wildlife-based private industry and recreation all have the real potential for pathogen introduction. However, the difference in motivating factors behind these activities presents managers with widely varying degrees of risk. State agency administrators must successfully blend science, policy, and common sense in order to reduce this threat to an acceptable level.

2. WHITE-NOSE SYNDROME IN BATS

Gary F McCracken, Department of Ecology and Evolutionary Biology, College of Arts and Sciences, University of Tennessee, Knoxville, Tennessee, USA

White-Nose Syndrome (WNS) is a newly emerged infectious disease of hibernating bats in North America that is caused by a previously unknown pathogenic fungus, *Geomyces destructans* (Gd). First documented in winter 2006-2007 in a commercial cave in eastern upstate NY, the disease has spread rapidly and now affects at least 7 species of bats in 22 US States and 5 Canadian Provinces. The fungus also has been found on three additional species of bats that do not yet show evidence of disease. As of 2012, USFWS estimated that 5.7 to 6.7 million bats have died from WNS, and population declines in much of the infected range exceed 80% for some bat species. Bat species are differentially susceptible to the disease, with growing evidence that ecological, behavioral and physiological attributes of the different species influence their susceptibility. Immediate cause(s) of death are energy depletion due to frequent arousals during hibernation, and dehydration and electrolyte depletion; the latter caused by the immunological response to invasive fungi and resulting tissue erosion of flight membranes. Genetic evidence supports a European origin for Gd which was most probably transported to the US by humans. The fungus does not cause the same tissue erosion or mortality in European bats. Major questions concern the possibility of evolved resistance in North American bats, the limits to the distributional spread of this cold-loving fungus, and identification of any practicable strategies for disease control.

3. OVERVIEW OF THE 2ND INTERNATIONAL SYMPOSIUM (ISR) ON RANAVIRUSES

VG Chinchar, Department of Microbiology, University Mississippi Medical Center, Jackson, Mississippi, USA

Although identified nearly 50 years ago, ranaviruses (family Iridoviridae) have only been viewed as significant pathogens of ectothermic vertebrates for the last 20 years. The 2nd ISR was organized to bring together a diverse group of investigators (ecologists, virologists, immunologists, and pathologists) in an effort to share information related to this emerging infectious agent. Platform and poster presentations addressed the prevalence and geographic distribution of ranavirus infections, the principal viral species responsible for disease, anti-ranaviral immune responses, viral genes that control virulence, diagnostic and treatment methodologies, and environmental and life history features that impact disease severity. Frog virus 3-like viruses (and other ranaviruses) infect multiple species of ectothermic vertebrates and contribute to considerable morbidity and mortality. Infections may be subclinical or fulminant, and are influenced by a variety of environmental factors. Young animals often succumb to disease, whereas immunocompetent adults mount an immune response that provides protection from severe clinical disease. Putative virulence genes have been identified and their deletion may generate attenuated viruses that may serve as protective vaccines. Additional information on the 2nd ISR can be found on the website for the Global Ranavirus Consortium. In addition, detailed protocols for the detection of ranavirus infections are located on the website of the World Organization for Animal Health (www.oie.org).

4. EMERGING AND RE-EMERGING LETHAL INFECTIOUS DISEASES OF WILD AMPHIBIANS AND REPTILES IN SOUTHEASTERN USA

D. E. Green, USGS National Wildlife Health Center, Madison, Wisconsin, USA

Infectious diseases continue to be a major factor in morbidity, mortality, population declines and local extirpations of amphibians and reptiles (A&R) nationwide. Southern Appalachian Mountains (SAM) are well known for their herpetological biodiversity, especially among amphibians. However, the diversity of infectious diseases in A&R in SAM and nationwide remains inexplicably low compared to fish and birds. The major pathogens of importance in A&R are viruses, fungi, protozoa and possibly mycoplasmas. Ranaviruses (family: Iridoviridae) are a major cause of mortality in larval amphibians and adult turtles. The relationship of fish, amphibian and reptilian ranaviruses is being investigated by total genome sequencing. Major herpetological fungal infections usually are limited to the skin and include chytridiomycosis (*Batrachochytrium dendrobatidis*) of adult frogs and toads (rarely salamanders), and an emerging "snake fungal disease" linked to *Ophidiomyces* (formerly *Chrysosporium) ophiodiicola*. Mortality events due to protozoal infections occur predominantly in ranid tadpoles and are attributed to an unnamed, poorly characterized alveolate, often called Perkinsus-like organism, but also referred to as Dermocystidium-like and by other names. Other pathogens have been implicated in morbidities and mortalities of captive and semi-captive A&R but seldom cause observed mortalities in the field. Better diagnostic tools and continued investigation of field mortalities are warranted.

5. HEMORRHAGIC DISEASE AND THE MANY MEANINGS OF NO-SE-UM

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Hemorrhagic disease (HD) is caused by related orbiviruses in the bluetongue virus (BTV) and epizootic hemorrhagic disease virus (EHDV) serogroups. These viruses infect numerous wild ungulates in North American and are transmitted by biting midges in the genus *Culicoides*. White-tailed deer (*Odocoileus virginianus*, WTD) are highly susceptible to HD, but clinical disease and potential population impacts are highly variable throughout their range. In general, the disease is most severe in more northern latitudes where HD occurs sporadically and where population immunity is minimal. In contrast, areas of enzootic stability exist in areas of the Southwestern United States where high infection rates occur annually but clinical disease is rarely reported. In WTD, this variation in clinical response is believed to be associated with variation in both acquired and innate immunity. In fawns, passive immunity also may be protective but this has not been sufficiently evaluated. There is recent evidence that the epidemiology of both bluetongue and epizootic hemorrhagic disease are changing globally. The mechanisms behind this change are not clearly understood and most likely involve multiple and interrelated climatic factors affecting the vectorial capacity of *Culicoides*. In Europe, numerous recent outbreaks involving different BTV serotypes have been reported in domestic ungulates, and extensive outbreaks of BTV-8 have occurred in areas were these viruses previously did not exist. Likewise, EHDV related disease has been reported in cattle from Israel, Turkey, and Réunion Island. In the United States, multiple exotic serotypes of both BTV and EHDV have been detected since the late 1990s, and in the case of EHDV-6 which was first detected in 2006, genetic reassortment with indigenous EHDV-2 has occurred. Potential wildlife disease problems associated with these introductions has been demonstrated in experimental infection of WTD with EHDV-6 and EHDV-7, and recently (2012) by widespread WTD mortality associated with EHDV-6 infections. Potential impacts associated with HD range expansion are not well documented or understood but based on historic data, there appears to be a northern expansion of HD in the Northeastern and Midwestern United States that also may be associated with an increase in disease frequency and intensity. There is very limited information related to the ability of new viruses to successfully invade areas where HD currently occurs, and the potential impacts associated with such introductions are unclear. Likewise, the ecological drivers behind these introductions and the changing epidemiologic patterns of HD are not adequately identified.

6. PATHOGENS, PESTS AND ECONOMICS: DRIVERS OF HONEY BEE COLONY DECLINES AND LOSSES

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The Western honey bee (*Apis mellifera*) is a semi-free ranging, managed agricultural species responsible for ecosystem services (pollination) worth U.S. $215 billion annually worldwide. While the number of managed colonies has increased 45% globally since 1961, steady declines have been reported in the last half-century in Europe and the U.S.A. This has led to significant research interest along with scientific, environmental policy and public debate on the causes and the environmental implications of this phenomenon. In my talk, I will review recent research on the causes of colony losses and bee population declines. The data suggest that the most important drivers of a decline in the number of colonies are political and socioeconomic factors while the spread of introduced pathogens and pests also leads to significant annual colony losses. I conclude that, while other causal hypotheses have received substantial attention scientifically, the role of pathogens, pests and management issues have been neglected and require our attention.

7. USING AN INDIVIDUAL-BASED MODEL TO STUDY THE SPREAD AND CONTROL OF PSEUDO-RABIES VIRUS IN FERAL HOGS IN THE GREAT SMOKY MOUNTAINS NATIONAL PARK

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For over two decades, the Park Service has been removing feral hogs from Great Smoky Mountains National Park (GSMNP) in an attempt to control the population. In 2005, the first seropositive cases of pseudo-rabies virus (PRV) were recorded in harvested individuals. We developed an individual-based model (IBM) for the feral hog population in Great Smoky Mountains National Park (GSMNP) and surrounding regions to test theories on the spread of pseudo-rabies virus (PRV) in GSMNP. Because there is limited understanding of the spread of the disease in feral populations, an IBM is well suited to test both modes and effectiveness of transmission. Another advantage of the IBM approach is the ability to model the efficiency of control methods (harvesting) for mitigating disease spread. IBMs can be used to compare changes in location, time, and effort to determine optimal control strategies. Preliminary results on the effectiveness of the current harvesting strategy on the population density of hogs and the spread of PRV suggest that although the year-to- year variation in fall hard mast is a natural population regulator, harvesting has had an impact on the population.

8. CAUSES OF MORBIDITY AND MORTALITY OF WILDLIFE SPECIES PRESENTED TO A WILDLIFE CLINIC IN EAST TENNESSEE, USA, 2000–2011

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A retrospective analysis using 14,303 records from cases presented to the University of Tennessee, College of Veterinary Medicine, was performed to determine the causes for presentation, overall mortality, and case fatality rate for certain presentations of wildlife between 2000 and 2011. The cases were categorized into herptile (reptiles and amphibians), mammal, or avian and then classified into different categories based on reason for presentation. The most common reasons for presentation were: trauma of unknown origin; found abandoned/orphaned; hit by automobile; cat-related injury; and dog-related injury. Overall mortality was 45.3% for the herptile cases, 57.6% for mammal cases, and 65.1% for avian cases. This study demonstrates that many animals present to wildlife clinics because of interactions with humans or their pets; based on these results, steps in communities could be taken to reduce the morbidity and mortality associated with these causes for presentation.

9. DETECTION AND EPIDEMIOLOGY OF TRICHOMONAS GALLINAE IN PEREGRINE FALCON NESTLINGS IN KENTUCKY

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Peregrine falcons (*Falco peregrinus*) are considered threatened and significant funds have been allocated for falcon conservation efforts. Avian trichomonosis, caused by the protozoal parasite *Trichomonas gallinae*, is considered one of the most important diseases for Peregrine falcon population recruitment. Since 2008, the Kentucky Department of Fish and Wildlife Resources (KDFWR) personnel have obtained oral swabs from 101 falcon nestlings, in conjunction with nestling banding and morphometric analysis, from various locations within the state. Swabs were inoculated into In-Pouch™ TF kits, for overnight transport to our laboratory. In-Pouch™ TF kits were incubated at 37 C and microscopically examined daily for at least five days for trichomonad growth. Nucleotide sequences of the internal transcribed spacer (ITS)-1, 5.8S, and ITS2 regions of the ribosomal RNA gene were analyzed from the positive trichomonad samples to determine the *T. gallinae* genotype. Of the 101 tested nestlings, seven nestlings (6.9%) were positive for trichomonad growth by culture. All seven ITS-5.8S sequences belonged to the rock pigeon genotype. Three positive nestlings, originating from the same nest, had identical ITS-5.8S sequences suggesting that a single infected prey item was likely responsible for infection of the three nestlings. The KDFWR will continue to monitor falcon nests and test nestlings for *Trichomonas* for at least the next 3 years.

10. UNUSUAL WINTER MORTALITY EVENTS IN MULTIPLE ATLANTIC SEABIRD SPECIES

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In December 2012, an irruption of live razorbills (*Alca torda*) began in Florida and other southeastern states. Within weeks, reports of dead razorbills were coming in from the same region, and would ultimately rise to several hundred individuals. In subsequent months, hundreds of dovekies (*Alle alle*) and murres (*Uria* spp.) were found dead along the east coast, but the worst mortality event in decades affecting Atlantic puffins (*Fratercula arctica*) began in the northeastern U.S. and in the U.K. In addition to the alcids, hundreds of common loons (*Gavia immer*) were also affected. Necropsies, performed at multiple laboratories, showed most birds were thin or emaciated with no gross indication of disease. Contrasting results in a small number of razorbills from North Carolina and Virginia suggested death due to internal damage from over-consumption of fish. Potential contributions of winter storms, oceanographic impacts, or altered prey recruitment in these die-offs are proposed, and roles of social media, local, state, regional, and federal wildlife groups as well as the national Wildlife Health Event Reporter in defining the timing, scope, and extent of these mortalities are emphasized.

11. PREVALENCE OF RANAVIRUS AND BD IN HELLBENDER POPULATIONS IN TENNESSEE AND ARKANSAS

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The Hellbender, *Cryptobranchis allenganiensis*, is a large aquatic salamander containing two subspecies (Ozark hellbender, *C. a. bishopi* and Eastern hellbender, *C. a. alleganiensis*) from the Ozark mountains and eastern U.S., respectively. Both subspecies have seen population declines over the past 25 years, especially in *C. a. bishopi* which is federally endangered. Habitat degradation and possibly low genetic diversity may lead to secondary infections with amphibian pathogens such as Ranavirus and *Batrachochytrium dendrobatidis* (Bd). The objective of this study was to determine prevalence of these pathogens in both subspecies as a first step in understanding the role of emerging amphibian pathogens in *C. alleganiensis* declines. We collected tail tissue and skin swabs from *C. a. bishopi* and *C. a. alleganiensis* individuals from Arkansas and Tennessee, respectively, during the summers of 2011 and 2012. We used qPCR analysis to determine presence of Ranavirus and Bd from tail samples and skin swabs, respectively. Overall, for *C. a. bishopi*, we detected 20% prevalence of Bd and no cases of ranaviral infections; for *C. a. alleganiensis*, we detected 7% prevalence of Bd and 5% prevalence of Ranavirus. Additionally, we observed leeches parasitizing many individuals and identified one *C.a. allenganiensis* leech positive for Ranavirus. This data reveals that Bd is present in these populations and, as Bd is known to favor keratinized tissue, may play a role in causing physical deformities (e.g., missing and fused toes) seen in *C. a. bishopi*. Furthermore, early analyses of Ranavirus suggest a link to watershed health and ectoparasitism

12. INFECTIOUS CAUSES OF DERMATOLOGIC DISEASE IN FREE-RANGING WHITE-TAILED DEER (*ODOCOILEUS VIRGINIANUS*) FROM THE SOUTHEASTERN UNITED STATES

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White-tailed deer (*Odocoileus virginianus*) are susceptible to a variety of dermatologic diseases that can have dramatic and highly visible lesions notable by hunters, wildlife biologists, and the general public. In this retrospective study we identified and described the most frequently diagnosed infectious causes of primary dermatologic disease in white-tailed deer from the southeastern United States. We reviewed 2,569 white-tailed deer cases submitted to the Southeastern Cooperative Wildlife Disease Study (SCWDS) between January 1975 and April 2012. Infectious causes of primary skin diseases were diagnosed in 104 individuals (4.1%). Demodicosis (n=38; 36.5%), dermatophilosis (n=19; 18.2%), and cutaneous fibromas (n=18; 17.3%) were the most common diagnoses. Deer with demodicosis were characterized by patchy to generalized alopecia. Microscopic lesions included epidermal crusts and cutaneous nodules (apparent grossly in severe cases) with mild perifollicular, lymphoplasmacytic dermatitis. Dermatophilosis was characterized by crusting, erythema, and alopecia of the face, ears, and distal extremities. Histologic lesions were characterized by extensive serocellular crusts comprised of degenerate neutrophils, keratin, and necrotic debris with intralesional filamentous chains of bacteria characteristic of *Dermatophilus congolensis*. Deer with cutaneous fibromas had characteristic lesions consisting of multiple, plaque-like to pedunculated, smooth, alopecic, fibrocutaneous nodules often on the head and neck. Less common diagnoses included other bacteria (n=13; 14.8%), fungi (n=5; 5.7%), ectoparasites (chiggers, lice, mites, and ticks; n=11; 12.5%), and larval nematodes (n=7; 8.0%). Population-level effects of these diseases are likely minimal. However, their occasionally dramatic presentations can be of concern to wildlife enthusiasts and, in some cases, may have zoonotic potential.

13. THE UNDISCOVERED COUNTRY: BATS, EMERGING INFECTIOUS DISEASES, MANAGEMENT STRATEGIES, AND CONSERVATION

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Bats are reservoirs for etiological agents of global health importance. Misguided attempts at disease management have led to widespread killing of bats. However, reduction of bat populations is not effective, nor compatible with the critical role of bats in ecosystem health, compounded with the highly threatened status of many populations. Recent analyses indicate that even culling of vampires may be ineffective. Holistic approaches addressing diseases are needed, employing multiple strategies, compatible with basic tenets of population ecology, vector control, health economics, and conservation biology. Examples include: public education regarding the value of bats, coupled with appreciation to preventing exposure to pathogens, such as filoviruses; vaccination of livestock, to protect agricultural investments, and lessen threats posed by bat-borne henipaviruses; proper use of Personal Protection Equipment (PPE), to minimize hazards associated with histoplasmosis at roosts. Rabies exemplifies these approaches in a One Health context. Education is key, regarding exposure avoidance. Those at risk require PPE. Rabies vaccination of domestic animals is routine to protect against spillover infections of bat lyssaviruses. Bat exclusion from human living quarters minimizes direct contact. Testing of suspect bats provides reliable diagnosis and aids exposure risk assessments. Postexposure prophylaxis is highly effective after bite. Moreover, oral rabies wildlife immunization with novel recombinant vaccines provides a unique tool for future consideration of some bat diseases under particular circumstances. These examples demonstrate solutions to problems arising at human, domestic-animal, and wildlife interfaces. Such challenges demand collaboration and multi-disciplinary approaches, involving researchers, biomedical professionals, ecologists, conservation biologists, and policy makers.

14. BAT RABIES: AN ANCIENT DISEASE WITH MANY UNKNOWNS

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Rabies is caused by viruses in the genus Lyssavirus, family Rhabdoviridae. Bats are principal reservoir hosts of lyssaviruses. In the New World, only rabies virus (RABV) is present in bats and carnivores, whereas in the Old World, bats harbor lyssaviruses of several other viral species. Why RABV is not present in Old World bats remains unclear. This phenomenon may be a result of viral extinction, or perhaps existing surveillance systems are inadequate to detect RABV in Old World bats. Regardless, new bat lyssaviruses have been discovered increasingly during the last several years, including recent findings, such as Bokeloh bat lyssavirus in Germany and France, and a West Caucasian-like bat lyssavirus in Spain. Although several prior controversial reports suggested that bats excrete RABV in saliva without demonstration of clinical signs, the current body of evidence indicates that bats suffer from rabies and die, similar to other mammals. However, virus-host interactions between bats and lyssaviruses do appear somewhat variable from those in carnivores, which is reflected in circulation patterns at the population level. Comparatively, bats seem less susceptible to lyssaviruses, and a majority of exposures may lead to peripheral abortive infection with the development of acquired immune responses, rather than leading necessarily to fatal cases. Clearly, many facets of these features remain unknown, and require further investigations to be able to better predict and manage bat rabies, particularly as bats cause the majority of human rabies cases in developed countries, and are involved frequently in spill-over events and host shifts of infection.

15. SPILL-OVER INFECTIONS AND HOST SHIFTS OF BAT RABIES VIRUSES TO CARNIVORES: RECENT EXAMPLES FROM NORTH AMERICA

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Rabies virus (RABV) is the type species of genus Lyssavirus. The RABV is distributed globally among carnivores, but in bats is present in New World only. In the Old World bats harbor several lyssavirus species, but not RABV. It was suggested that bats are the primary evolutionary hosts of lyssaviruses, and further adaptation to carnivores occurred through host switch. Although this hypothesis does not explain many facets of natural history of lyssaviruses, RABV can evidently spill-over and shift from bats to carnivores. Phylogeny demonstrates that RABV lineages from the US south-central skunk, Mexican skunk, and raccoon are related to bat RABV lineages. Spill-over infections of bat RABV are documented in carnivores and livestock every year. Moreover, a rabies outbreak that occurred during 1993 among red foxes on Prince Edward Island, Canada, was caused by a RABV variant associated with bats of the genus *Myotis*. At least three outbreaks occurred in striped skunks and gray foxes in Arizona during 2001-2009 and each resulted from independent incursions of RABV associated with big brown bats (*Eptesicus fuscus*). In Oregon, at least two outbreaks caused by RABV variants of *Myotis* spp. and *E. fuscus* were documented in gray foxes during 2009-2010. A virus similar to those circulating among Mexican free-tailed bats (*Tadarida brasiliensis*) caused an outbreak in coatis in Mexico during 2008. One suggestion offered to explain why some bat RABV variants shift to carnivores and others do not is the substitution S242T in the RABV glycoprotein. However, this hypothesis needs additional research, as do other relevant aspects of RABV thought to be associated with host shifts.

16. USAID PREDICT WILDLIFE SURVEILLANCE IN MEXICO

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PREDICT is a program for the global surveillance of zoonotic disease in wildlife funded by USAID and designed to detect new viruses and predict viruses of zoonotic potential. Wildlife disease surveillance is important to human and domestic animal health; 70% of emerging infectious diseases are reported to be of animal origin, and of that total, 75% have wildlife origins. In particular, bats have been proposed as hosting a higher number of zoonotic viruses than other orders. Disease surveillance in bats is important to understand the current virological pool for both conservation and public health purposes. PREDICT Mexico used PREDICT ecological modeling to target bat disease surveillance at a variety of human-wildlife interfaces. This presentation focuses on the importance of wildlife disease surveillance, in particular in the face of the potential spread of white-nose syndrome and the fungus that causes that disease (*Geomyces destructans*), as well as the discovery of novel coronaviruses and other viruses in bats.

17. A TISSUE EXPLANT MODEL TO INVESTIGATE THE PATHOGENESIS OF WHITE-NOSE SYNDROME OF BATS

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Experimental infection trials are necessary to answer many basic questions about white-nose syndrome. However, such trials are faced by many challenges including variable host response, husbandry of bats, and constraints imposed by the timing of hibernation. As an alternative, we have refined the use of tissue explants, consisting of skin biopsies, which enable us to limit many variables inherent in experimental infections and to limit the number of bats that must be sacrificed for such experiments. Biopsies can be taken from live bats or many samples can be collected from recently euthanized animals. Each sample collected can be used as a replicate in applicable experiments. We have been able to maintain the tissues on nutritive media, with minimal changes, for up to two months. The most significant change has been the slight accumulation of fluid between epithelial cells. However, within the epidermis, no changes were observed in cell membranes, cell junctions, organelles, keratin layers, or the basement membrane. Spores of *Geomyces destructans* applied to skin explants germinated and colonized the tissues. This fungus was capable of colonizing and invading the tissues of species not susceptible to significant mortality, such as gray bats (*Myotis grisescens*), suggesting that behavioral and environmental factors may also play a role in progression of the disease. Experiments to assess innate resistance of tissues from additional species to infection are ongoing.

18. INVESTIGATING THE USE OF MUNITIONS BUNKERS AS ARTIFICIAL BAT HIBERNACULA

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White-nose syndrome is an infectious fungal disease of bats that emerged in 2006 and is caused by the pathogen *Geomyces destructans* (Gd). This disease is associated with high mortality rates in several bat species, particularly the little brown bat (*Myotis lucifugus*). One proposed intervention for controlling white-nose syndrome is to hibernate bats in human-built structures that can be disinfected between each season to reduce or eliminate the infective load of Gd in the environment, and increase bat survival. In this project we assessed the suitability of conditions for cave dwelling bat hibernation in concrete munitions bunkers located on a National Wildlife Refuge in Massachusetts. Temperature and humidity of six bunkers maintained with different conditions (airflow, insulation, and water addition) were measured hourly for 10 months. Bunker interior surfaces were sampled in February and July 2012, and samples were tested for presence of Gd and other *Geomyces* species using quantitative PCR. Bunker temperature ranges at the start of the project on 11 October 2011 were 14.1°C to 15.6°C, and the lows were reached on 14 February 2012 and ranged from 2.2°C to 5.0°C. Relative humidity ranged from 92.5% to 103.6% on 11 October 2011, and reached a low of 63.8% to 108.9% on 16 January 2012. PCR analysis of swabs showed that Gd was not present at the time of sampling. Our results indicate that concrete munitions bunkers can be modified by adding full insulation, and minimizing airflow to create suitable hibernacula for the specific temperature and humidity requirements of the *Myotis* species.

19. A SYSTEMATIC HEALTH ASSESSMENT OF THE INDIAN OCEAN BOTTLENOSE DOLPHIN (*TURSIOPS ADUNCUS*) AND THE INDO-PACIFIC HUMPBACK DOLPHIN (*SOUSA CHINENSIS*) INCIDENTALLY CAUGHT IN SHARK NETS OFF THE KWAZULU-NATAL COAST, SOUTH AFRICA

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Coastal dolphin populations are indicators of coastal marine environmental health and may be sensitive to anthropogenic influences. An increase in serosal nodules during necropsies of dolphins incidentally caught in shark nets off the KwaZulu-Natal coast, South Africa prompted the first systematic health assessment. Thirty five *Tursiops aduncus* (Indian Ocean bottlenose dolphin) and five *Sousa chinensis* (Indo-Pacific humpback dolphin), caught between 2010 and 2012, were evaluated using a detailed protocol for necropsy and sampling of small cetaceans developed for this purpose. All animals were considered to be in good nutritional condition based on blubber thickness. All animals had lesions with definite or presumed parasitic aetiology, including pneumonia (34/40), bronchiolar epithelial mineralization (33/40), gastroenteritis (28/40), hepatitis (24/39), endometritis (11/26), serosal inflammation of various abdominal and thoracic organs (30/40) and splenic serosal tags (18/40). Five parasites (*Halocercus* sp., *Crassicauda* sp., *Anisarkis* sp., Brachycladiinae, and *Xenobalanus globicipitis*) were recovered. Non-specific meningoencepahalitis (7/18) and myocardial fibrosis (10/39) were relatively common. Adrenal cortical hyperplasia (18/37), possibly related to chronic stress, was also found. Pulmonary pneumoconiosis and foreign material accumulation in the marginal lymph node of the lung, possibly indicating exposure to polluted air, was seen in three animals. Lesions suggestive of morbillivirus, *Toxoplasma gondii* or *Brucella* spp. tested negative with special stains and immunohistochemistry. The first confirmed cases of lobomycosis and sarcocystosis in South Africa were documented. Most lesions were mild and apparently did not affect nutritional state, although the high (and apparently increasing) prevalence of parasitic lesions may indicate that the host/parasite interface is changing. This may be attributed to anthropogenic factors, stress or environmental pollution, suggesting degradation of the marine environment. A changing marine ecosystem could also negatively impact on the human populations using the same environment for recreation, food and industry. Therefore continued health monitoring of the cetaceans populations and further research into disease pathophysiology and anthropogenic factors affecting these populations is needed.

20. IDENTIFICATION AND CHARACTERIZATION OF AVIAN INFLUENZA ISOLATED IN THE CENTRAL REGION OF CHILE

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Waterfowl and shorebirds are the main reservoirs of avian influenza viruses (AIV) in nature, particularly for low pathogenicity (LPAI) strains. Bird migration is considered one of the main routes of viral spread throughout large geographical areas. Chile forms part of the Pacific Migratory flyway, a bird migration route that stretches from the furthermost tip of Alaska to the South American Patagonia. However, influenza surveillance along this flyway has been scarce. Between July and August 2012, 1689 environmental feces samples were collected; 747 of them belonging to wild birds and 942 to domestic poultry. A total of 10 samples tested positive by real-time RT-PCR for the influenza M gene with a prevalence of 0.13% in wild birds and 0.95% in poultry. Viral isolation was successful on one specimen that originated from waterfowl (*Anas georgica spinicauda*), and genetic analysis revealed a non-pandemic H1N1 virus. Its hemagglutinin (HA) gene is closely related to one other South American wild bird isolate, while its neuraminidase (NA) gene relates to both South and North American wild bird AIV isolates. This is the first isolate of AIV from a wild bird in Chile, hence the importance of its finding. Furthermore, pathogenicity studies in BALB/c mice showed no weight loss or disease, although viral particles could be detected in lung homogenates until day six post-infection. This finding highlights the importance of influenza surveillance in order to fully understand the spread and impact of AIV on wildlife, poultry production and human health in Chile and other South American countries.

21. CORRELATING ANTHROPOGENIC CAUSES OF WILDLIFE MORTALITY WITH HUMAN POPULATION DENSITY ESTIMATED BY NIGHT-LIGHT RADIANCE IN THE CANADIAN MARITIMES

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Night-light radiance obtained by satellite imagery has been correlated to human population counts in urban areas, and thus used as an alternative indicator of human population density instead of difficult-to-obtain census data. Visible-Infrared Imager-Radiometer Suite (VIIRS) night-light imagery, collected in April and October 2012 and prepared by the National Oceanic and Atmospheric Administration, was used to evaluate the correlation between human population density and anthropogenic causes of wildlife mortality in the Canadian Maritimes (New Brunswick, Nova Scotia and Prince Edward Island) during a single year. Mortality of wildlife data, as recorded in 2012 by the Canadian Cooperative Wildlife Health Centre, Atlantic region, included over 500 individual reports. Causes of mortality were organized into three categories: non-anthropogenic, anthropogenic and unknown. Night-light radiance values, as derived from the VIIRS images at an approximate resolution of 500 m^2 (15 arc-second grid), were assigned to each mortality's GPS location. A linear regression, with night-light radiance as the outcome, was used to assess the association between human population density and cause of mortality, and the interaction between cause of mortality and season, province and species. Night-light radiance was found to adequately reflect human population density in the Canadian Maritimes, and to be useful in evaluating its effect on anthropogenic mortality in wildlife. How much human population density results in anthropogenic wildlife mortality will be presented.

22. CARRY-OVER EFFECTS OF ENVIRONMENTAL CONDITIONS AND STRESS DURING PREVIOUS MOULT ON REPRODUCTIVE SUCCESS IN NORTHERN COMMON EIDERS FACING ANNUAL AVIAN CHOLERA OUTBREAKS

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Environmental factors can have immediate consequences for individual condition and fitness, but may also have consequences at later stages. Carry-over effects (COE) occur when events in one season affect an individual's performance in a subsequent period. COEs have the potential to affect population dynamics; however, identifying linkages is challenging due to difficulty in tracking migratory species across seasons and locations. Since 2005, annual outbreaks of avian cholera have caused large-scale mortality in a Northern common eider (*Somateria mollissima borealis*) breeding colony in the Canadian Arctic. Feather corticosterone (CORTf) can be used as an integrated measure of stress experienced by common eiders during feather growth. In an earlier study, we showed that CORTf is correlated with climatic variables during the moulting period. In this study, path analyses were used to examine how CORTf may reveal COEs from environmental conditions at moult on reproductive success and survival in the subsequent breeding season, during avian cholera outbreaks. Individuals with higher CORTf delayed their arrival date at the breeding colony and were in lower body condition. We found cascading effects of arrival date and body condition on laying date and reproductive success. Early birds in better condition laid their eggs earlier and had better reproductive success. Finally, eiders that had reproductive success (hatched at least one egg) were more likely to survive during an avian cholera outbreak. Therefore, conditions during moult may have direct and indirect COEs on reproduction and survival in eiders.

23. THE EFFECTS OF LONG-TERM PRESCRIBED BURNING ON TICK-BORNE PATHOGEN PREVALENCE AND DISEASE RISK IN SOUTHWEST GEORGIA

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Prescribed fire is a common forest management tool and is thought to have potential for controlling tick populations. In this study, 21 sites in southwestern Georgia with variable long-term burn regimes were sampled for ticks and tick-borne pathogens to better elucidate the effects of long-term prescribed fire on prevalence of tick-borne pathogens and disease risk. Ticks were captured via flagging on a monthly basis for two calendar years (2010 and 2011). In total, 3,546 ticks (3,062 *A. americanum*, 75 *A. maculatum*, 381 *I. scapularis*, two *I. brunneus*, and 26 *D. variabilis*) were tested for one or more bacterial pathogen(s) including *Rickettsia* spp., *Borrelia* spp., and *Ehrlichia* spp. In general, prevalences of each organism in appropriate tick species and lifestage (*Rickettsia* 7-67%, *Borrelia* 0-2%, *E. chaffeensis* 0-1%, *E. ewingii* 0-7%, and Panola Mountain *Ehrlichia* 0-4%) were similar to what has been reported in other regions of Georgia and the southeastern US. Pathogen prevalence did not vary significantly between burned and unburned sites with the exception that Rickettsia-infected *A. americanum* from burned habitats had significantly lower minimum infection prevalence compared with *A. americanum* from unburned habitats. In general, burning did not affect pathogen prevalence; however, it significantly decreased tick populations which results in a reduction in the density of infected ticks. Burned sites had an average of 0.02 infected ticks/ hour whereas unburned sites had 0.7 infected ticks/ hour. This study provided valuable data on pathogen dynamics in a rarely studied region and indicates that long-term prescribed fire is an effective tool for reducing disease risk.

24. DISEASES IN INVASIVE SPECIES: INVESTIGATIONS IN FREE-RANGING RACCOONS (*Procyon lotor*) IN GERMANY

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The North American raccoon is an introduced species in Europe. Germany is the core area for this population with two main groups settled in the country: one in the center and the other in the northeastern region. Although both population groups are increasing and expanding to neighboring countries, investigations on diseases of these animals are lacking. Considering the role raccoons play regarding infectious disease ecology in North America, we aim to investigate the occurrence of diseases in raccoons in Germany. Carcasses of raccoons (n=156) from a National park in Northeastern Germany (n=108) and Berlin's metropolitan area (n=48) were collected and necropsied. Fur and intestines were examined for presence of parasites. Organ samples were collected for histopathology as well as analyses for selected viral and bacterial agents. Activation of the lymphoid tissue of the spleen and interstitial pneumonia were the most common histopathologic findings. In ten animals the trematode, *Alaria alata*, was identified and three cases of *Sarcoptes scabiei* infection were reported. Additionally, in December 2012, a canine distemper outbreak started amongst wild carnivores from Germany including Berlin. Tissue samples of 37 infected raccoons were collected for further diagnosis and strain characterization. The occurrence of these infectious diseases within the populations suggests that raccoons closely interact with other wildlife species and that the non-native raccoons can expand the host range for pathogenic organisms. Moreover, the comparison between urban and rural raccoon populations can help to understand the importance of this introduced species in Germany.

25. AN INVESTIGATION OF HATCH-YEAR MORTALITY IN AN ONTARIO CAPTIVE BREEDING PROGRAM FOR THE ENDANGERED EASTERN LOGGERHEAD SHRIKE (*Lanius ludovicianus migrans*), 2006-2011

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In 1991, the Eastern loggerhead Shrike (*Lanius ludovicianus migrans*) was listed as an endangered species in Canada. Environment Canada launched a captive breeding and release program in 1997 and has successfully released captive-reared shrikes in Ontario since 2001. A growing concern about recent increasing mortality among hatch-year birds prompted an investigation to determine whether there has been a significant increase in mortality since 2006 and, if so, whether there was significant variation in mortality among facilities. Associations between fledgling survival and the following variables were also explored: clutch number, site, parent hatch year, number of fledglings per nest, and breeding outcome of the mother in the previous year. Mortality among these birds has been largely unexplained due to a lack of pathogen-specific lesions in birds submitted for post-mortem examination. Breeding data were obtained from the three main captive breeding facilities. Multi-level logistic regression with random intercepts for breeding pair and nest was used to identify significant variables associated with fledgling survival. After controlling for year and breeding location, the odds of fledgling survival were lower in nests with fewer fledglings and among second clutches. The number of fledglings and/or the clutch number may reflect the overall health of the nest, changes in environmental conditions, and/or the impact of additional breeding stress on parenting behaviour. Wild shrikes seldom raise a second brood; additional analyses need to be completed to determine whether encouraging birds to second clutch is beneficial to the breeding program.

26. CAUSE OF DEATH AND TRENDS OF MORTALITY FOR BALD EAGLES (*Haliaeetus leucocephalus*) IN MICHIGAN OVER A 25-YEAR PERIOD, 1987-2011.

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Necropsy to determine cause of death (COD) was performed on all bald eagle (*Haliaeetus leucocephalus*) carcasses recovered within the state of Michigan, USA over a 25-year period from 1987-2011. A primary COD was determined for each of 1001 bald eagles while many individuals were assigned additional secondary diagnoses. Mortality rates increased proportionally with the growing number of nesting territories throughout the 25 year study period. Mortality rates also significantly increased with productivity from 2007-2011, indicating that the population may be reaching carrying capacity causing more eagles to search for alternative food sources during winter months. When primary COD's were compared, mortality due to trauma and poisoning were two of the leading causes of bald eagle mortality. When these two categories were broken down to determine specific causes, vehicular trauma and lead poisoning attributed the greatest amount of bald eagle mortality. Analyses of the data suggest that these COD's have increased, specifically within the last 5 years, indicating an increased utilization of prey scavenged from road and hunter-killed carcasses. If agencies could move road-killed carcasses, especially of white-tailed deer (*Odocoileus virginianus*) from the main thoroughfare to the back of the right-of-way, the food source would still be available to the eagles with decreased risk of vehicular trauma. A potential reduction in lead poisoning might be accomplished by requiring use of nontoxic alternatives to lead ammunition for hunting deer and other game. These changes would decrease risks to bald eagles and other scavengers impacted by vehicular trauma and lead poisoning.

27. IDENTIFICATION AND CHARACTERIZATION OF AVIAN INFLUENZA ISOLATED IN THE CENTRAL REGION OF CHILE

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Waterfowl and shorebirds are the main reservoirs of avian influenza viruses (AIV) in nature, particularly for low pathogenicity (LPAI) strains. Bird migration is considered one of the main routes of viral spread throughout large geographical areas. Chile forms part of the Pacific Migratory flyway, a bird migration route that stretches from the furthermost tip of Alaska to the South American Patagonia. However, influenza surveillance along this flyway has been scarce. Between July and August 2012, 1689 environmental feces samples were collected; 747 of them belonging to wild birds and 942 to domestic poultry. A total of 10 samples tested positive by real-time RT-PCR for the influenza M gene with a prevalence of 0.13% in wild birds and 0.95% in poultry. Viral isolation was successful on one specimen that originated from waterfowl (*Anas georgica spinicauda*), and genetic analysis revealed a non-pandemic H1N1 virus. Its hemagglutinin (HA) gene is closely related to one other South American wild bird isolate, while its neuraminidase (NA) gene relates to both South and North American wild bird AIV isolates. This is the first isolate of AIV from a wild bird in Chile, hence the importance of its finding. Furthermore, pathogenicity studies in BALB/c mice showed no weight loss or disease, although viral particles could be detected in lung homogenates until day six post-infection. This finding highlights the importance of influenza surveillance in order to fully understand the spread and impact of AIV on wildlife, poultry production and human health in Chile and other South American countries.

28. DEMOGRAPHIC AND SPATIOTEMPORAL PATTERNS OF AVIAN INFLUENZA VIRUS INFECTION AT THE CONTINENTAL SCALE, AND IN RELATION TO ANNUAL LIFE CYCLE OF A MIGRATORY HOST

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To identify ecological determinants and spatiotemporal patterns of avian influenza virus (AIV) infection in long distance migratory waterfowl in North America, generalized linear models with binominal distribution were fitted to analyze results from 13,574 blue-winged teal (*Anas discors*) sampled in 2007 to 2010 during AIV surveillance programs in Canada and the United States. Our analyses revealed that during late summer staging (August) and fall migration (September-October), hatch year (HY) birds were more likely to be infected than after hatch year (AHY) birds; however, there was no difference between age categories for the remainder of the year (winter, spring migration, and breeding period). Probability of infection increased non-linearly with latitude, and was highest in late summer prior to fall migration when densities of birds and the proportion of susceptible HY birds in the population are generally highest. Blue-winged teal in the Pacific, Central and Mississippi flyways were more likely to be infected compared to those in the Atlantic flyway. Seasonal cycles of AIV infection were largely driven by HY birds, which exhibited more prominent cycles and spatial variation of infection compared to AHY birds. Our results demonstrate clear demographic as well as seasonal, latitudinal and flyway trends across Canada and the US, while illustrating the importance of migratory host life cycle and age in driving cyclical patterns of prevalence.

29. CANADA GEESE (*Branta canadensis*) AND INFLUENZA A VIRUSES: WHAT CAN WE LEARN?

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Influenza A viruses (IAVs) are widespread viruses of global importance, and understanding the epidemiology of IAVs is important for veterinary and human health. Most of our data on IAVs in their natural hosts is derived from detection of viral shedding by virus isolation or molecular techniques. Serology is also a valuable tool because persistent antibodies can be detected after viral shedding ends; however, it is often underutilized. Previous research on Canada geese suggests that they could be effective sentinels for IAV transmission. This study was conducted to further evaluate the role geese play in the epidemiology of IAVs. Samples were collected from 3,782 geese in five states (MN, NJ, PA, WA, and WI) from 2009-2012 and 44 Canada goose eggs in 2012. Overall, 930 (25%) of samples had antibodies to IAVs. A subset of these positive samples was tested for subtype-specific antibodies to six hemagglutinin subtypes. Interestingly, 99% of the tested samples had reciprocal titers >64 against the H5 subtype, while only nine (H3) and two (H9) samples had titers >64 against from any of the other five subtypes tested, including H4 and H6 subtypes. Antibodies to IAVs were detected in 66% (29/44) of yolks from goose eggs. This research indicates that Canada geese are frequently exposed to IAVs; however, the antibodies detected were not to subtypes that commonly circulate in dabbling ducks in the fall. This indicates more research needs to be done to understand the epidemiology of IAVs in geese, especially viruses of the H5 suptype.

30. A NOVEL AVIPOXVIRUS ASSOCIATED TO CUTANEOUS AND DIPHTHERIC DISEASE IN MAGELLANIC PENGUINS (*Spheniscus magellanicus*) IN BRAZIL

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A novel avipox virus caused diphtheric disease in two and cutaneous lesions in ten Magellanic penguins (Spheniscus magellanicus) housed in outdoor enclosures in a Rehabilitation Centre in Santa Catarina (27° 35' 49" South, 48° 32' 58" West), Brazil. Diagnosis was based on clinical signs, histopathology and polymerase chain reaction (PCR). Clinical signs in the penguins included cutaneous papules and nodules around eyelids and beaks, depression and restriction on weight gain. The most common gross lesions were severely congested and hemorrhagic lungs, splenomegaly and cardiomegaly. Histological examination revealed Bollinger inclusion bodies in cutaneous lesions, mild to severe pneumonia, moderate periportal lymphocytic hepatitis, splenic lymphopenia and lymphocytolysis. Other frequent findings included necrotizing splenitis, enteritis, esophagitis, dermatitis and airsaculitis. Cytoplasmic inclusion bodies were also seen within esophagical epithelial cells in two animals. DNA from all samples was amplified from skin tissue by PCR using P4b-targeting primers already described in the literature for avipox virus. The sequences showed a different virus strain belonging to the genus *Avipoxvirus* of the Chordopoxvirinae subfamily, being totally divergent from Penguinpoxvirus and Avipoxvirus already described in Magellanic penguins in Patagonia and segregating within a clade of canarypox-like viruses implicated in diphtheric and respiratory disease. This novel avipox virus seems to be a threat to the Magellanic penguins for its lesions on gastrointestinal and respiratory tissues. As a similar virus was never described in the wild, the birds were not released. We are grateful to the Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq) and São Paulo Research Foundation (FAPESP 2010/51801-5), IBAMA and Santa Catarina's Environmental Military Police.

31. ASSESSMENT OF RECOMBINANT POXVIRUSES AS VACCINE VECTORS FOR BATS THROUGH IN VIVO IMAGING

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Bats (Order Chiroptera) are an abundant group of mammals with tremendous ecological value as insectivores and plant dispersers, although their role as reservoirs of significant zoonotic diseases has become more appreciable in the last decade. Here we tested two recombinant poxviruses, Modified Vaccinia Ankara (MVA) and Raccoonpox virus (RCN), as feasible vaccine vectors in the Mexican Free-tailed Bat (*Tadarida brasiliensis*) through the use of in vivo imaging studies. Animals were infected with recombinant poxviral vectors expressing the luciferase gene (MVA-luc, RCN-luc) through oronasal or intramuscular routes, and sequential imaging revealed the pattern of viral gene expression over time. No clinical illness was noted after exposure to the vectors by either route. The imaging study revealed evidence that both viral vectors can express the luciferase gene and are potential viable oral vaccine vectors in *T. brasiliensis*. To assess immune response to this vector, data is being collected on serologic responses after vaccination to RCN-vectored vaccination against the rabies glycoprotein (RCN-G). Poxviral vectors can accept large insertions of foreign DNA for the production of protective antigens and have been shown to be effective in wildlife vaccine campaigns in the past. Orally available vaccines can be distributed to groups of bats as a liquid or paste while they roost or are otherwise congregated. By engineering recombinant RCN-based vaccines against lyssaviruses and other important transmissible diseases, we can generate immunity in free-ranging bat populations, offering the opportunity for “up-stream” interventions of important zoonoses and other bat diseases.

32. ASSESSMENT OF PHYSIOLOGICAL EFFECTS OF WHITE-NOSE SYNDROME IN BATS USING DOUBLY LABELED WATER AND CLINICAL CHEMISTRY

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The physiological effects of white-nose syndrome (WNS) and mechanisms of mortality due to infection with *Geomyces destructans* in hibernating bats are not fully understood. Associated wing damage is hypothesized to disrupt vital physiological functions, and preliminary evidence indicates increased arousal frequency, water loss, and electrolyte imbalances occur. We used the doubly labeled water (DLW) method in hibernating bats infected with *G. destructans* in the laboratory to evaluate the role of water balance and energy use in WNS pathogenesis. Blood chemistries were analyzed to assess physiologic disturbances. Preliminary analyses indicate bats with WNS increased total body water content over the course of the experiment compared to sham-treated bats, supporting the hypothesis that bats utilize fat reserves at a faster rate when infected with *G. destructans*. Additionally, bats with WNS demonstrated a primary respiratory acidosis characterized by elevated carbon dioxide levels (PCO_2) and lower blood pH than controls. Renal compensation, evidenced by elevated bicarbonate (HCO_3^-), was not sufficient to normalize blood pH. Potassium concentrations were also higher in infected bats. There were no differences in sodium concentrations, but chloride was marginally lower in infected bats likely due to secondary renal excretion. Blood glucose levels were also lower in infected bats, but there was no evidence of lactic- or keto-acidosis. Although normal blood chemistry reference values for microchiropterans do not exist, significant differences observed between infected and control bats in this study demonstrate increased energy use among bats with WNS together with life-threatening respiratory acidosis, providing a mechanistic explanation for mortality during hibernation.

33. AN EXPERIMENTAL TRIAL INDUCES AVIAN VACUOLAR MYELINOPATHY IN PAINTED TURTLES (*Chrysemys picta*)

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Avian vacuolar myelinopathy (AVM) is a neurologic disease that primarily affects birds of southeastern U.S. reservoirs. AVM is thought to develop via ingestion of submerged aquatic vegetation (SAV) colonized by a novel, toxin-producing cyanobacterium (order Stigonematales); consuming invertebrates feeding on toxic SAV; or consuming birds with AVM. Aquatic turtles also consume SAV and/or invertebrates, yet AVM has never been described in any chelonian. Their natural history and diet might expose turtles to the toxin, but turtles affected by AVM may go undetected because they may be predated, or die and sink. To determine if turtles are susceptible to AVM, we conducted a feeding trial. We hypothesized turtles would develop AVM-like clinical signs and lesions after consumption of a toxic invasive SAV species, *Hydrilla verticillata*. Wild-caught painted turtles (*Chrysemys picta*; n=10) were divided into 2 treatment groups for 95 days. Five turtles received verified “toxic” hydrilla in gelatin capsules and free-floating hydrilla ad libidum (at ~ 2mg/kg/day). Five control turtles received the same amount of verified non-toxic hydrilla. Between 80 to 95 days later, all treatment turtles displayed abnormal physical or neurologic signs and were euthanized. Two turtles became very weak and anorexic, and three displayed varying degrees of neurologic signs such as listing, dragging the hind limbs, knuckling, and hypermetria. A complete necropsy was performed and examination of the brain at the level of the optic tectum and spinal cord revealed only AVM-like lesions in experimental turtles. This is the first report of AVM-like signs and lesions in a chelonian.

34. EFFECTS OF UPPER RESPIRATORY TRACT DISEASE ON MOVEMENT AND BEHAVIOR OF GOPHER TORTOISES (*Gopherus polyphemus*)

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We assessed the long-term effects of upper respiratory tract disease (URTD) on gopher tortoise (*Gopherus polyphemus*) movement and thermoregulatory behavior using a tortoise population with historically high prevalence of *Mycoplasma agassizii* antibodies. Tortoises at Ichauway (Baker County, Georgia, USA) were tested for antibodies to two *Mycoplasma* species. Behavioral assessments of 30 tortoises from Green Grove (GG), a focal area of Ichauway were completed using radio-telemetry and temperature data loggers. Site-wide (Ichauway), ten tortoises with severe URTD were monitored for comparison with GG tortoises. Home ranges of tortoises with severe clinical signs were significantly larger (172.86 ha) than year-long home ranges of GG asymptomatic (1.16 ha) and GG mild URTD tortoises (1.76 ha) ($p= 0.0081$). GG tortoises moved an average of 30m between tracking events, whereas severe tortoises moved as far as 755m in one day, contradicting the hypothesis that chronically-infected tortoises are less likely to emigrate. *Mycoplasma agassizii* antibody prevalence was similar among the three groups (98% overall), but *M. testudineum* seroprevalence was lowest in the asymptomatic (7%) and mild groups (14%) compared with severe (50%) ($p= 0.0019$). Severe tortoise temperature ranges differed from the average temperatures of GG tortoises ($H= 17.142$, $df= 2$, $p= 0.0002$), which suggested differences in thermoregulatory behavior of severely ill tortoises. Despite the high seroprevalence documented in 1997, population density in GG has remained constant over time. However, emigration of animals with clinical disease may play an important role in dispersal of these pathogens into naive populations.

35. BIOASSAY DETECTION OF CHRONIC WASTING DISEASE PRIONS IN SOIL

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Studies suggest that environmental deposits of chronic wasting disease (CWD) prions play an important role in the transmission and persistence of CWD among captive and wild cervids. Furthermore, studies indicate that the prion molecule forms a close association with clays and other soil components, enhancing its persistence and, surprisingly, the transmissibility of the infectious agent. Investigation of PrP^{CWD} presence in soil has been particularly challenging due to limited sensitivity of existing laboratory assays. To date, detection of prions in field samples has been unsuccessful. Our objective was to use an existing bioassay technique with CWD susceptible transgenic mice to demonstrate presence and estimate amount of PrP^{CWD} in soil. A prion-soil titration curve was created by orally inoculating mice with one of 5 dilutions of PrP^{CWD} positive elk brain homogenate with 10% whole soil in sucrose. Second, additional groups of mice were either orally inoculated with, or housed on, soil originating from captive cervid research facilities where CWD occurred in herds. These soils, one from the Colorado Division of Wildlife research facility and the other from the Wyoming Fish and Game research facility, were considered “naturally contaminated” with PrP^{CWD}. Preliminary results from time point sacrifices and clinically ill mice indicate that the use of a mouse bioassay successfully demonstrated the presence of prions in naturally contaminated soil samples. The amount of infectious PrP^{CWD} present in these naturally contaminated soils as compared to our established bioassay titration curve is estimated.

36. ROLE OF THE HYPERMUCOID PHENOTYPE IN THE RESISTANCE OF *Klebsiella pneumonia* TO OXIDATIVE AND SERUM KILLING IN NON-HUMAN PRIMATES

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Klebsiella pneumoniae is a zoonotic, Gram-negative, member of the family Enterobacteriaceae, and the causative agent of nosocomial septicemic, pneumonic and urinary tract infections. Recently, pathogenic strains of *K. pneumoniae* sharing a hypermucoviscosity (HMV+) phenotype have been attributed to multisystemic abscessation and mortality events of non-human primates. The biological significance of the HMV phenotype to virulence and disease processes in non-human primates is currently unknown. To increase the body of knowledge of this enigmatic pathogen, an in vitro cellular model was used to assess serum resistance and oxidant-mediated killing of HMV+ and HMV- *K. pneumoniae* previously isolated from clinical cases in African green monkeys (*Chlorocebus aethiops sabaeus*) (AGV). The results indicate that HMV+ isolates were significantly more resistant to serum killing. Heat-inactivation of serum abolished the killing properties of the serum, indicating involvement of the complement cascade. Moreover, the HMV+ isolates were also significantly more resistant to the microbicidal action of oxidants including hydrogen peroxide (H_2O_2) and hypochlorous acid (HOCl) when compared to HMV- isolates. Together this data indicates that the HMV phenotype is an important virulence trait in the pathogenesis of *Klebsiella pneumoniae* in non-human primates.

37. ECTOPARASITES AND THEIR RELATIONSHIP TO THE NOVEL BABESIA DETECTED IN THE ENDANGERED FLORIDA PUMA (*Puma concolor coryi*)

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Florida pumas are an endangered population (estimated 100-150) of *Puma concolor* in southern Florida. In 2006, a novel *Babesia* species was detected in numerous Florida pumas. We provide new biological, serologic, and molecular data on the *Babesia* that will be used to formally describe it. Prevalence in adult pumas is high (>90%), and infected pumas show no evidence of anemia. Testing of over 900 bobcats from the eastern U.S. suggests that this *Babesia* is restricted to southern Florida and pumas, although screening of domestic cats is pending. No evidence of congenital infection in kittens (n=24) of *Babesia*-infected female pumas was noted. Genetic analyses revealed high diversity in the ITS1 rRNA region, which suggests that the parasite is endemic. Serologic cross-reactivity (1:256) was noted between serum from *Babesia*-infected pumas and *B. odocoilei*, *B. canis*, and *B. bovis* antigens. Ixodid ticks transmit many *Babesia* species, but no vector has been identified for any felid *Babesia*. Ectoparasite surveys conducted for the past 18 years on Florida pumas indicate that both *Dermacentor variabilis* (81% of all pumas with ticks; mean 6 ticks/infested puma) and *Ixodes scapularis* (75% of pumas with ticks; mean 13 ticks) were common. Transmission studies are underway to determine if either of these two tick species is a competent vector. Although *Babesia* infections in wildlife are usually asymptomatic, catastrophic events such as viral outbreaks or severe stress may allow these parasites to become pathogenic. We believe that identification of the vector will facilitate understanding of the ecology of this novel *Babesia*.

38. SURVEILLANCE OF FILARIAL NEMATODES IN FREE RANGING MOOSE FROM MINNESOTA

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Moose (*Alces alces*), a culturally and economically valued species, have historically occupied northern forests of Minnesota. However, since 2006 total population numbers have decreased by approximately 50%. The cause of the decline is currently unclear. *Elaeophora schneideri*, a filarial parasite of deer, is associated with moose morbidity and mortality and although not commonly reported in Minnesota, may contribute to the population decline. To detect filarial parasites in moose with suspected nematode infections, brain tissue and arterial blood samples were tested using a PCR assay with nematode-specific primers targeting the 18S rRNA gene or internal transcribed spacer regions. To investigate the prevalence of filarial nematodes, banked blood samples from hunter-killed and live-caught moose were screened microscopically for microfilariae utilizing a modified Knott's test. DNA sequences of brain tissue PCR products revealed 19 (65.5%, n=29) moose contained sequences similar to *E. schneideri*. Within 2 (40%, n=5) arterial blood samples, sequences of an unidentified filarial parasite most closely related to *Mansonella ozzardi* (80% maximum identity) were identified. At present, it is unknown if the *Mansonella*-like parasite is pathogenic in moose. Microscopic screening of hunter-killed and live-caught moose blood revealed 22.4% (n=125) contained microfilariae, with size ranges of 150-185µm (length) and 2-5µm (width) and a single sample containing additional microfilariae measuring 280x13µm, similar to the size range reported for *E. schneideri*. These data suggest *E. schneideri* is harbored within the Minnesota population; however, further surveillance is needed to better understand the eco-epidemiology and transmission of both filarial parasites and their role in moose populations.

39. Echinococcus multilocularis AND *E. canadensis* IN WOLVES FROM WESTERN CANADA

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The prevalence and genetic diversity of *Echinococcus* in Canadian wolves (*Canis lupus*) is described using combined morphological and molecular techniques. *Echinococcus* adult cestodes were morphologically identified to genus level and harvested from two 10% aliquots of the intestinal contents of each of 38 of 93 wolves (41%) from the Northwest Territories, Manitoba, and Saskatchewan. To definitively identify *E. canadensis* and *E. multilocularis*, 2-9 cestodes from each of 29 wolves were successfully characterized using primers designed to amplify 470 bp and 395 bp regions of the NADH dehydrogenase subunit 1 (NAD1) mitochondrial gene, respectively. *Echinococcus canadensis* was detected in 23 and *E. multilocularis* in 12 wolves, and both parasites were present in all locations sampled. Mixed infections of the G8 and G10 genotypes of *E. canadensis*, and *E. canadensis/E. multilocularis* were observed in 3 and 6 wolves, respectively. This is the first North American report of wolves naturally infected with *E. multilocularis*, as well as the first report of wolves harbouring mixed infections with multiple species and genotypes of *Echinococcus*. These observations provide important information regarding the distribution and diversity of zoonotic species of *Echinococcus* in western North America and may be of interest to those conducting public health or wildlife surveillance.

40. BARTONELLA INFECTION PREVALENCE IN CARDIAC VALVES OF COYOTES, A NATURAL RESERVOIR IN CALIFORNIA

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Bartonella are hemotropic bacteria infecting a wide variety of domestic and wild animal species. In dogs and humans, *Bartonella vinsonii* subsp. *berkhoffii* (*B. v. berkhoffii*) is a cause of severe valvular endocarditis, predominantly infecting the aortic valve. Coyotes are its main reservoir in California (35% seropositive and 28% bacteremic out of 109 coyotes tested). Natural reservoirs of *Bartonella* are often asymptomatic, but it is not known if *B. v. berkhoffii*-infected coyotes develop endocarditis or similar morbidity/mortality as dogs.
Methods: Seventy coyote hearts from Northern California were dissected and examined for the presence of gross pathologic lesions associated with endocarditis. Presence of *Bartonella* DNA was investigated on aortic and mitral valves and spleens (as control for ongoing bacteremia) by PCR. Final species identification by molecular techniques (RFLP and partial sequencing) was performed on PCR-positive samples.
Preliminary Results: No valvular lesions associated with endocarditis were observed. To date, PCR has been performed on 56 (80%) aortic valves, and 46 (66%) mitral valves. Of these, 10 (18%) aortic and 2 (4.3%) mitral valves were *Bartonella* PCR-positive, a statistically significant difference (Fischer's Exact Test; p-value = 0.03).
Conclusions: No endocarditis was observed, but 89% of the samples were from juvenile (0-2 years) coyotes. In dogs, endocarditis is usually detected in middle-age animals (3-6 years). Therefore, it is likely that an early infection stage was detected, prior to development of vegetative valvular lesions. However, our data points toward aortic valve localization of *Bartonella* infection as a preliminary step to the development of endocarditis.

41. 25 YEARS POST REINTRODUCTION: SEROSURVEY OF SELECT PATHOGENS IN A POPULATION OF AMERICAN MARTEN IN MICHIGAN

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American marten (*Martes americana*) were reintroduced into the Upper Peninsula (UP) and Northern Lower Peninsula (NLP) of Michigan during the 20th century. While the marten population in the UP has grown, marten in the NLP are regionally rare. There are no studies examining pathogen exposure in martens in Michigan. This study examines the seroprevalence to canine distemper virus (CDV), *Toxoplasma gondii*, and *Leptospira* spp. in the NLP American marten population. Serum and urine samples from 22 live-trapped American marten from the Manistee National Forest (MNF) were obtained between May 2011 and December 2012. Overall, 9% (n=2) were seropositive for CDV, 50% (n=11) for T. gondii, and 0% for *Leptospira*. In addition, urine samples from 18 marten were negative for *Leptospira* spp. using real-time polymerase chain reaction or indirect fluorescent antibody. Nine marten were re-captured and tested for *T. gondii* and eight for CDV. Six re-captured marten seropositive for *T. gondii* at the initial exam remained positive 4 to 12 months later. One marten seroconverted during the study and two marten were consistently seronegative for *T. gondii* 8-12 months later. Two martens seropositive for CDV had persistent titers 4-7 months later. Thus, marten in the MNF are exposed to CDV and *T. gondii*, while exposure to *Leptospira* spp. was not detected in this study. These results indicate that further testing of both the UP and NLP marten populations is warranted to determine if disease is limiting the NLP population and to evaluate the risk of disease introduction in any future reintroduction.

42. CONTACT BETWEEN BIGHORN SHEEP AND DOMESTIC LIVESTOCK

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Seventeen bighorn sheep (*Ovis canadensis*) with known or suspected contact with domestic ruminants on public or private land were removed to prevent possible disease transmission. Live bighorns maintained in captivity were monitored for evidence of respiratory disease. Cattle contact (n=4) occurred from December to February while most contacts with domestic sheep (n=10), goats (n=3) or both (n=1) occurred between April and October. Four bighorns died within 7 days following capture and 10 survived from 47 days to 57 mo in captivity. Five bighorns had gross and/or histological evidence of pneumonia. Pasteurellaceae were isolated from 17/18 bighorns, and domestic ruminants contacted by 4 bighorns. Isolates included multiple biovariants of *Mannheimia* spp. and *Bibersteinia trehalosi*, and *Pasteurella multocida* subspecies and biotypes. Pasteurellaceae from pneumonic lungs included *Mannheimia* spp. biovariant 1, *P. multocida multocida* a, and *B. trehalosi* biovariant 2B. The *Mannheimia* spp. biovariant 1, isolated from two pneumonic bighorns and contacted domestic sheep, had restriction fragment length pattern similarity coefficient values of 1.0 indicating high similarity and likely sharing between the species. Management implications include the need for species separation and rapid responses to contact situations since 28% of the bighorns died with evidence of respiratory disease likely associated with domestic ruminant contact.

43. CANINE DISTEMPER VIRUS: AN EMERGING DISEASE IN WILD ENDANGERED AMUR TIGERS (*PANTHERA TIGRIS ALTAICA*)

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Fewer than 500 Amur tigers (*Panthera tigris altaica*) remain in the wild. Due to low numbers and their solitary and reclusive nature, tiger sightings across their range in the Russian Far East (RFE) and China are rare; sightings of sick tigers are rarer still. Serious neurologic disease in two wild tigers in 2001 and 2004 coupled with observation of similar abnormal neurologic behavior in wild tigers in 2010 suggested disease emergence in this endangered species. Here we show that in 5 adult tigers that died or were destroyed in 2001 (n=1), 2004 (n=1), or 2010 (n=3), canine distemper virus (CDV) infection caused the observed neurologic disease in two and was definitively established in a third. Non-suppurative encephalitis with demyelination and eosinophilic nuclear viral inclusions, and IHC and ISH staining consistent with CDV were present in brain from both tigers with available brain samples. CDV phosphoprotein (P) and hemagglutinin (H) gene products were obtained from brain samples from these two tigers by RT-PCR and a short fragment of CDV P gene sequence was detected in lymph node of a third tiger. Phylogenetically, Amur tiger CDV groups with Arctic-like strains in Russia. Our results, coupled with documented lack of CDV antibodies in wild Amur tigers prior to 2000, suggest recent emergence of CDV as a conservation threat to endangered Amur tigers in the Russian Far East.

44. BLUETONGUE VIRUS 10 AND 11 INFECTION IN TWO DESERT BIGHORN SHEEP

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In September 2012, a female desert bighorn sheep (*Ovis canadensis nelsoni*) was found dead on the shore of Canyon Lake, Arizona. A moderate amount of yellow pleural effusion with fibrous adhesions between lobes of the lungs and between the lungs and the thoracic wall was found on necropsy. A second ewe was observed coughing and separated from a nearby herd by the Arizona Game and Fish Department during a survey of the population. The ewe was euthanized and at necropsy we found a mild pericardial effusion. Histologically, only mild changes were seen with the first ewe having pulmonary congestion and pulmonary edema with minimal alveolitis, and the second ewe having essentially normal tissues. Bluetongue virus (BTV) serotype 11 and serotype 10 were found in lung tissue from the first and second bighorn sheep, respectively, with a real-time reverse transcriptase PCR method specific for the M6 gene of BTV. Subsequent serotype determination was made via PCR targeting the serotype-specific genome segment 2 encoding BTV outer-capsid protein VP2 and sequencing of the amplicon. A serological survey of the population found ten of 27 (37%) bighorn sheep positive for bluetongue virus; most had higher titers to BTV 17 than either serotype 10 or 11. Serological testing of the same population in 2010 found 9 of 30 (30%) bighorn sheep with antibodies to bluetongue virus. None had a notable titer to BTV 10 and only one had a high titer to BTV 11. This case adds to the limited reports of clinical BTV in bighorn sheep.

45. OUTBREAK OF MYCOBACTERIAL DERMATITIS AND CELLULITIS IN FOUR TASMANIAN DEVILS (*SARCOPHILUS HARRISII*)

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Tasmanian devils (*Sarcophilus harrisii*), the largest extant carnivorous marsupials, are threatened with extinction due to a transmissible neoplasm, Devil Facial Tumour Disease. Conservation efforts include the creation of a multi-zoo captive contingency population. Skin lesions were identified in four animals held in a mainland Australian zoo. Lesions included incompletely healed scabs, discrete, subcutaneous masses and indurated, thickened skin with fistulous tracts. Fine needle aspirates and punch biopsies of skin were taken. All samples demonstrated pyogranulomatous dermal and subcutaneous inflammation. Beaded, filamentous, acid fast bacilli were noted in two animals. Biopsy samples were also submitted for PCR and culture. All were negative for *Mycobacterium tuberculosis* complex, *Mycobacterium avium* and *Mycobacterium intracellulare* on PCR. Culture yielded *Mycobacterium fortuitum* complex in all cases. Three of the four animals were given 5-6 weeks of enrofloxacin. The fourth animal was given long-acting amoxicillin at the time of examination. Although lesions appeared to resolve, histopathology and/or culture of biopsy samples revealed persistence of infection. All animals were then given sulfadiazine/trimethoprim in combination with enrofloxacin. Upon receipt of sensitivity results, sulfadiazine/trimethoprim was discontinued. Enrofloxacin was given for three months to three animals and 7 months to the fourth. One animal, euthanized after three months therapy still had typical histopathological changes despite apparent clinical resolution. Infection appears to have resolved in the remaining three animals with histological confirmation in two cases. This case will be compared to two previous reports of mycobacterial infections in single Tasmanian devils and subcutaneous mycobacterial infections in another carnivorous marsupial, the tiger quoll (*Dasyurus maculatus*). The case described here is unique in that four cases were identified over a brief period. Epidemiological factors will be discussed.

46. HEALTH SURVEILLANCE AS AN IMPORTANT TOOL IN WILDLIFE CONSERVATION: EXPERIENCES WITH THE EURASIAN LYNX

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The Eurasian lynx (*Lynx lynx*) was reintroduced to Switzerland in the 1970s, resulting in two distinct populations (Jura and Alps). Ecological and pathological investigations were initiated in 1983. Living and dead lynx have been systematically sampled for genetic research since the 1990s, and screenings for various infectious agents started in 2001. An official management plan was implemented in 2004, requiring submission of all dead lynx to one institution responsible for veterinary examinations and hosting a sample archive. Veterinary examination of lynx caught alive contributed to the development of health screening protocols for translocation and the improvement of field procedures (e.g. captures). Genetic analyses revealed a loss of variability and increasing inbreeding mainly in the Alps, urging for genetic management. Infectious agents such as *Cytauxzoon*, feline hemotropic mycoplasmas and parvovirus circulate in lynx apparently without associated morbidity. However, cases of mange, distemper, congenital malformations and fatal cardiomyopathy have been newly diagnosed. Archived samples revealed a high prevalence of subclinical heart lesions in Alpine lynx, and heart murmurs were repeatedly noticed in live lynx from this population, raising concerns about an inbreeding depression. Recent observations of active parvovirus infections, distemper emergence in wildlife within the lynx range, and cardiac abnormalities together with reduced heterozygocity in the Alps now require a revision of management strategies at several levels. These experiences underline the necessity of long-term health surveillance of reintroduced and small isolated wildlife populations, the value of multidisciplinary collaboration and of archived samples, and the need for adaptive management based on scientific data.

47. IMPACTS OF HOST DENSITIES ON THE EVOLUTION OF *TOXOPLASMA GONDII* TRANSMISSION ROUTES

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Toxoplasma gondii is a fascinating parasite for its ability to infect almost all mammal species, to often exhibit a low level of virulence, to use different routes of transmission and to be present in environments contrasting in host abundances and species. Given that cats (*Felis catus*) and rodents are major hosts of this parasite, humans obviously impacted *T. gondii* ecology and evolution through their impact on these host species. Indeed, the expansion of agriculture has offered a unique and ideal environment for *T. gondii* by concentrating both the feline definitive host (DH) and its prey intermediate host (IH) at the same place. In this study we investigate how host densities may impact on the evolution of the different transmission routes of *T. gondii*. We test the hypothesis that the concentration of cat DHs and rodents IHs in rural areas has favored the evolution of alternative transmission routes, such as transmission from oocysts, i.e. the free living stage of the parasite, to cats; vertical transmission in intermediate hosts and transmission via carnivorism in IHs. Under the assumption that the parasite cannot optimize simultaneously all these transmission routes, we show that rural environments are at the interface of pressures for the different routes. Interestingly, we also show that while wild environments favor manipulation of intermediate host behavior, rural environments may favor vertical transmission in intermediate hosts. This may have consequences on other domestic animals, such as sheep in which vertical transmission causes economical losses.

48. CAN NEW AND TRANSLOCATED SPECIES OF *EIMERIA* ASSIST IN THE MANAGEMENT OF AUSTRALIA'S PEST EUROPEAN RABBIT (*ORYCTOLAGUS CUNICULUS CUNICULUS*) POPULATION?

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European colonizers of Australia introduced European rabbits (*Oryctolagus cuniculus cuniculus*) as early as 1788, and continued to regularly import them, primarily as an easily housed and managed source of protein, but also for hunting. The species is now Australia's worst pest animal. Australia's management of its pest population of rabbits has been benefited by the successful introductions of myxomatosis in 1950 and rabbit haemorrhagic disease virus (RHDV) in 1995-saving agricultural industries c. $70 billion. However, as expected with pathogen/host relationships, the viruses have changed and genetic resistance has developed. In the search for additional biological control agents for the pest rabbits, new and translocated species of *Eimeria* have been proposed. Rabbit parasites, in particular *Eimeria* spp, may have substantial negative effects upon host fat, suggesting a reduction in condition. Further, these mass reductions could potentially have detrimental effects on host fecundity. Numerous species of rabbit *Eimeria* are not recorded in Australia. *Eimeria intestinalis* and *E. flavescens* are reported from south-west Western Australia, but not from other regions, and their translocation to other regions may assist rabbit management. In addition, the co-infection of both myxomatosis, endemic in Australia, and *Eimeria* spp. may influence the impact of these parasites on rabbit populations.

49. CONTROL APPLICATIONS IN WILDLIFE DISEASE MODELS

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Some examples of wildlife disease models with research supported by the National Institute of Mathematical and Biological Synthesis will be presented. Vaccine bait distribution in models for managing rabies in raccoons will be illustrated using optimal control techniques. Modeling *Toxoplasma gondii* will also be discussed.

50. ROAD PROJECTS, TURTLE RELOCATION AND RANAVIRUS: LESSONS FOR US ALL

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Ranavirus infections in wild North American chelonians, first recognized in Florida (1992), now exist in 11 states. Epizootic mortality attributed to ranavirus is most commonly reported among Eastern box turtles; however, at least four native chelonian species demonstrate susceptibility. Challenges of mortality detection among free-ranging solitary species combined with low pathogen prevalence reported in wild turtles surveyed outside of epizootic events and the potential for subclinical infections make it difficult to recognize pathogen presence in a population. This proves problematic when large-scale human encroachment into turtle habitat necessitates management action to ensure turtle survival; one such mitigation strategy is the relocation of displaced individuals. A significant outbreak involving Eastern box turtles relocated as mitigation for a road project highlight potential impacts of ranavirus on local populations. In Montgomery Co., Maryland (2008-2011), a study evaluating the effects of translocation distance on displaced turtles identified 26% mortality (27/105) among tracked turtles from confirmed or suspected ranavirus infection at the relocation site. Physical examination and quarantine of unhealthy turtles was employed prior to release to new areas. Clinical signs developed within the first year following relocation and continued throughout the study. The ranavirus outbreak was unexpected as this pathogen had not been detected before in box turtles from Montgomery or adjacent counties; however, it has been recognized in Maryland since the mid 1990's. Increased statewide surveillance and rehabilitator education has been instituted to determine the geographic distribution and significance of the ranavirus outbreak in wild turtles and amphibians.

51. FUNGAL DERMATITIS IN TWO FREE-LIVING SNAKES ASSOCIATED WITH *CHRYSOSPORIUM OPHIODIICOLA* AND *ACREMONIUM* (*SAROCLADIUM*) *STRICTUM*

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Fungal dermatitis in free-living snakes may be an emerging threat, particularly to species already threatened or endangered due to other stressors. Recent reports describe severe facial dermatitis in two species of rattlesnakes (eastern massasauga [*Sistrurus catenatus catenatus*] and timber [*Crotalus horridus*] rattlesnakes) from which the newly identified fungus *Chrysosporium ophiodiicola* was isolated in many but not all cases. Information on common fungal organisms of skin and their potential pathogenicity in free-living snakes is lacking. Also lacking is an understanding of how widespread fungal dermatitis may be among various snake species throughout the United States and elsewhere. This report details fungal dermatitis in two free-living snakes recovered from the state of New Hampshire, USA: a ringneck snake (*Diadophis punctatus*) and a black racer (*Coluber constrictor*). Infections in these snakes were associated with two different fungal organisms*, C. ophiodiicola* and *Acremonium (Sarocladium*) *strictum*, respectively, identified via PCR. While *C. ophiodiicola* was isolated from the ringneck snake, the lesions in this snake were not markedly similar to those reported in rattlesnake species. Conversely, lesions in the black racer were similar to the facial lesions reported in rattlesnakes but were associated with *A. strictum*. Descriptions of skin lesions in a variety of snake species and accurate identification of organisms involved are needed to elucidate the potential threat to free-living snakes from fungal skin infection.

52. CAPABILITY OF RANAVIRUS TO CAUSE EXTINCTION IN LOCAL POPULATIONS OF WOOD FROGS

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The ability for ranavirus to affect population dynamics or cause extinction in local populations of host species is currently unclear. To examine this possibility, we created a stage-structured population model for the wood frog (*Lithobates sylvaticus*) and investigated the influence of ranavirus introduction at different life stages and different exposure frequencies on population size and extinction probability. For model simulations, we used mortality data from laboratory transdermal challenges with ranavirus on egg, hatchling, larval, and metamorph life stages in wood frogs, which reported 60, 95, 100 and 100% mortality after 14 days, respectively. Model simulations were run 1000 times and 1000 years for each life stage and exposure frequency (2, 5, 10, 25, and 50 years). Exposure to ranavirus in the larval and metamorph stages resulted in extinction in several model runs for all exposure intervals, with extinction probability and time to extinction increasing as years between exposures decreased. Ranavirus exposure during the hatchling stage caused extinction if exposure occurred at least every 10 years, with 100% of populations going extinct when ranavirus was present at least every 2 years. If ranavirus was introduced during the egg stage, extinction never occurred. Our simulations demonstrate that ranavirus can affect wood frog population dynamics and cause local extinction under certain scenarios. Wood frogs are one of the most susceptible anurans to ranavirus; thus, future work needs to explore the consequence of ranavirus introduction on less susceptible species.

53. LIME DISINFECTION OF FISH PONDS: EFFECTS ON VIRUSES AND ON INVERTEBRATE COMMUNITIES

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The disinfection of fish ponds is an important hygienic method for the inactivation viruses and the prevention of virus infections in aquaculture. Quick lime (calcium oxide) and slaked lime (calcium hydroxide) are traditionally most commonly used as disinfectants for the disinfection of natural fish ponds. Disinfection with both is achieved by an increase in pH. It is generally suggested that a pH of 11 or 12 be achieved following a disease outbreak. However, the effects of these treatments of natural ponds on important viruses have never been sufficiently tested. The effect of the effluent water with an increased pH on macroinvertebrate-communities in streams located close to aquaculture-sites has also never been sufficiently studied. For this purpose the effect of different concentrations of quick lime and slaked lime on koi herpesvirus and viral haemorrhagic septicaemia virus was tested in the laboratory and during disinfection of affected ponds. In addition, macroinvertebrate-samples were collected in potentially affected streams before and after disinfection.

54. CORAL DISEASE-WHERE ARE THE WILDLIFE HEALTH EXPERTS?

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Coral reefs comprise less than 1% of the earth's surface but harbor ca. 25% of its diversity, but climate change and disease is threatening their very survival. In the Western Atlantic, coral cover has been reduced by 80%, mainly because of disease. Diseases threaten corals globally, but 40 years on, their causes remain mostly unknown. This is in large part because standard approaches to animal disease investigations including histopathology are not used to understand what at the cellular level is killing corals. Indeed, the wildlife and animal health community has been notably absent in this saga. Presently, causation of disease is assigned based on appearance of gross lesions alone along with use of molecular and immunological tools in absence of objective data on cell pathology. A review 415 papers on coral diseases published between 1965 and 2011 reveals that pathology comprised 6% of diagnostic effort and 40% of "known" causes of coral disease are now refuted or cannot be confirmed. Unlike most animal diseases that are an interaction between agent, host, and environment, coral disease is a unique case where the animal is the environment; lose the corals and you lose the environment. By helping understand causes and management of coral disease, wildlife health professionals could play a profoundly disproportionate role in marine conservation. Pathology and pathogenesis of disease of mucosal surfaces could serve as a useful model for diseases of corals thereby easing biomedical experts with knowledge of animal diseases into a field where they are sorely needed.

55. PREVALENCE OF TWO AMPHIBIAN DISEASES, RANAVIRUS AND CHYTRIDIOMYCOSIS, IN CONTAMINATED AND UNCONTAMINATED SITES ON THE SAVANNAH RIVER SITE

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A variety of natural and anthropogenic stressors have been hypothesized to increase the emergence of wildlife diseases in amphibians (eg. ranavirus, chytridiomycosis) via increased host susceptibility. In South Carolina, a high incidence of *Batrachochytrium dendrobatidis* in bullfrog larvae was observed in constructed wetlands on the Savannah River Site (SRS), where there are also elevated levels of copper, zinc, and mercury. However, no studies to date have explicitly examined the linkages between metal contaminants and the disease ecology of ranavirus or chytridiomycosis in amphibians, and this knowledge gap impedes our understanding of disease transmission. We sampled adult and larval amphibians from three contaminated and two reference wetlands on the SRS. We examined 215 individual amphibians representing 4 frog and 1 toad species. None of the 80 samples from our uncontaminated reference sites tested positive for *B. dendrobatidis* or ranavirus. Significantly higher proportions (50%) of animals with *B. dendrobatidis* were observed in contaminated sites versus uncontaminated sites, while no difference was observed for ranavirus (3%). Nonetheless, our preliminary data indicated that while ranavirus occurred at low prevalence it was only detected in contaminated sites. In total, we found *B. dendrobatidis* and ranavirus in four and two species sampled from the contaminated wetlands.

56. TRENDS IN RANAVIRUS PREVALENCE AMONG PLETHODONTID SALAMANDERS IN THE GREAT SMOKY MOUNTAINS NATIONAL PARK

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Emerging infectious diseases are a potential contributor to worldwide amphibian declines. Ranaviruses, which infect ectothermic vertebrates and are common in aquatic environments, have been implicated in mass mortality of at least 72 amphibian species worldwide. As a majority of these surveillance studies have focused on pool-breeding amphibians, the primary objective of our study was to evaluate trends in ranavirus infection within a salamander assemblage (Family Plethodontidae) in the Great Smoky Mountains National Park, USA. We sampled a total of 691 plethodontid salamanders representing 16 species at a total of eight sites over a six-year period (2007 – 2012). We identified ranavirus positive individuals in 11 of the 16 (69%) sampled species, with salamanders in the genus *Desmognathus* having greatest infection prevalence. We observed species-specific effects of elevation on infection prevalence with individuals sampled at lower elevation sites having greater infection prevalence compared to high-elevation sites. Infection prevalence was significantly different by year and was greatest in 2007, with 82.5% of sampled individuals testing positive for ranavirus. We hypothesize that extremely low rainfall amounts during 2007 was responsible for high infection prevalence. Body condition was not a significant predictor of ranavirus infection; however, average body condition for the five most commonly captured individuals was greatest during the year (2010) with lowest infection prevalence. Overall, our results indicate that natural history differences among streamside salamander species along with elevation and environmental stressors may play a profound role in the way that ranavirus infections occur in plethodontid salamanders.

57. RANAVIRAL DISEASE IN THE UK – COMMON FROGS AND COMMON TOADS ARE NOT CREATED EQUAL: EXPERIMENTAL ASSESSMENT OF VIRULENCE AND HOST SPECIFICITY OF UK RANAVIRUS ISOLATES IN RANA TEMPORARIA AND BUFO BUFO TADPOLES

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Ranaviruses are emerging pathogens in amphibians that were first reported in UK common frogs (*Rana temporaria*) in the late 1980s/early 1990s. To date, only preliminary assessments of host-specificity and virulence have been conducted in native UK species. Here, we assess the relationship of infection, signs of disease, and mortality with viral isolate and dose for four UK ranavirus isolates from two UK amphibian hosts in both *R. temporaria* and *Bufo bufo* tadpoles. In *R. temporaria* tadpoles, those exposed to low doses of strains that originated from *R. temporaria* experienced higher mortality than those exposed to strains from *B. bufo*. There was no such difference at the high dose. This result suggests some degree of host-specificity at low dose. The origin of the isolate had no significant effect on the presence of infection, or signs of disease at death at the high dose. The most common sign of disease was abdominal haemorrhages and/or bloating. In *B. bufo*, reduced survivorship, the presence of infection, and signs of disease at death were all associated with dose, not isolate. The most common sign of disease at death for *B. bufo* tadpoles was skin sloughing. Taken together, these experiments demonstrate host specificity at low doses, which is lost at higher doses; it also suggests that *R. temporaria* is the primary host of the ranavirus in the UK since virulence can be higher in a primary host where secondary hosts exist.

58. HEALTH ASSESSMENT OF EASTERN INDIGO SNAKES (*Drymarchon couperi*) IN GEORGIA

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The eastern indigo snake (*Drymarchon couperi*) has experienced population declines across its range primarily as a result of extensive habit loss, fragmentation, and degradation. There is minimal information regarding health and disease of free-ranging eastern indigo snakes. The objectives of this study were to develop a database for health, infectious disease, reproductive, and nutritional parameters for free-ranging eastern indigo snakes and evaluate the effects of environmental contaminants on the health and reproductive status of this species. Biological samples used in this study included blood, feces, stomach wash contents, skin biopsies, and various tissues from necropsy which were collected opportunistically from snakes that were found dead on the road (DOR), live snakes brought in for rehabilitation, and live snakes that were involved in mark-recapture and radio-telemetry research studies. Representative prey items of the indigo snake were collected DOR for complete nutritional analysis. Prey items found in the gastrointestinal contents were identified. Significant findings included extremely elevated plasma calcium, plasma vitamin D, and measurable levels of blood mercury. Hepatazoon sp. was identified in 62.3% of the snakes evaluated. Histopathological evaluation of skin biopsies taken from snakes with winter time vesicular skin disease revealed severe, subacute, heterophilic, hyperplastic, pustular, and ulcerative dermatitis with intralesional bacterial rods and intralesional fungal hyphae. The most common necropsy finding in vehicular trauma cases was granulomatous inflammation in the gastrointestinal tract related to migrating parasites. Necropsies conducted on 3 snakes found moribund or dead in the field had systemic fungal infections.

59. PAIN MANAGEMENT STRATEGIES IN CHELONIANS AND PHARMACOKINETICS OF TRAMADOL AND O-DESMETHYLTRAMADOL IN THE LOGGERHEAD SEA TURTLE (*Caretta caretta*)

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Trauma is the most common reason for sea turtles to be presented to the Georgia Sea Turtle Center for rehabilitation. Boat strike injuries account for over 20 percent of our caseload and these injuries are likely to be extremely painful. Although pain management in reptiles has made some recent advances, data are lacking for sea turtles. The objective of this study was to determine the pharmacokinetics of two orally administered doses of tramadol (5 and 10 mg/kg) and its major metabolite (O-desmethyltramadol) in loggerhead sea turtles (*Caretta caretta*). After oral administration, the half-life of tramadol administered at 5 mg/kg and 10 mg/kg was 20.35 and 22.67 hours, whereas the half-life of M1 was 10.23 and 11.26 hours, respectively. The maximum concentration (Cmax) for tramadol after oral administration at 5 mg/kg and 10 mg/kg was 373 and 719 ng/mL, whereas that of M1 was 655 and 1376 ng/mL, respectively. We were able to determine that tramadol, administered orally to loggerhead sea turtles at both dosages provided measurable plasma concentrations of tramadol and O-desmethyltramadol for several days with no adverse effects. Plasma concentrations of tramadol and O-desmethyltramadol remained ≥ 100 ng/ml for at least 48 hours and perhaps as long as 72 hours when tramadol was administered at 10 mg/kg. Based on therapeutic levels that are achieved in humans, a dose of 10 mg/kg every 72 hrs or 5 mg/kg every 48 hours should produce similar levels but further studies are needed to confirm this information including multi-dose and pharmacodynamic studies.

60. SOUTHEASTERN WILD TURTLES ARE RESERVOIRS OF *SALMONELLA SPP* BUT DO NOT SHED AFTER BEING STRESSED

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Salmonella spp. are a leading cause of bacterial diarrheal disease. The majority of cases are associated with food hygiene; however, “non-foodborne” cases are on the rise, particularly in Southern USA. Although most have historically been associated with pet turtles, the source for many cases is unknown. A multi-state outbreak involving >347 people infected with diverse Salmonella serotypes occurred in 2012 and only about 70% reported contact with a turtle. Additionally, it is widely accepted that captivity-associated stress promotes shedding in reptiles. We conducted an investigation to determine: 1) the prevalence in wild aquatic turtles and 2) if stress induced shedding in painted turtles. Turtles were captured and held overnight in clean containers to collect feces. *Salmonella* prevalence varied by species (n=146, 5 species; prevalence range 15-100%) and sampling month (highest in July). Wild-caught painted turtles (n=17) were placed in captivity and tested weekly. Contrary to previous suggestions that “stress” induces shedding, our captive turtles stopped shedding *Salmonella* after one week in captivity. Except for spiny softshell turtles (n=4; 100%), shedding rates of wild turtles is low and stress did not induce shedding. We propose that overcrowding/poor hygiene during transport/shipping contributes to higher rates of *Salmonella* in captive-reared turtles. However, wild turtles are harvested for pets and food, and serotypes isolated from these turtles are commonly reported to cause human salmonellosis. In addition, the diversity of serotypes (n>7) shed by these long-lived species places other aquatic wild animals at risk for exposure; highlighting its significance for both people and other wildlife.

61. PHENOTYPIC AND GENOTYPIC HOMOGENEITY AMONGST *Streptococcus iniae* ISOLATES RECOVERED DURING CARIBBEAN REEF FISH OUTBREAKS

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Members of the genus *Streptococcus* (specifically *S. iniae* and *S. agalactiae*), are amongst the most destructive and lethal bacteria known to affect cultured and wild fish species. The agents are not only extremely important pathogens in fresh water and marine environments; but they are also zoonotic agents that can cause severe diseases and mortality in humans and other mammals. During the last decade, outbreaks of Streptococcosis in a wide range of reef fish have occurred in the Caribbean. In this project, fifteen *S. iniae* isolates recovered from different islands and different fish species were characterized. The species identity was confirmed by biochemical identification and amplification and sequence of the 16S rRNA gene. Repetitive element palindromic PCR (rep-PCR) fingerprinting, biochemical and antimicrobial susceptibility profiles suggest that a single strain was responsible for the different outbreaks. The inciting cause for this cluster of mortalities caused by *S. iniae* is unknown.

62. STUNTING AND MORTALITY OF CAPTIVE RAISED LOWLAND LEOPARD FROG (*Lithobates yavapaiensis*) TADPOLES AND RECENT METAMOPHS ORIGINATING FROM WILD COLLECTED EGG MASSES

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Lowland leopard frog tadpoles originating from egg masses collected at three native localities during fall in Arizona were captive-raised at densities of 5 to 15 in seven liter polycarbonate containers containing carbon filtered (20%) and reverse osmosis (80%) water at approximately 24ºC, under 5% UVB fluorescent lights and fed spirulina algae supplemented with fish food flakes, bee pollen and egg whites. Initially water NH3 and phosphate levels were often higher than acceptable (>0.5 mg/l and >0.5 mg/l, respectively) and this was managed with water changes, decreased feed amount and lower density. Of tadpoles living 5 days post-hatch (N=298), 57% survived and 27% completed metamorphosis by 180 days. Ranavirus PCR on selected mortalities was negative. Tadpoles and metamorphs failing to undergo complete metamorphosis were euthanized at 180 days and had extreme variation in weight (0.2 to 2.4 grams) as did complete metamorphs (1.0-2.7 grams) that died prior to 180 days. Chronic myodegeneration (32%), nephrocalcinosis (23%), water mold infection (19%) and ocular lens degeneration (10%) were observed in tadpoles and metamorphs (N=102) examined microscopically. Tadpoles with chronic myodegeneration had decreased growth rate, anorexia and often exhibited erratic swimming for days prior to death or euthanasia. Microscopically, chronic myodegeneration was characterized by progressive dropout of striated muscle (up to 70%) and was accompanied by hepatic atrophy. Water mold infection was observed in both normal-sized tadpoles and those with myodegeneration but decreased in frequency when water quality improved. Documentation of non-infectious lesions may be useful for evaluation of genetic, toxic or environmental parameters.

63. EPIDEMIC MORTALITY DUE TO TRICHOMONOSIS IN A DECLINING BAND-TAILED PIGEON POPULATION

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Avian trichomonosis is a protozoal disease of birds that is typically caused by infection with *Trichomonas gallinae*. Despite their variable resistance to clinical signs and lesions, some columbid species experience significant population or recruitment losses from trichomonosis outbreaks. The Pacific Coast band-tailed pigeon (*Patagioenas fasciata monilis*, BTPI) is a migratory upland game species at risk for population decline. During a multi-year opportunistic and syndromic surveillance effort, we analyzed the prevalence, genetic diversity, and pathogenesis of trichomonad parasite infections in BTPI of California. Infections were most common in adult BTPI and prevalence was high in birds sampled at mortality events (96%) and rehabilitation centers (36%) compared to hunter-killed (11%) or live-caught (4%) birds. Only in the second year of surveillance did we detect mortality events in late winter and early spring in the Sierra Nevada and central coast regions of California that lead to an estimated cumulative loss of >1,500 BTPI. Both *T. gallinae* and a *T. vaginalis*-like organism, *T. stablerae* sp. nov., were isolated during outbreaks and, less frequently, in healthy birds. Our analyses indicate that host-parasite ecology and inter-annual variation in climate and resource abundance may have a greater influence on epidemic transmission and susceptibility to severe disease than parasite genetic background.

64. THE DISTRIBUTION AND EXTENT OF HEAVY METAL ACCUMULATION AND BLOOD PARASITES IN SONG SPARROWS OF ARIZONA'S UPPER SANTA CRUZ RIVER WATERSHED

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Heavy metals play a persistent role in the environment, and runoff of metals into riparian zones may present a threat to ecosystems, as plants and wildlife are susceptible to long-term exposure and bioaccumulation. We investigated the distribution and cascading extent of heavy metal accumulation and blood parasites in Song Sparrows (a resident riparian species) in Arizona's upper Santa Cruz River watershed. This study had three goals: 1) quantify the degree of heavy metal accumulation in sparrows and determine the distributional patterns among six study sites, 2) compare concentrations of metals found in this study to those found in studies performed prior to a wastewater facility upgrade, and 3) assess the condition and hematozoan prevalence levels in Song Sparrows among sites with differing potential levels of exposure. We examined six study sites that reflect different potential sources of contamination. Body mass residuals and leukocyte counts were used to assess sparrow condition. Eight metals in blood and feathers showed significant patterns in abundance among sites. Cadmium, copper, mercury, nickel, and selenium exceeded background levels at some sites, but were generally lower than or similar to earlier studies performed prior to the international sewage treatment plant upgrade. Recaptured birds showed higher concentrations in 2012 than 2011 for two and five metals in blood and feathers, respectively, suggesting possible bioaccumulation. We found no cascading effects as a result of metal exposure but did find higher blood parasite prevalence with increased contamination and that metal levels were reduced following the international wastewater treatment plant upgrade.

65. BALD EAGLE NESTLING MORTALITY DUE TO PARASITISM BY TICKS AND SUCCESSFUL MANAGEMENT WITH NEST REPLACEMENT

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From 2009 to 2011, eight bald eagle nestlings died at a nest site located near the confluence of the Verde and Salt Rivers on Salt River Pima-Maricopa Indian Community land in Arizona. The nest pair had consistently raised 3 fledglings annually for several years. The nest was located in a mature cottonwood tree (*Populus fremonti*) and as part of a population monitoring program, was regularly observed during the nesting season. The nestlings were all found under the nest between 8 and 12 weeks after hatching. The nestlings presented with depression, muscular weakness and partial flaccid paralysis of the pelvic limbs. All were anemic, and had heavy tick infestations. Necropsy findings for five of the fledglings included subcutaneous hemorrhages, external parasites; three were also positive for West Nile Virus. Samples of ticks from the fledglings and nest were analyzed and based on mtDNA two species of ticks were identified, *Argas radiatus* and *Argas ricei*. Argasid ticks have been associated with a neurotoxin mediated paralytic syndrome. One affected fledgling survived with supportive care and manual removal of all larval ticks. Topical and environmental applications of pyrethrins and treatment of the affected areas of the tree with a sealant were ineffective at preventing subsequent nestling mortality. In the fall of 2011, the infested nest was removed and an artificial nest was erected in a nearby tree. A measure of the success of the management action was provided in 2012 when two bald eagles fledged from the artificial nest.

66. IDENTIFICATION OF LYMPHOPROLIFERATIVE DISEASE VIRUS IN WILD TURKEYS (*MELEAGRIS GALLOPAVO*) IN NORTH AMERICA

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Historically, retroviral-associated neoplasia in North American wild upland game birds has been associated with reticuloendotheliosis virus infection. In 2009, lymphoproliferative disease virus (LPDV), an uncommon source of lymphotumoral disease in domestic turkeys in Europe and Israel, was first identified by PCR and sequence confirmation in a wild turkey (*Meleagris gallopavo*) from Arkansas with lymphoid tumors in multiple visceral organs. Since then, LPDV proviral DNA has been identified in wild turkey diagnostic cases from 19 different states in the eastern United States. Based on gross and microscopic lesions, lymphoid neoplasia was determined to be the cause of morbidity or mortality in a minority of the LPDV positive wild turkeys. Phylogenetic analyses of partial gag sequences (p31 and capsid) of 58 North American viruses identified two major lineages: one consisting of the vast majority of viruses, while the other contained of a small subset of four viruses from South Carolina. Interestingly, the prototype strain from Israel, recovered in 1978, clustered within the small monophyletic clade of South Carolina viruses suggesting a direct link between North America and Europe. The cases reported herein are novel as they represent the first reports of LPDV infection in wild turkeys and the first identification of LPDV in North America. Current research efforts are currently underway to better understand the natural history, epidemiology, and significance of this virus for agriculture and wildlife.

67. COMMON LOON HEALTH ASSESSMENTS IN NEW YORK'S ADIRONDACK PARK, 2003-2012

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Health assessments were conducted on 149 Common Loons (*Gavia immer*) in New York's Adirondack Park from 2003 to 2012. Birds were captured using nightlighting and playback techniques. Blood samples were collected from the tibiotarsal vein from 103 adult and 46 juvenile loons for complete blood counts, chemistry profiles, heavy metal analyses, and to determine exposure to pesticides. Not all analyses were conducted on all birds. Complete blood counts (n=138) and chemistries (n=30) were similar to previously published results. Adult loons had higher average packed cell volumes and heterophil counts than juveniles, Blood parasites including trypanosomes, microfilaria, and *Leukocytozoon* sp. were observed on blood smears from 7 birds. Eleven of 42 (26%) loons had one or more endoparasites, including trematodes, *Eimeria* sp., and *Digenea* sp., in opportunistically collected fecal samples. Lead levels were elevated in 98 (6%) of the loons, indicating probably ingestion of lead fishing tackle. Mercury levels high enough to impair reproductive success were observed in 32% of the loons (n=99). Exposure to other heavy metals (arsenic, cadmium, and thallium) was negligible or nonexistent (n=98). Sixty-five percent (37/57) and 94% (34/36) of loons evaluated had residues of metabolites of PCB's and DDE respectively, indicating potential ongoing exposure to banned persistent environmental contaminants. There was little or no evidence of exposure to other contaminants, such as aldrin, BHC, dieldrin, endosulfane, chlordane, endrin, heptachlor, and lindane. This study provides a baseline for assessing health parameters and contaminant exposure in loons evaluated for rehabilitation or in catastrophic events, such as oil spills.

68. WEST NILE VIRUS IN GEORGIA- A TEN-YEAR STUDY

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Invasive pathogens can have deleterious effects on human and wildlife populations as depicted with the introduction of WNV into North America in 1999. In this study we examined the molecular evolution of WNV in Georgia by sampling virus isolates over a 10-year period. We tracked the frequency and distribution of nucleotide and amino acid substitutions that arose. The nucleotide changes reflect the nature of the error-prone polymerase of WNV as it evolves as well as functional constraints on the virus possibly due to the transmission cycle. The majority of amino acid changes were detected at very low frequencies, indicative of near neutral mutations in a large population of viruses. There were a few mutations that appeared to be conserved; the most notable was the previously reported V159A amino acid in the E gene. Our data set enabled us to identify the percent of displacement of the NY99 strain in Georgia. This displacement occurred from 2001-2004 having all viruses after 2004 recognized as the NW02. Phylogenetic work indicates that the Georgia isolates fall into four distinct clades. The overall topology of the tree is most likely due to the continual introduction of virus into Georgia from migratory birds as well as small-scale transmission events within the state. This data provides additional support for the role of migratory birds in the intercontinental spread of WNV in North America.

69. NESTLING TREE SWALLOWS EXPOSED TO OIL SANDS-RELATED EMISSIONS: ASSESSMENT OF BIOLOGICAL EFFECTS

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We conducted a study to assess the biological impact of natural exposure to oil sands-related emissions on wild birds. This is meant to complement toxicological studies on vertebrates and invertebrates exposed to oil sands processed water. We erected nest boxes to attract breeding tree swallows (*Tachycineta bicolor*) at two sites in proximity (within 5 km) to active oil sands mining, extraction and processing (data combined), and at two reference sites (>100 km from active mine sites). We deployed passive air monitors at all study sites to measure nitrogen dioxide (NO2), sulphur dioxide (SO2), volatile organic compounds (VOC) and polycyclic aromatic compounds (PACs). We examined the nestlings at days 9 and 14 post-hatching, euthanizing a subsample for pathology, hormonal, enzyme and residue analyses. Compared to the reference nestlings, birds from the industrial sites showed: 1) similar hatching success and mortality rates ($p>0.05$), 2) increased hepatic biotransformation enzymes ($p<0.001$), 3) decreased liver somatic index ($p=0.02$), 4) reduced T-lymphocyte response ($p=0.01$), 5) decreased bursa of Fabricius size ($p<0.001$) and, 6) decreased skeletal size at day 9 ($p=0.014$) but not at day 14 post hatching ($p=0.24$). Contaminants in air were higher at the oil sands sites for NO2 and SO2 (5-fold), VOC (6-fold) and PACs (up to 5-fold). Our results indicate health effects on liver (induction of detoxification enzymes, yet reduced organ size) and the immune system (reduced lymphocyte function and bursal size) of nestlings from the exposed sites. Impacts of these effects on the long-term health of the birds require further investigation

70. THE PERPLEXING PROBLEM OF AVIAN POX IN HAWAIIAN FOREST BIRDS

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Although malaria and pox are widely cited as primary factors in the demise of Hawaiian forest birds direct evidence that avian pox has caused declines or extinctions of these endemic birds is very scant. Transmission of both diseases by a common mosquito vector, susceptibility of native birds to avian malaria, and high frequency of concurrent pox and malaria infection makes it challenging to understand the epidemiological patterns and demographic impact of pox in Hawaii. We conducted a three- year study of pox (and malaria) infection in marked birds on Hawaii at three different elevations. We analyzed longitudinal (capture-recapture) data using a Bayesian state-space multistate model to estimate capture, survival, pox infection, and recovery rates for three native Hawaiian forest birds. We found elevation and species differences in rates of pox infection and recovery. Pox infection rates were highest in low-elevation forests, intermediate at mid-elevation, and lowest at high-elevation. The rate of recovery from pox infection was very highest in Apapane and lowest in Hawaii Amakihi. For high-elevation birds, infection rates appeared to be higher in Iiwi, but our estimates were highly variable. Our primary finding was that infection with avian pox had no demonstrable impact on survival rates of the three species we studied. A somewhat puzzling result was that capture rates of pox infected Amakihi were much lower than uninfected birds, which would artificially lower pox prevalence estimates in traditional cross-sectional disease studies. High recovery rates indicate that pox infections may be similar to those for malaria.

71. SURVEILLANCE GAPS AND BIODIVERSITY OF INFLUENZA A SUBTYPES IN WILD BIRDS

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Wild aquatic birds are recognized as the natural reservoir of avian influenza A viruses (AIV), but across high and low pathogenic avian influenza strains, scientists have yet to rigorously identify all competent hosts and subtypes. In the years that followed the emergence of the highly pathogenic Asian H5N1 strain, surveillance of wild birds for all subtypes was unprecedented. However, over time, priorities have shifted with surveillance efforts increasingly focused on strains that threaten the poultry industry. Our examination of 12,429 GenBank records provided insight into patterns of global AIV subtype diversity as well as striking, new testable hypotheses on potential novel avian host species and drivers of AIV subtype richness. We conducted an extensive literature review and communicated directly with scientists to accumulate 49 study locations and over 250,000 birds sampled. We built regional and global subtype sample-based accumulation curves to better estimate sample size targets that capture a specific percentage of virus subtype diversity. Our study identifies surveillance steps needed to develop a more balanced approach that can explore the influence of host and virus subtype biodiversity on emergence and transmission, and a targeted sampling scheme to detect 75% percent of global and regional circulating virus subtypes.

72. EVIDENCE FOR NEGATIVE IMPACT OF LEAD EXPOSURE ON GENERIC INDICES OF HEALTH IN FREE-RANGING DUCKS

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Numerous experiments under controlled conditions and extensive investigation of waterfowl mortality have demonstrated that exposure to lead from spent gunshot is detrimental to the health of waterfowl. However, few studies have focused on examining the sub-lethal effects of lead toxicity on free-ranging ducks under field conditions. Our studies in North-Eastern Argentina's wetlands, where hunting with lead gunshot is substantial, have shown that exposure to lead, as measured by lead pellet ingestion and lead concentrations in liver, bone and blood of ducks, is very high. To assess the health status of ducks exposed to varying amounts of lead under natural conditions, we measured body weight, sex, age class, and body condition (keel angle) from 415 hunter-killed ducks, and 70 live-trapped ducks. In addition, spleen weight was recorded in hunted ducks and basic hematology and aminolevulinate dehydratase were determined in live duck blood. Pellet ingestion and lead concentration in liver and bone (killed ducks), and blood (live ducks) were also measured. Using multivariable linear models, we found that, when controlling for the potential confounding effect of site, year, species and age, lead levels in the liver were negatively associated with body condition and spleen mass. Spleen mass was also lower in ducks with higher lead levels in their bones. In live ducks, blood lead levels were negatively associated with hematocrit values. These findings suggest a relationship between lead exposure and impoverished health that could have serious implications for duck conservation. This evidence further supports the need for urgently banning lead shot.

73. PATHOLOGY OF DISEASE CAUSED BY WELLFLEET BAY VIRUS, AN EMERGING PATHOGEN OF COMMON EIDERS (*SOMATERIA MOLLISSIMA*)

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Previously unrecognized virus, now named Wellfleet Bay Virus (WFBV), was first isolated from a Common Eider (*Somateria mollissima*) from Cape Cod, Massachusetts in 2006 from carcasses submitted for necropsy to the USGS National Wildlife Health Center (NWHC) during a mortality event. Based on genetic analysis of five different RNA segments, the virus was determined to be a novel orthomyxovirus (family Orthomyxoviridae, genus *Quarjavirus*). Since 2006, the NWHC has continued to investigate the disease caused by WFBV in both free-flying eiders during subsequent die-offs, and through laboratory inoculation trials in juvenile eiders. Pathologic findings in free-flying eiders infected with WFBV were variable, but consistently included hepatic necrosis and lymphoid depletion. In 2010, healthy eider ducklings were inoculated with WFBV in a controlled laboratory setting. Twenty-five percent of inoculated eiders became severely ill and had to be euthanized. Inoculated eiders developed serum antibodies by Day 4 following inoculation. At necropsy, lesions consistent with those seen in free-flying eiders were present in inoculated birds that became ill; control birds were unaffected. Virus was re-isolated from multiple tissues from affected birds, completing the fulfillment of Koch's postulates for WFBV in Common Eiders.

74. NEUTRALIZING ANTIBODIES TO INFLUENZA A VIRUSES IN STAGING MALLARDS

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Serologic testing of ducks for antibodies to influenza A viruses (IAV) has largely targeted antibodies to internal viral proteins. Although results have application to identifying avian species that have been infected with IAV, results provide little information related to population immunity. At present, subtype specific tests are limited to hemagglutination inhibition (HI) and virus neutralization (VN) formats; VN primarily has been used to test mammalian serum. Currently, it is unknown if either of these tests provide reliable and specific information that can be used to assess levels of flock immunity in free-living avian populations. This problem is further complicated by unknowns associated with: 1) the duration of the detectable subtype specific antibody response, 2) potential for cross reactions between related HA or neuraminidase (NA) antigens; 3) changes in the immune response associated with repeated infections; and 4) an inability to relate detectable antibody titer to functional immunity. A technical problem associated with these tests also relates to the serum demand associated with testing against 16 hemagglutinin (HA) subtypes. In order to begin to address these issues, we tested experimentally infected and field caught mallards (*Anas platyrhynchos)* by VN against IAV representing HA 1-12. Wild birds were sampled in northwestern Minnesota during August and September of 2009-2012 and virus isolation results were available for all of these birds. With experimentally infected mallards, VN had a high sensitivity and specificity although there was some indication of cross reactions with matched NA antigens. Results from free-living mallards during all years mirrored virus isolation results, and with few exceptions, gave a reliable indication of predominant HA subtypes infecting hatch year (HY) mallards. This was not the case for after hatch year mallards (AHY), suggesting that AHY birds develop a very broad antibody response associated with previous exposure to multiple IAV subtypes. Most birds that were virus isolation positive tested negative for antibodies to that HA subtype suggesting the detection of antibodies may be predictive of subtype specific immunity. Based on HA specific antibody prevalence estimates, flock immunity in HY birds from their first encounter with multiple IAV subtypes during peaks in IAV prevalence during late summer/fall staging are relatively low. However, challenge experiments are needed to fully relate these detectable antibody responses to functional immunity.

75. THE ROLE OF PASSERINES AND OTHER TERRESTRIAL BIRDS IN AVIAN INFLUENZA VIRUS EPIDEMIOLOGY

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Although passerines and peridomestic birds have been involved in influenza A virus (IAV) poultry outbreaks, there is little historic evidence for their involvement as reservoirs. However, recent reports of IAV detection by polymerase chain reaction (PCR) have challenged this paradigm and suggested additional research into the role of passerines as IAV hosts is warranted. To address this, we reviewed the published literature on IAV for 829 passerines and other terrestrial birds and conducted surveillance for IAV in 100 terrestrial avian species. In total, 3,868 serum samples and 901 swab samples were collected from four states, including Georgia, New Jersey, Delaware, and Minnesota. Of these, 310 of the Minnesota samples were collected on two domestic poultry farms that had recently experienced a H7N9 low pathogenic IAV outbreak. Serologic testing was performed with a commercial blocking ELISA (bELISA) and swab samples were tested using real-time reverse transcriptase polymerase chain reaction assay (RRT-PCR) and virus isolation in chicken eggs. Antibodies to IAV were detected in 4/3,868 serum samples (0.1%), including a Baltimore oriole (*Icterus galbula*), American robin (*Turdus migratorius*), American redstart (*Setophaga ruticilla*) and European starling (*Sturnus vulgaris*), all from Minnesota. The seropositive starling was the only bird sampled on the poultry farm that was seropositive and H7 subtype hemagglutinin inhibition testing was negative. All 901 swab samples were virus isolation and RRT-PCR negative. Data from the literature review and prospective study provide no evidence to suggest that passerines or other terrestrial birds are important in IAV natural history.

76. *TOXOPLASMA GONDII* IN SCANDINAVIAN BROWN BEARS

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Toxoplasma gondii is a ubiquitous parasite with serious implications for public health and conservation. Human infection typically occurs via ingestion of oocysts shed in felid feces or consumption of undercooked meat from intermediate hosts. The smaller number of domestic cats and greater game consumption, compared to the United States, makes exposure via the latter a proportionally greater concern in Scandinavia. To better understand the public health risk and possible effects on bear fitness, this study used serology to investigate exposure of brown bears (*Ursus arctos*) to this parasite. Serum samples collected from two areas in Sweden from 1995 to 2012 were tested; detailed demographic and ecological data were accessed from the Scandinavian Brown Bear Project database. Logistic regression and generalized linear mixed models were used to assess risk factors and attributes associated with exposure. Overall seroprevalence was 25% (n=541); there were 55 incidences of seroconversion and three of seroreversion. Only 2% of yearlings were seropositive, with limited evidence of vertical transmission. The preferred logistic regression model showed significant interactive effects between age and both sex (p=0.0018) and study site (p=0.02). Risk of exposure increased with age, with the effect more pronounced in males; prevalence was higher in the southern area. These effects may be due to sex and site-based differences in physiological, ecological, and climatic factors. Associations between exposure and body condition, reproductive success, and survivorship were also explored. The results of this study assess the impact of this zoonosis on bear fitness and highlight the need for hunter awareness of the pathogen.

77. STUDY OF PATHOLOGY IN BRUSHTAIL POSSUMS (*TRICHOSURUS VULPECULA*) IN AN URBAN AUSTRALIAN SETTING

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Possums have been recently hailed as a sentinel species for environmental and human health in the urban environment, making it prudent to review the pathology of these animals. Pathology records for brushtail possums (*Trichosurus vulpecula*) presented to Taronga Wildlife Hospital in Sydney were retrieved from the Australian Registry of Wildlife Health for review. 208 records dating from 1982 to early 2013 were included in this study. These cases represented free-ranging animals from within zoo grounds and animals presented to the wildlife hospital for care from surrounding suburbs. Case distribution included 150 adult (males = 66; females = 80; unknown = 4), 52 juvenile (males = 34; females = 16; unknown = 2), and 6 animals of unknown age (males = 1; females = 1; unknown = 4). Most common pathologic conditions apart from trauma (n = 40) included: exudative dermatitis (n = 14), nonsuppurative meningoencephalitis (Wobbly possum syndrome; (n = 23)) and pulmonary marsupostrongylosis (n = 21). Zoonotic diseases identified included toxoplasmosis (n = 5), listeriosis (n = 1) and neuroangiostrongylosis (n = 1). Rodenticide ingestion (n = 6) was the most common form of intoxication documented and lymphosarcoma (n = 4) was the most common form of neoplasia. Brushtail possums are a common urban wildlife species susceptible to multiple diseases that also affect the human population, including neuroangiostrongylosis (*Angiostrongylus cantonensis*), which is responsible for multiple cases of human death and disability in the Sydney area. Continued surveillance of the brushtail possum population in addition to other urban wildlife species is warranted under the auspices of environmental and public health.

78. INVESTIGATION OF *GIARDIA DUODENALIS* INFECTION IN A LABORATORY COLONY OF PRAIRIE DOGS, *CYNOMYS LUDOVISIANUS*

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Since 2005, black-tailed prairie dogs (*Cynomys ludovicianus*) have been collected for use as research animals from field sites in Kansas, Colorado, and Texas, with the most recent collection from Texas (2011) coming from a city farm that was irrigated with treated waste water. In January of 2012, *Giardia* trophozoites were identified by histology in the lumen of the small intestine and colon of an animal euthanized because of extreme weight loss. With giardiasis suspected as the cause of weight loss, a survey of *Giardia duodenalis* in the laboratory colony of prairie dogs was initiated. Direct immunofluorescence testing of feces revealed active shedding of *Giardia* cysts in 40% (n= 60) of animals held in the vivarium. All tested fecal samples (n=29) from animals in another holding facility where the first mortality originated were PCR positive for *G. duodenalis* with assemblages A and B identified from sequencing *tpi*, *gdh*, and *β-giardin* genes. Both assemblages are considered zoonotic, thus the parasites in prairie dogs are potential human pathogens. During the investigation, four more animals died during or after treatment with fenbendazole; however, no pathologic evidence of trophozoites was seen. Molecular testing for other protozoan gastrointestinal parasites revealed no *Cryptosporidium* infections but identified a novel *Enterocytozoon bieneusi* genotype in the 2011-collected group of prairie dogs but not the 2009 animals. These cases of *G. duodenalis* in prairie dogs highlight the occurrence of zoonotic subtypes and the potential for morbidity and mortality associated with such infections.

79. EVALUATION OF THE GAMBIAN POUCHED RAT (*CRICETOMYS GAMBIANUS*) AS A POTENTIAL MONKEYPOX RESERVOIR USING BIOLUMINESCENT IMAGING

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Monkeypox (MPX) is a zoonosis similar to smallpox that has recently been on the rise in central Africa. Despite attempts to isolate the virus from wild rodents and other small mammals, no reservoir host has been identified. Several rodent hosts have been proposed as the most likely, including the Gambian pouched rat (*Cricetomys gambianus*) and Rope Squirrel (*Funisciurus anerythrus*). To investigate the suitability of the Gambian pouched rat as a reservoir host, we infected 6 animals with Monkeypox virus that expresses firefly luciferase ; 3 animals each by intranasal and intradermal routes. We used bioluminescent imaging (BLI) to track replicating virus through time, monitored clinical signs and collected blood, urine, ocular, nasal, oral, and rectal swabs. Swabs, blood and urine were analyzed using real time PCR and virus isolation. Pathology was varied in each animal, but intradermal infection resulted in clinical signs of Monkeypox in 2 of 3 animals. One severely ill animal was euthanized. The other clinically affected animal recovered and was clinically normal 34 days post-infection. Intranasal infection resulted in subclinical infection in all 3 animals. All 6 animals shed virus in oral secretions and several animals shed through one or more of the other routes. Additionally, BLI identified viral replication in the skin without grossly visible lesions. This study indicates that Gambian Pouched Rats may be a potentially important transmission host for humans, as they are hunted for consumption. They can become infected with Monkeypox virus and shed infectious virus with no clinical signs.

80. INITIAL ECOLOGICAL INVESTIGATIONS OF HEARTLAND VIRUS IN AREAS ADJACENT TO HUMAN CASE SITES

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In 2009, a novel phlebovirus called Heartland virus was isolated from two independent patients in Missouri, both with a history of tick bites. Nymphal *Amblyomma americanum* ticks collected in 2012 from habitats adjacent to the initial human cases tested positive for Heartland virus RNA by RT-PCR. Subsequent isolation of the virus from RT-PCR positive tick homogenates implicates them as suspected vectors. Genetic characterization of the virus has demonstrated it to be most similar to Severe Fever with Thrombocytopenia Syndrome virus (SFTSV,) the only other tick-borne phlebovirus known to elicit human disease. Serosurveillance of birds and mammals was performed in areas near the human case sites. A total of 139 birds, 101 wild mammals, and 38 domestic mammals were sampled to assess serum neutralizing antibody and for virus isolation attempts. Ticks, if present, were collected from animals at the time of sampling. Animals with Heartland virus neutralizing antibodies included white-tailed deer (9/14), raccoons (27/49), horses (5/23), dogs (1/13) and opossums (1/24). Experimental infections with raccoons (n=6) failed to elicit viremia following subcutaneous inoculation with 10,000 PFU of Heartland virus, thus ruling them out as the likely reservoir hosts. Two of the 6 raccoons seroconverted by 28 days post-infection. Additional experimental inoculations of domestic chickens, laboratory rabbits, hamsters and C57B6 mice all demonstrated no susceptibility to the virus. These preliminary studies indicate the need for experimental infection studies of white-tailed deer and further ecological studies to characterize the enzootic maintenance cycle of this novel viral agent.

81. ENHANCED RABIES SURVEILLANCE IN ALASKAN WILDLIFE: DETECTION OF NEW HOST RANGE AND RISKS TO TRAPPERS

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Historically, rabies surveillance in Alaska was limited to a public health laboratory evaluation of brain from suspect animals by direct fluorescent antibody (dFA) test following exposure to a human or pet. In 2006, the Centers for Disease Control and Prevention (CDC) validated the direct rapid immunohistochemistry test (dRIT) using tissue unsuitable for standard techniques. This rapid test doesn't require fluorescent microscopy or opening the skull to retrieve appropriate samples. Beginning in 2011, wildlife agency staff, certified by CDC, utilized dRIT on neurologic tissues of free-ranging wildlife obtained as trapper/hunter-killed, found dead, killed in vehicular collisions, culled for management or euthanized. The enhanced surveillance effort evaluated over 1100 specimens representing 18 species. All dRIT positive and 10% of negative tests were verified by CDC. Among 403 trapper-killed red foxes, 1.8% were positive whereas 4% of 100 arctic foxes found dead or killed as rabies-suspects were positive. We documented the first case of rabies in a wolverine in North America (1 of 42 tested) and rabies in a wolf where rabies has not been detected since the 1940's. High specificity and sensitivity was obtained using dRIT on foxes however false positive results were increased in some species and techniques not reported here. Enhanced surveillance identified the risk of rabies transmission to trappers within the fox rabies enzootic region and detected rabies in a wolverine (also a trapper target). Continued utilization of the dRIT for rabies surveillance will enhance our ability to rapidly detect rabies outbreaks and changes in species or geographic distribution.

82. ARE AFRICAN NONHUMAN PRIMATES A RESERVOIR FOR HUMAN YAWS INFECTION?

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In humans, *Treponema pallidum* causes syphilis (subsp. *pallidum*) as well as the non-sexually transmitted diseases yaws (subsp. *pertenue*) and endemic syphilis (subsp. *endemicum*). Infection with *T. pallidum* has been reported in baboons and other West African monkey species (Fribourg-Blanc and Mollaret 1969), as well as great apes (Levrero et al. 2007). In East Africa, the pathogen has been identified mainly in baboons (Harper and Knauf 2013). Clinical manifestations in non-human primates (NHPs) differ markedly between species, similar to the different symptoms in humans caused by *T. pallidum*. While baboons in West Africa are reported to have small lesions around the muzzle, eyelids, and armpits (Fribourg-Blanc and Mollaret 1969), which resemble the characteristics of yaws infection, baboons in East Africa harbor a strain associated with severe genital ulceration (Knauf et al. 2012). The geographic distribution of *T. pallidum* infection in African NHPs and a report of sustained human infection following experimental inoculation with a simian isolate (Smith et al. 1971) suggest the potential for cross-species infection between humans and NHPs. Yet, genetic data from simian and human *T. pallidum* strains circulating in Africa is scarce. Recently, a *T. pallidum* strain collected from olive baboons at Lake Manyara National Park in Tanzania was, on the basis of currently available data, indistinguishable from human yaws-causing strains (Harper et al. 2012). While the first yaws eradication campaign, carried out in the mid-20th century, was tremendously successful in reducing the number of human yaws cases, eradication has not yet been achieved. Given the suggestive body of evidence, NHPs should be considered a potential reservoir for *T. pallidum*.

83. FECAL VIRAL DIVERSITY AS AN INDICATOR OF HEALTH IN FREE-RANGING GREAT APES IN THE SANGHA REGION OF THE REPUBLIC OF CONGO

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Concrete information on pathogen diversity within free-ranging great apes is lacking. The collection of fecal samples can allow a snapshot of viral diversity in individual animals and in populations at larger scales. To investigate viral diversity, we used consensus PCR and degenerate primer pairs to test 135 gorilla samples and 28 chimpanzee fecal samples collected near Odzala-Kokoua National Park in the Sangha Region of the Republic of Congo. These samples were tested for the following viruses and their families: flaviviridae, paramyxoviridae, filoviridae, poxviridae, bocaviridae, herpesviridae, adenoviridae and simian immunodeficiency virus (SIV). Genetic sequencing and phylogenetic analysis led to the identification of 19 viruses within two viral families; herpesviridae and adenoviridae. No zoonotic viruses were found. Overall, 26.4% of 163 samples tested positive for herpesvirus, and 49.1% tested positive for adenovirus. We found evidence of co-infections with multiple herpesviruses and/or multiple adenoviruses in gorillas and chimpanzees. We detected more than 1 type of viral sequence from 30.7% of the samples. Overall, 27.4% of 135 gorilla samples and 46.4% of 28 chimpanzee samples had more than 1 type of virus. Spatial mapping was performed to determine the geographic distribution of these pathogens. These results will form a basis for understanding the types of viruses circulating within free-ranging chimpanzee and gorilla communities in this region. The findings may shed new insight on the ecological factors shaping great ape co-infection, as well as how these viruses are shared between species and across the survey zones.

84. *BORRELIA* INFECTIONS IN *IXODES* SPECIES TICKS (ACARI: IXODIDAE) ALONG LATIDUDINAL GRADIENTS IN THE SOUTHEASTERN COASTAL UNITED STATES

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The classic Lyme borreliosis (LB) cycle, involving the vector *Ixodes scapularis* and the etiological agent *Borrelia burgdorferi s.s.* (Bbss) has been well documented in the Northeastern US, where this disease is becoming increasingly prevalent in humans and canines. In the Southeast, however, human LB prevalence is much lower and the disease cycle is not well understood. We are investigating whether the geographic pattern of human disease corresponds with geographic variation in Bbss prevalence in the vector ticks. We have found higher prevalence of Borrelia spp. infection among I. affinis than I. scapularis from Virginia (*I. affinis* 58% N=12; *I. scapularis* 14% N=132) through northern coastal North Carolina (*I. affinis* 33% N=15; *I. scapularis* .004% N=432), which confirms a similar recent finding in NC (Maggi et al. 2010). Although active at different times of year, these two tick species are morphologically difficult to differentiate and only *I. scapularis* is known to bite humans. Winter counts of I. scapularis increased as we surveyed southwards into South Carolina and Florida. As counts increase, the probability of finding infected ticks would increase, however we have found no infected ticks of either species south of middle NC. Middle North Carolina currently appears to represent a line of demarcation for the southwards spread of the Northeastern Lyme disease endemic region. Further spring tick counts during the peak seasonal activity period of *I. affinis* are planned to test hypotheses about the relative importance of these two species in the LB cycle. Data with regard to southwards spread of northern-clade *I. scapularis* will also be discussed.

85. Diseases at the livestock–wildlife interface in the United States: Status, challenges, and opportunities

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In the last half century, significant attention has been given to animal diseases; however, our understanding of disease processes and how to manage them at the livestock–wildlife interface remains limited. In this study, we conduct a systematic review of the scientific literature to evaluate the status of diseases at the livestock–wildlife interface in the United States. Specifically, the goals of the literature review were three fold: first to evaluate domestic animal diseases currently found in the United States where wildlife may play a role; second to identify critical issues faced in managing these diseases at the livestock–wildlife interface; and third to identify potential technical and policy strategies for addressing these issues. We found that of the 86 avian, ruminant, swine, and lagomorph diseases that are reportable to the World Organization for Animal Health (OIE), 53 are present in the United States; 42 (79%) of these have a putative wildlife component associated with the transmission, maintenance, or life cycle of the pathogen; and 40% are known to be zoonotic. At least six of these reportable diseases—bovine tuberculosis, paratuberculosis, brucellosis, avian influenza, rabies, and cattle fever tick—have a wildlife reservoir that is a recognized impediment to eradication in domestic populations. The complex nature of these systems highlights the need to understand the role of wildlife in the epidemiology, transmission, and maintenance of infectious diseases of livestock. Successful management or eradication of these diseases will require the development of cross-discipline and institutional collaborations. Despite social and policy challenges, there remain opportunities to develop new collaborations and technologies to mitigate the risks posed at the livestock–wildlife interface.

86. A BIOECONOMIC DECISION MODEL FOR DISEASE MITIGATION AT THE WILDLIFE-LIVESTOCK INTERFACE

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The economics of managing diseases at the wildlife-livestock interface have received heightened attention as agricultural and natural resource agencies struggle to tackle growing risks to animal health. In the fiscal landscape of increased scrutiny and shrinking budgets, resource managers seek to maximize the benefits and minimize the costs of disease mitigation efforts. To address this issue, USDA APHIS developed a benefit-cost analysis (BCA) decision model designed to help users make informed choices about whether and how to target disease management efforts in wildlife and livestock populations. This model provides a structural framework that can be used to identify, assemble and measure the components vital to the biological and economic efficiencies of animal disease mitigation efforts. Our model can be applied to commercially-raised and free-ranging species at various levels of management – from detailed intervention strategies to broad programmatic actions. The ability of BCA to illustrate the benefits of disease management projects per-dollar-spent allows for the determination of economic efficiency of alternative management actions. Although this bioeconomic framework was developed to inform policy and program decisions within USDA APHIS, we believe it will be useful to the broader natural resource management community to maximize returns on financial and other resources invested in wildlife and livestock disease management programs.

87. PROPOSAL TO CREATE A US NATIONAL FISH AND WILDLIFE HEALTH NETWORK

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Disease threats to free-ranging fish and wildlife populations transcend state and national borders, cross jurisdictions and have multiple societal and ecological impacts. Thus, there is a need for intersectoral and multidisciplinary partnerships to effectively address these issues of mutual concern. We are proposing the creation of a National Fish and Wildlife Health Network designed to build a collaborative, operational framework by which government agencies, tribes, universities and professional conservation organizations will cooperate to assist tribal, state and federal agencies in their responsibilities to manage these diseases. The mission of the Network will be achieved through collaborative partnerships and the collective, voluntary adoption of protocols and actions to address fish and wildlife health issues. A Coordinating Committee will oversee and coordinate implementation of the Network. The Network will consist of agencies and organizations with the technical expertise to implement the guidelines and plans. The primary stakeholders are the tribal, state and federal government agencies responsible for managing the health of free-ranging fish, wildlife and marine animal populations. Specific areas of focus for the Network will include: 1) wildlife diagnostic laboratory protocols; 2) disease information management and dissemination; 3) coordinated disease surveillance; 4) interagency communication and response plans; 5) species specific health issues. The Network will endeavor to address deficiencies in fish and wildlife disease monitoring and prevention programs where they exist, and facilitate the work of existing systems. The creation of this Network will be an important step in addressing the critical need to protect the Nation's fish and wildlife health.

88. CITIZEN SCIENCE AS A TOOL FOR WILDLIFE DISEASE SURVEILLANCE: THE EVOLUTION OF THE GARDEN WILDLIFE HEALTH PROJECT IN GREAT BRITAIN

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Zoological Society of London has a strong track record of utilising citizen science schemes to conduct wildlife disease surveillance since the early 1990s. Close collaboration between veterinarians and non-governmental organisations with natural history expertise has underpinned this research. The first schemes comprised public reporting of wild animal mortality incidents solely on an ad hoc basis. These covered a range of taxa, including marine and terrestrial mammals, amphibians and wild birds. Whilst such schemes provide a wealth of information, the potential for reporting bias limits data interpretation. In 2005, the Garden Bird Health initiative was launched to investigate causes of mortality of garden birds across Great Britain. A combination of two independent but complementary surveillance schemes was employed: opportunistic reports of garden bird mortality incidents were solicited from the public and systematic surveillance was undertaken by a citizen science network where both the presence and perceived absence of mortality was recorded on a weekly basis throughout the calendar year. Post mortem examinations were performed on a subset of incidents following a standardised protocol and set case definitions. Integration of surveillance data with relative abundance trends enabled quantification of the impact of disease at the population level.

The Garden Wildlife Health project builds on this successful dual surveillance model and integrates garden bird, amphibian, reptile and hedgehog (*Erinaceus europaeus*) disease surveillance using web-based reporting. Citizen science offers a practical and cost-effective solution to achieve wildlife disease surveillance in peri-domestic habitats and is ideally suited to these positively-perceived species, many of which are of conservation concern.

89. NATIONAL *ECHINOCOCCUS* SURVEILLANCE USING A NOVEL PCR TEST FOR FOX FECAL SAMPLES

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The fox dwarf tapeworm *Echinococcus multilocularis* (EM) was detected in Sweden for the first time in 2011 after 10 years of screening around 300 hunted red fox (*Vulpes vulpes*) annually. An intensified national surveillance screening using segmental sedimentation and counting technique of intestines from almost 3,000 foxes followed, detecting a total of four EM-positive foxes from three different counties. To test a more cost efficient method of surveillance, an intensive collection of fox scats was done in one of the three positive areas in 2011. The intention was to analyze four fox scats per 4 km2 from an area with 25 km radius surrounding the positive finding. Almost 800 fox scats were collected from 267 of the 535 4 km2 grid reference areas. Samples were analyzed with a new SVA-developed protocol that applies template fishing in a semi automated magnetic bead based capture probe DNA extraction method and real time PCR assay. Using this test, six samples (0.8%) were positive for EM. Fox scat collection and PCR analysis is presently being used for the second national large scale surveillance of EM in Sweden, initiated in 2012. A network of hunters from all 290 municipalities in Sweden has been established to ensure systematic sampling of 4,000 fox scats from the whole country. Surveillance results are published on SVA´s website and are updated weekly in tables and a map.

90. EFFECTS OF GONADOTROPIN-RELEASING HORMONE VACCINATION (GONACON-B) ON FERTILITY IN FREE-RANGING FEMALE ROCKY MOUNTAIN ELK (*CERVUS ELAPHUS NELSONI*)

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We evaluated the safety and efficacy of the immunocontraceptive, gonadotropin-releasing hormone vaccine, GonaCon-B, in free-ranging elk. In January 2008, 120 mature (> 2 yr) female elk were captured in Rocky Mountain National Park (CO) and randomly assigned to treatment (n = 60; 1.5 mls GonaCon-B) or control (n = 60; 1.5 mls 0.9% NaCl) groups. During the following three winters females were recaptured and euthanized (2009, n = 20; 2010, n = 25; 2011, n = 34). At the time of capture and at necropsy pregnancy status was determined. Tissues were collected from organs associated with the hypothalamic-pituitary-gonadal (HPG) axis. Injection sites were relocated, tissue collected, and culture performed when gross evidence of inflammation was present. There were no differences in pregnancy rates between groups at the time of treatment (P = 0.558). In the following three years saline administered control females (n = 36) had a mean pregnancy rate of 0.83 (0.71 - 0.95). Pregnancy rate in the treatment group was 0.0 (0.0 – 0.22, P = 0.0001) year one, 0.33 (0.12 – 0.61, P = 0.05) year two, and 0.65 (0.43 – 0.83, P = 0.17) year three. No evidence of lameness or external swelling at the injection site was observed; however, all treatment females in had internal pyogranulomatous inflammation whereas none was observed in the control group. Microbes were rarely present (~5%). No consistent changes were observed within the HPG axis. GonaCon-B is effective at reducing pregnancy for two years post-vaccination and is strongly associated with sterile injection site inflammation.

91. PARADIGM SHIFT IN WILDLIFE RABIES SURVEILLANCE TO SUPPORT ORAL RABIES VACCINATION

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Laboratory-based surveillance is a cornerstone of effective wildlife rabies management. Enhanced rabies surveillance includes the testing of road-killed animals, ill carnivores, and those observed with aberrant clinical signs, within proximity to established oral rabies vaccination (ORV) zones, or in related areas where rabies research and management is conducted. Such enhanced surveillance, in concert with public health activities, better defines the spatial distribution of specific rabies virus variants. A direct, rapid immunohistochemistry test (dRIT) was developed for rabies diagnosis and allows for more real time virus detection in the field by use of light microscopy. Wildlife Services (WS) has conducted the dRIT since 2005 through a cooperative program with the Rabies Team at CDC to improve sample turnaround time and reduce the burden of increased samples on the public health system. From 2005-2012, WS tested 57,868 enhanced surveillance samples using the dRIT, representing 82% of USDA-collected surveillance specimens during that time. Fifteen of 21 states confirmed 1,031 rabid animals that would not likely have been tested through exposure-based public health surveillance. Rabid animal cases comprised 1.8% of all samples tested with the dRIT. Enhanced surveillance samples tested by WS using dRIT comprised 6-8% of all rabies surveillance specimens tested in the U.S. annually. This paradigm shift has enabled WS and cooperators to better delineate the distribution of rabies and the predicted direction of disease spread for strategic ORV baiting, as well as establish a system to better evaluate program success by sampling a broader spectrum of suspect rabid animals.

92. CHALLENGES OF DEVELOPING A GLOBAL WILDLIFE HEALTH INFORMATION MANAGEMENT SYSTEM PART I: LESSONS LEARNED FROM A DATA ANALYSTS' PERSPECTIVE

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The USAID Emerging Pandemic Threats - PREDICT project is a multi-country endeavour led by the University of California - Davis One Health Institute to develop the global capacity to detect emerging zoonotic diseases of wildlife origin. Standardized data collection of surveillance data and test results from 5 organizations and 20 countries has been an essential aspect of this initiative. The 5-year project is now mid way through the 4th year and data analysis efforts to uncover patterns and trends in the surveillance and test data set are now underway. As in any large dataset, as data increases in volume, complexity and value, the preservation and maintenance of the data, also known as data curation, becomes increasingly important, especially when integrating heterogeneous data sources. As a result of these curation efforts, the Global Animal Information System (GAINS) information management team has gained insight and critical skill sets that could be considered when developing surveillance and test results data collection systems. Some examples of these are: the complexity of working with multiple organizations, countries and languages; developing a common language of database concepts between Information Management personnel and field staff; developing data tools in both connected and non-connected environments; and developing standard animal taxonomy to handle sampling of multiple animal taxa across geographical regions. These challenges have been mitigated with development of standard approaches to data entry and data summaries, including use of controlled vocabularies and existing taxonomic databases, regular data quality checks and reviews, careful analysis, and adaptive management.

93. CHALLENGES OF DEVELOPING A GLOBAL WILDLIFE HEALTH INFORMATION MANAGEMENT SYSTEM PART II: LESSONS LEARNED FROM A WILDLIFE EPIDEMIOLOGIST'S PERSPECTIVE

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There is a positive trend in the wildlife health discipline towards large, interdisciplinary and inter-institution collaborative endeavours, such as the multi-agency West Nile and avian influenza surveillance projects over the last decade. Management of the data derived from these projects presents multiple challenges, from effectively communicating user needs to IT specialists to implementing a data terminology and taxonomy that is sufficiently flexible and comprehensive to capture the data necessary to achieve the project's objectives. PREDICT is a five-year project funded by the United States Agency for International Development and led by the University of California at Davis, with a goal of improving the global capacity to detect emerging viral zoonotic pathogens of wildlife. PREDICT operates in almost 20 countries in Latin America, Central and East Africa, and Asia. In this talk, we discuss the unique data and information management challenges such a large and geographically dispersed project has presented from the non-IT specialist perspective, complementing the IT specialists' perspective. Specifically, we explore the process of bridging the gap between an epidemiologists' in-depth understanding of data content (with a naïve understanding of data management) and a database analysts' broad understanding of data management (but limited knowledge of data content). We feel this oft overlooked exploration is important as we move towards "big data" underpinning increasing portions of our discipline.

94. WHITE-TAILED DEER DEMOGRAPHY IN A HIGH-PREVALENCE CWD-ENDEMIC AREA OF WYOMING

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We examined the effects of chronic wasting disease (CWD) on vital rates and population sustainability in a free-ranging white-tailed deer (*Odocoileus virginianus*) herd in Wyoming. To determine demographic effects of CWD, white-tailed deer were captured, CWD-tested, radio-collared, pregnancy tested, and vital rates were determined for four cohorts in Wyoming annually (2003-2010). We hypothesized CWD impacts populations by lowering survival of CWD-positive deer, lowering the finite rate of growth (λ), and lowering recruitment. We monitored CWD-positive and CWD-negative deer (n = 175) via radio-telemetry and global positioning system (GPS) collars to determine demographic and disease indices, annual survival, and λ . The CWD prevalence was higher in females (42%) than males (28.8%). Pregnancy and recruitment did not differ by CWD-status. Hunter harvest and clinical CWD were the leading causes of mortality and CWD-positive deer were over-represented in harvested deer and total mortalities based on baseline CWD prevalence in population. Survival was lower for CWD-positive deer and they were 4.5 times more likely to die than CWD-negative deer. Based on Cox's proportional hazards model, dispersal was moderately protective against CWD-related mortality. Slope of age-specific CWD incidence was steeper for bucks, but does had higher overall incidence; no CWD-negative deer older than 6.5 years-old acquired CWD. The population model calculated λ at 0.8960. Eliminating female harvest would produce a sustainable population ($\lambda \geq 1.0$). Mortality due to harvest and CWD caused the population age structure to be dominated by fawns, yearlings, and 2.5 years-old deer. It is not known what effects this young age structure will have on long-term population viability.

95. CACTUS BUCKS, TESTICULAR LESIONS, AND EPIZOOTIC HEMORRHAGIC DISEASE IN COLORADO MULE DEER

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Antler abnormalities are occasionally seen in many species of deer and often result from testicular lesions and decreased levels of testosterone, preventing normal cycles of antler growth. Affected bucks have antlers with numerous short, misshapen points (cactus bucks), retained velvet, and failure to shed these abnormal antlers annually. In Colorado, multiple herds of mule deer have recently been observed to have an unexpectedly high (10-20% of bucks) occurrence of cactus bucks, coinciding with a high seroprevalence (nearly 100%) of epizootic hemorrhagic disease virus (serotype EHDV-2). Histologic findings in the testes of these animals include nonspecific end-stage lesions of chronic inflammation, fibrosis, and mineralization. To examine earlier stages of testicular lesions, and to screen for the presence of EHDV in the testes, we sampled 16 mule deer bucks from affected areas during the 2012 fall hunting season. Sampling was targeted for bucks with normal antlers (n=14) or retained velvet only (n=2). Testicular lesions identified included necrotizing vasculitis (n=2), hemorrhage (n=6), edema (n=2), seminiferous tubule necrosis (n=5), orchitis (n=5), epididymitis (n=10), hypospermia (n=6), and end-stage lesions of tubular loss (n=2), fibrosis (n=2), and mineralization (n=2). Of testes with two or fewer of the lesions listed above, one of 11 (9%) was positive for EHDV by RT-qPCR. Of testes with more than two of the lesions listed above, six of six (100%) were positive for EHDV, including testes from both bucks with retained velvet. The vascular lesions found in some of these cases suggest that the pathogenesis of end-stage fibrosis and mineralization may involve a vascular insult. The role of EHDV infection remains uncertain, although our findings suggest an association between testicular lesions and the presence of EHDV RNA in the testis.

96. DIFFERENTIAL MORTALITY AND CLINICAL PATHOLOGY OF SEMI FREE-RANGING MOOSE ASSOCIATED WITH *FASCIOLOIDES MAGNA* IN ELK ISLAND NATIONAL PARK, ALBERTA

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Two distinct moose (*Alces alces*) subpopulations exist within Elk Island National Park, Alberta (north of Highway 16 and south), that have identical habitat but are separated by a four-lane highway and a 1.8 metre high page wire fence. The two subpopulations exhibit markedly divergent historical population growth rates. Ongoing investigation since 1987 indicates giant liver fluke (*Fascioloides magna)* only occurs in the northern subpopulation. Thirty-eight adult female moose (19 north, 19 south) were radio-collared in January 2010 and 2011 to determine cause-specific sources of mortality. Moose from the north had significantly elevated red blood cell indices and eosinophilia, as well as elevated liver enzymes, serum proteins, and urea at capture compared to moose from the south. Mortality rate was significantly higher in the north (37.3 compared to 13.7 per 100 moose-years of risk, p=0.036) and was associated with *F. magna* infection in 64% of north mortalities. Two distinct syndromes were observed in *F. magna* infected moose; an acute toxemic syndrome and a chronic hepatic failure syndrome. No mortality has been associated with *F. magna* in the south to date. Our data provide strong support that the markedly different population trajectories of these two subpopulations is a direct result of giant liver flukes as other mortality causes due to habitat, environmental differences, or diseases do not seem to be involved. Wildlife managers need to seriously consider *F. magna* as a significant source of mortality and morbidity in free-ranging moose populations in North America and Elk Island National Park provides a unique setting for this natural experiment.

97. PREVALENCE AND EFFECTS OF CHRONIC WASTING DISEASE IN ELK FROM ROCKY MOUNTAIN NATIONAL PARK

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Chronic wasting disease (CWD) can have long-term, negative impacts on deer populations, but there is little known about the ecology of CWD in free-ranging elk (*Cervus elaphus*). We measured the efficacy of rectal biopsies to diagnose prion infection and the impact of CWD on elk survival and population growth in Rocky Mountain National Park, Colorado. Sensitivity of rectal biopsy samples increased with follicle count and was maximized at 85% (95% Bayesian credible interval (BCI) = 60, 98). Rectal biopsy test results were similar to brainstem samples, but neither tissue contained prions in the earliest stages of infection that were only detected in retropharyngeal lymph nodes. Minimum prevalence was estimated to be 9.9% (BCI = 5.7, 15.7), but this estimate rose to 12.9% (BCI = 8.0, 19.1) when we included four elk that were likely misdiagnosed at initial capture. Following removal of all known individuals with CWD, the annual survival rate was relatively high during the initial year of the study, but subsequently declined due to increases in CWD-related mortalities (2008 survival = 0.97 [BCI: 0.93, 0.99], 2009 = 0.90 [BCI: 0.83, 0.95], 2010 = 0.85 [BCI: 0.75, 0.93]). Population declines were predicted to occur due almost solely to CWD-caused mortality when prevalence exceeded 13% (BCI = 0, 35) in this population. These results suggest rectal biopsies can be a useful research tool, but can miss elk in the earliest stages of prion infection; and CWD can reduce the survival of adult females and lower the population growth of elk herds.

98. INCORPORATING HUMAN ACTIVITY RISK FACTORS INTO CHRONIC WASTING DISEASE SURVEILLANCE

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Information from the field regarding human-activity disease risk factors is not readily available in the literature and can enhance surveillance in areas of potential disease entry and exposure. Surveillance for chronic wasting disease (CWD) in New York State has been conducted since 2002. In 2005, two captive locations and two wild white-tailed deer tested positive and were linked with taxidermy and deer rehabilitation. We have revised our sample targets to take into account potential risk factors for reintroduction of CWD into New York. Locations of captive cervid farms, taxidermy businesses, and meat processors that may receive deer from out-of-state were identified and mapped; each was given a risk value of 1. New quotas were calculated by 1) population estimates and 2) proportion of cumulative risk locations within the county. Concurrent with the hunting season, we instituted a field survey of 391 taxidermies, 369 processors, and 22 combined operations to gather information on incoming deer parameters, disposal of parts, and to distribute informational material. We worked with NYS Department of Agriculture and Markets to collect information on captive cervid farms from a questionnaire completed by their field veterinarians, which included species, importation, disposal, fence quality, and additional businesses involving cervids. Importation of captive cervids increased over the last 5 years. Out-of-state deer carcasses going to processors or taxidermists comprised less than 5% of the total business. Half of these businesses disposed of carcasses and parts in landfills, the remainder used rendering (25%), composting, and pits. We will use this information to refine and inform New York's CWD surveillance and response plans by apportioning more sampling to areas that greater density of high risk activities.

99. IMPROVING HUNTER HARVEST AS A TOOL FOR CWD MANAGEMENT

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Hunter harvest remains the primary tool available to wildlife agencies that struggle to contain or reduce the spread of CWD in wild deer populations. Alberta began surveillance for CWD in 1998 and detected it in 2005. In our landscapes CWD currently is in the order of 10x more likely to occur in mule deer than white-tailed deer, 2x more likely to occur in males than females, and it has an increased occurrence among related individuals and within contiguous riparian areas. Transmission seems to be facilitated by increased size and duration of winter mule deer populations, and within female-dominated social groups. Theoretical models identified plausible mechanisms that could result in male-biased CWD prevalence including: (1) higher susceptibility in males, (2) higher environmental transmission due to higher exposure, (3) higher transmission within male groups, and (4) higher rate of transmission from females to males than males to females. All four mechanisms represent frequency-dependent transmission. This presentation reviews the surveillance, management, and research data to date and proposes a long-term harvest management experiment targeting mule deer older males, younger males, or female groups for increased harvest in enzootic areas as likely to have the greatest effect on subsequent transmission. The proposed experimental outline is designed to focus on perceived drivers of natural transmission in prairie and parkland habitats recently invaded by CWD.

100. THREATS TO THE SURVIVAL OF CALIFORNIA CONDORS: IMPACTS OF HUMAN DISTURBANCE ON A CRITICALLY ENDANGERED SCAVENGER

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Investigations into factors threatening survival of endangered species populations and the effects of mitigation directed at species conservation are often limited by a lack of data, yet this insight is crucial for directing monitoring and conservation efforts. Our investigation, made possible by intensive and collaborative field monitoring efforts combined with epidemiologic analyses, provides critical insight into threats to survival and conservation of the California condor, a once extirpated species now struggling to recover a self-sustaining population. Our preliminary results show that average annual mortality rates for the population over the past 20 years exceeded levels necessary for recovery of a naturally sustainable population. Furthermore, only 50% of condors survived to an age at which they generally reproduce in the wild. Therefore even with intensive management, survivorship has been too low for recovery, and continued releases from the captive breeding program are necessary to sustain the condor population. Despite lead ammunition regulations within the condor range, lead poisoning from ingestion of spent lead ammunition in carrion remains a leading cause of death, accounting for the highest proportion of adult mortality, and the most significant challenge to recovery. Utility line collision and wildfire were also important mortality factors, and although potentially less formidable, present potential long-term threats to the population with increasing development, energy demands, and climate change. Given the increasing recognition of worldwide declines of scavenging bird populations, the approaches used here have broad application for investigating factors influencing survival in vulnerable populations for which reasons of decline are poorly understood.

101. WHICH FACTORS DRIVE TUBERCULOSIS TRANSMISSION? IDENTIFYING SUPER-SHEDDERS IN WILD BOAR POPULATIONS

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Infected host individuals that excrete more organisms of a given pathogen than others are known as super-shedders. Super-shedders (S-S) are important drivers of infection maintenance within populations, and are important targets for disease control. Regarding tuberculosis (TB), those individuals with more disseminated disease involving the lung are likely S-S. We hypothesized that the distribution of S-S within a naturally TB infected host population would depend on specific risk factors. We studied 472 hunter-harvested Eurasian wild boar (*Sus scrofa*) in Toledo (Spain), the wildlife population with the highest known *Mycobacterium tuberculosis* complex MTC infection prevalence (56%). TB status was assessed through culture and pathology scoring. Data on individual (sex, age, body condition) and population risk factors (abundance, management, TB prevalence) were analyzed by GzLMM. Based on the pathology score we defined S-S as those individuals with more disseminated disease involving the lung (9.4%). None of the factors analyzed had a significant effect on S-S. We defined the characteristics of S-S and analyzed their distribution. The characterization of S-S is of paramount importance in TB epidemiology and particularly for assessing the success of ongoing vaccination trials. We expected to find more S-S among individuals presenting certain TB risk factors, such as a poor condition or those living at higher densities or in high-prevalence sites. However, contrary to our expectations, S-S were homogeneously distributed among the population. This opens new avenues for research including other possible factors such as strain pathogenicity and host resistance. Acknowledgements: EU FP7 grant 278976 ANTIGONE and Plan Nacional grant AGL2011-30041.

102. PHYLOGENETIC ANALYSIS, AND QUANTITATIVE PCR SURVEILLANCE OF A NOVEL HERPESVIRUS OF NORTHERN FUR SEALS (*Callorhinus ursinus*) RELATED TO THE CARCINOMA-ASSOCIATED OTARINE HV1

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Herpesviruses are large, enveloped, double stranded DNA viruses with high host fidelity. In marine mammals, at least 19 herpesviruses have been characterized with partial polymerase sequences. Three have been reported from otariids: Otarine Herpesvirus 1 (OtHV1) is strongly associated with urogenital carcinoma in California sea lions (CSL*, Zalophus californianus*), and is a major cause of mortality in some populations; OtHV2 was identified from an ocular swab of a CSL with conjunctivitis, and OtHV3 was found in 30.7% of CSL samples surveyed. We report a new Otarine herpesvirus found in Northern Fur seals (NFS, *Callorhinus ursinus*), here termed OtHV4. This virus was initially found in a vaginal swab of a female NFS in 2011. We obtained partial sequences of the polymerase gene and the glycoprotein B gene using established protocols. OtHV4 is closely related to OtHV1 (95-97% of similarity at protein level). There are reports of breeding between CSLs and NFSs8, and this may represent a host jump. Alternatively, these viruses may have codiverged with their hosts. We developed qPCR assays to determine the prevalence of OtHV4 in NFSs. OtHV4 has not been associated with urogenital carcinoma. qPCR results, confirmed with specific PCR and sequencing, show that a healthy population of NFS has a OtHV4 prevalence of 21%. Future comparative genomics of OtHV1 and OtHV4 may identify candidate oncogenic genes. OtHV4 may have utility as a potential vaccine to prevent OtHV1 infection.

103. HOST UNGULATE RICHNESS INCREASES TUBERCULOSIS RISK IN SOUTH SPAIN

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Life history affects pathogen virulence, transmissibility and specificity as well as host defenses and life strategies, which can determine whether richer assemblages of hosts increases or decreases disease risk. We used the presence of pulmonary TB to measure species and community competence in 45 wild ungulate (1752 wild boar *Sus scrofa*, 1910 red deer *Cervus elaphus*, and 329 fallow deer *Dama dama*) and extensive cattle populations (1309 individuals) in Southern Spain, with species richness ranging from 1 to 4. We found a 49% increase in community competence for TB in richer assemblages, and this was not attributable to changes in the abundance of the most competent hosts. While highlighting the benefit of a community-based approach to study infectious diseases, our findings illustrate that increases in biodiversity do not necessarily reduce disease risk. Much of the infection patterns of microparasites such as mycobacteria causing TB are determined by their ability to multiply directly within the host, regardless of the host life history traits, so a possible explanation is that a mass-action mode of transmission would benefit from increased niches offered by higher host diversity, resulting also in increased and more diverse networks of direct and indirect contacts (trophic relationships and host aggregation). These facts may apply specially for multi-host pathogens such as mycobacteria that also persist in the environment. We therefore must consider both natural variations in life histories of pathogens and host communities to characterize the impact of biodiversity conservation on human and animal health.

104. SIMULATING THE POPULATION IMPACT OF CANINE DISTEMPER VIRUS ON AMUR TIGERS (*PANTHERA TIGRIS ALTAICA*) IN RUSSIA

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Lethal infections with canine distemper virus (CDV) have recently been diagnosed in Amur tigers (*Panthera tigris altaica*), but the implications for the population have not been determined. The objective of this study was to assess the impact of CDV on the growth and persistence of a key tiger population in Sikhote-Alin Biosphere Zapovednik (SABZ). An individual-based stochastic, SIRD model was used to simulate infection through predation of infected domestic dogs and/or wild carnivores, and intraspecific transmission through tiger-to-tiger interaction. Simulations were based on scenarios where prevalence of CDV in predated carnivores remained constant, or fluctuated on 3, 5 and 7 year cycles. CDV prevalence and effective contact based on published and observed data was used to define plausible low and high-risk infection scenarios. CDV infection increased the 50-year extinction probability of tigers in SABZ by 2.1% (low risk) to 64.3% (high risk) compared to a control population without CDV. Simulations that adjusted duration of infectious period, or included epizootic infection waves had little or no additional impact. The study findings demonstrate that where tigers coexist and interact with other carnivores, multi-host pathogens such as CDV have the potential to reduce population growth and increase extinction probability.

105. DEAD OR ALIVE: ANIMAL SAMPLING DURING EBOLA HEMORRHAGIC FEVER OUTBREAKS IN HUMANS

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There are currently no widely accepted animal surveillance guidelines for human Ebola hemorrhagic fever (EHF) outbreak investigations to identify potential sources of Ebolavirus (EBOV) spillover into humans and other animals. Animal field surveillance during and following an outbreak has several purposes, from helping identify the specific animal source of a human case to guiding control activities by describing the spatial and temporal distribution of wild circulating EBOV, informing public health efforts, and contributing to broader EHF research questions. Using field surveillance data associated with EHF outbreaks, this review provides guidance on animal sampling for resource-limited outbreak situations, target species, and, in some cases, which diagnostics should be prioritized to rapidly assess the presence of EBOV in animal reservoirs. In brief, EBOV detection was 32.7% (18/55) for animals found dead and 0.2% (13/5309) for live captured animals. Our review indicates that for the purposes of identifying potential sources of transmission from animals to humans and isolating the suspected virus in an animal in outbreak situations, (1) surveillance of free-ranging non-human primate mortality and morbidity should be a priority, (2) any wildlife morbidity or mortality events should be investigated and may hold the most promise for locating virus or viral genome sequences, (3) surveillance of selected bat species is worthwhile to isolate and detect evidence of exposure even in the absence of clinical disease, and (4) morbidity, mortality, and serological studies of domestic animals should prioritize dogs and pigs and include testing for virus and previous exposure.

106. LACK OF *BATROCHOCHYTRIUM DENDROBATIDIS* AND RANAVIRUS INFECTIONS IN CANE TOADS (*RHINELLA MARINA*) FROM GUANACASTE COSTA RICA

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Worldwide, populations of amphibians are declining. Two pathogens, *Batrochochytrium dendrobatidis* (*Bd*) and ranaviruses (Rv), have caused extensive declines, and even extinctions in the case of *Bd*. The cane toad, *Rhinella marina*, is considered to be an asymptomatic reservoir of *Bd*, but susceptibility of this species to Rv is unknown. Because the cane toad is a successful worldwide invader, it could play an important role in the transmission of these and other pathogens; therefore, it is critical for amphibian conservation to understand the prevalence of these pathogens in cane toad populations. As part of a larger project to evaluate cane toad population health within artificial wetlands in the Guanacaste province of Costa Rica, we tested skin swabs (n=102) for *Bd* and liver (n=84) for Rv using PCR assays. All samples were negative. Failure to detect *Bd* at these field sites is likely due to climate as Guanacaste is in the lowlands whereas *Bd* infections in Costa Rica have been in cooler highlands. Ranaviruses have only recently been reported in Costa Rican amphibians at La Selva Biological Station, but not from cane toads. Further research is needed to determine environmental factors associated with transmission of *Bd*/Rv to cane toads, their reservoir potential, and pathogenicity of Rv for cane toads. Finally, it is critical to understand how the prevalence of *Bd*/Rv differs in their native and invasive ranges as they are reported in cane toads in their invasive range, and especially because few studies have investigated these pathogens within the native range.

107. ZOONOSIS AND SOCIETAL PERCEPTION OF WILDLIFE – A SWEDISH PERSPECTIVE

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As much as 60% of emerging infectious diseases has a zoonotic origin, of which a majority originate from wildlife. In addition, there seem to be a trend of steadily increasing number of incidences. Consequently, there is an increased public and scientific attention given to zoonotic diseases emerging from wildlife populations. Although justified from a public health perspective, one potential outcome of this is an increased awareness and fright of wildlife, in particular those in close vicinity to urban areas, houses and farms. There is also an aspect of short-term interest in acquiring grants for all-so-well-motivated scientific efforts with regard to zoonotic potential. Thus, a trade-off between public health, research funding, and induced detachment between man and nature emerge. In Sweden, we have a legal right of common access, “Legal Right of Access to Private Land”, which enables people to freely explore non-populated nature areas and also pick wild berries and mushrooms. This legal right, in association with an overall sparsely populated country, has most likely contributed to a strong societal interest and passion for nature and wildlife. Here, we address how an increased media, scientific, and overall societal focus on, in particular, zoonotic diseases affect this relationship. We also ask if this focus affects the overall incitement for preserving biological diversity and may shift the fundamental baseline for societal perception of wildlife. The implications of such a ‘shifting baseline’ is discussed based on results from regular enquires conducted to monitor societal perception of, and opinion about, wildlife populations.

108. LONG-TERM EFFECTS OF CAPTURE AND HANDLING: AN ISSUE FOR WILDLIFE RESEARCH, MANAGEMENT AND CONSERVATION THAT SHOULD NOT BE IGNORED

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Evidence of long-term harmful effects of capture and handling are being increasingly reported in the peer-reviewed wildlife literature. Although advances in radio-telemetry, data analysis techniques, and animal health diagnostics are likely influencing this trend, changes in attitude concerning the resiliency of wild animals to human intervention in their life histories may also be a causative factor. Long-term effects have been described in all classes of vertebrates and, while specific effects may vary from one animal to the next, they are generally categorized as behavioral, physiological, or a combination of the two in reference to the types of effects on individual animals. However, these effects are not only limited to individual animals, but may also manifest at the population level as reduced survival and reproductive output. Beyond citing supporting examples, I will place emphasis in this presentation toward discussing the significance of long-term capture and handling effects. Aside obvious ethical and animal welfare considerations, the implications of long-term effects may be broader. In the context of wildlife research, study results and interpretations may be unknowingly biased. In the context of wildlife management, actions directed toward conservation or recovery may prove more harmful than beneficial to the target population or species. It is unlikely that capture and handling will always result in long-term harmful effects, but the fact that it sometimes does should prompt wildlife professionals to both monitor for, and take actions to prevent or minimize, long-term effects.

109. STRESS AND PAIN MANAGEMENT IN WILDLIFE-THE NEW FRONTIER FOR WILDLIFE PROFESSIONALS

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Increasing levels of intensive management and research in wildlife has resulted in these species being subjected to more invasive surgical procedures for implantation of physiological monitoring devices plus more capture and translocation programs to accomplish management goals. Twenty years ago, stress management was never a topic of discussion in the wildlife community until there was a disastrous mortality event after a translocation. Today, every capture and post-capture mortality is examined. Two pivotal studies of the impact of managing pre-immobilization stress on hyperthermia in impala (*Aepyceros melampus*) have revolutionized thinking about handling of hoof stock prior to any immobilization or capture. These studies document the importance of either habituation or limiting fright response in the pre-darting environment to minimize hyperthermia-the major cause of mortality in capture events. Additionally, field experience in South Africa has indicated the advantages of using long acting neuroleptics to moderate the stress of transportation. Neuroleptics such as haloperidol, zuclopenthixol, and trilafon have been used in South Africa for years to reduce mortalities in transport; however, these are only recently available in the United States. Experiential field use indicates that haloperidol will reduce transport mortalities in species such as pronghorn (*Antilocapra americana*).

Like stress, pain management was never discussed in wildlife management circles but with the advances in pain management in domestic species, this topic must now come to the table. Currently and in the future, animal care and use committee's will demand that this subject as well as stress must be addressed in research protocols. Fortunately, we can utilize some of these advances in wildlife. Current pain management protocols utilizing pharmaceuticals such as fentanyl, butorphanol, buprenorphine, and meloxicam may be applicable to many of the species in wildlife research. Some of these pharmaceuticals are now used in a sustained release form that allows dosing every 48-72 hours.

110. WILDLIFE CAPTURE – AN ASSESSMENT AND RE-VISIONING OF THE PROCESS

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The capture of wild animals is an old science with many tricks of the trade. Improvements have occurred utilizing new formulations and combinations of drugs and equipment used for immobilization, monitoring and supportive care; however, there continues to be morbidity and mortality associated with free-ranging wildlife capture.

Capture records for moose (n=117), elk (n=309) and wolves (n=499) from the Idaho Department of Fish and Game and the Nevada Department of Wildlife for bighorn sheep (n=402) for both net-gun capture and field anesthesia were reviewed. Capture methods used by both states consisted of techniques that are also utilized by most wildlife management agencies in the western US and included aerial darting, ground darting, trapping, and helicopter net gun.

Injuries (n=63) during field immobilizations and net gun captures are primarily associated with trauma either from falls or the darts with the exception of injuries associated with foot hold traps (n=172). Mortalities (n=10) for both methods were secondary to severe trauma, drowning or secondary to hyperthermia or respiratory arrest. Recorded physiologic changes encountered with both capture methods included hyperthermia, hypoxemia and severe lactic acidosis. In general, a greater incidence of morbidity and mortality occurred during capture events that involved an aerial chase.

From the alternative livestock and domestic animal literature, it has been determined that species, individual genetics, herd dominance, sex, age, and human habituation, can all affect the level of psychological stress or fear in an animal and that fear can cause physiologic changes such as hyperthermia and lactic acidosis. We challenge wildlife professionals to incorporate this information into their planning as the next step, in the evolution of the science of wildlife capture and handling.

111. CAPTURE-RELATED MORTALITIES IN BROWN BEARS (*URSUS ARCTOS*) IN SCANDINAVIA 1984-2013: A REVIEW OF 1,824 CAPTURES

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The Scandinavian Brown Bear Research Project conducted a total of 1,824 brown bear (*Ursus arctos*) captures from 1984 through February 2013. Capture-related mortality rates during the capture event and during a 30-day post capture period were 0.8 % (n=14) and 0.1 % (n=2), respectively. From 1984 through 1991, bears were immobilized from a helicopter with either etorphine or medetomidine-ketamine and seven capture-related deaths (3.4 %) occurred in 174 captures. Six of these deaths occurred when bears were immobilized with etorphine: three due to stress, hyperthermia and/or respiratory depression (one of these animals had only one functional lung), two due to drowning, and one due to dart trauma (pneumothorax). In addition, one bear immobilized with medetomidine-ketamine was shot for human protection after a spontaneous recovery from anesthesia. From 1992 through 2012, a total of 1,625 captures were carried out from a helicopter with medetomidine-tiletamine-zolazepam (MTZ). Seven bears (0.4 %) died during the capture event using this protocol: three because of shock/circulatory failure, two due to drowning, and two due to dart trauma (penetration of the thoracic cavity). Two bears (0.1 %) died during the 30-day post capture period: one due to unknown causes after three days and one due to wound dehiscence 14 days after surgical implantation of an intraperitoneal radiotransmitter. We also conducted 25 captures of hibernating subadults during February-March in 2010-2013 with no mortality, using a modified anesthetic protocol based on medetomidine-ketamine-tiletamine-zolazepam (MKTZ). We recommend the current protocols for capture of denning (MKTZ) and non-denning (MTZ) brown bears.

112. TASER ELECTRONIC CONTROL DEVICE USE FOR WILDLIFE MANAGEMENT

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In some situations, the use of standard techniques to restrain wildlife (e.g. chemical immobilization) or modify their behavior (e.g. hazing with beanbag or rubber projectile, or noisemaker rounds fired from 12GA shotgun), may not be practicable or desirable. Wildlife managers need additional, safe methods provide short term (<1 minute) restraint of animals to allow manipulation (e.g. release from entanglements) as well as more effective hazing. We evaluated the impact and risk of capture myopathy with ECD application on moose compared with a 3 cc Cap-chur explosive dart delivery of chemical capture agents. Body temperature, salivary cortisol, as well as selected blood parameters were used as potential predictors of indicators of trauma, organ damage, or increased risk of capture myopathy. Behavioral responses to ECD and the associated painful stimulus included an immediate flight response after application and a prolonged aversion to human presence. Mean cortisol and lactate concentrations were 3 to 5 times higher with ECD compared to darting but there was no significant difference in body temperature and other parameters. Although we could detect a brief, elevated stress responses greater than with darted, we concluded that a short (<1 minute) application ECD was not more likely to induce capture myopathy than darting. While both darting and ECD are painful (the later only during application), the escape/flight behavior and prolonged aversion to human presence to ECD indicates the potential use of this technique as an alternative to destruction of animals that have become food conditioned and/or dangerous to the public.

113. WILDLIFE EUTHANSIA

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The euthanasia of animals is needed in some instances when handling or capturing wildlife. There are numerous considerations presented when dealing with free-ranging wildlife with regard to euthanasia and selection of appropriate methods to use. The American Veterinary Medical Association published the 2013 version of its Euthanasia Guidelines. Numerous groups including the American Association of Wildlife Veterinarians, the American Association of Zoo Veterinarians, the Association of Avian Veterinarians, The Wildlife Society, and others contributed to the guidelines as they pertain to free-ranging wildlife. The AVMA guidelines and similar ones published by the American Association of Zoo Veterinarians provide an exhaustive summary of euthanasia for wildlife species. These details will be summarized for this presentation for both the context and appropriate methods of euthanasia in free-ranging wildlife.

114. NEW DEVELOPMENTS IN BIO-LOGGING TECHNIQUES: PHYSIOLOGICAL SENSORS WITH A MORTALITY ALERT

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Biologging techniques are becoming integral to wildlife ecology, research and management. Here we report an implant designed to send temperature and heart rate data through the cell phone network or via satellite. This device includes an acceleration and temperature sensor. The acceleration sensor detects movement from the heart, and when inserted in the reticulum of ruminants, calculates heartbeat. In 2012 and 2013, we inserted this device into the reticulum of 48 moose*, Alces alces* and the peritoneal cavity of five brown bears, *Ursus arctos*. They were programmed to record body temperature and heart rate every 5 minutes, and send, with GPS positions, to a central database. In six moose, the implants were eructated shortly after insertion, one of these was irreparably damaged, four were lost and one was functioning and redeployed. Nine of 48 sensors in moose malfunctioned and only sent temperature data. In bears, implants were sterilized using ethylene oxide gas. One bear and two moose have died, and all collars sent mortality alerts by text messaging. This device allowed for collection of real-time physiological data including heart rate, body temperature, activity and movement. This data was used to determine normal body temperature ranges and to evaluate effects of capture, disturbance, hunting and seasonality on body temperature. This device also allows predation and mortality projects to arrive at a carcass while determining the cause of death is still possible and to determine if animals had an elevated temperature at the time of death, indicting stress, predation, inflammation or infection.

115. APPLIED VETERINARY MEDICINE AS A CONSERVATION TOOL FOR WESTERN LOWLAND GORILLAS (*GORILLA GORILLA*)

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Applied veterinary medicine can be a valuable tool in conservation efforts with wildlife and especially for endangered species. There are increasing examples across the globe where veterinarians have played integral roles in helping to sustain and conserve wildlife at both the individual and population levels. For different reasons and under different scenarios pro-active involvement of veterinarians and applied in-situ veterinary care and interventions with wildlife are sometimes welcomed, and sometimes rejected. There are complex reasons for this relationship, some based on subjective feelings and dogmatic approaches, some based on objective science and risk assessments. All these issues pertain to recent successful efforts to increase veterinary involvement, research and applied veterinary medicine to free-ranging, human-habituated western lowland gorillas (*Gorilla gorilla*) in the Central African Republic (CAR). A partnership between multiple conservation institutions, individuals, and other local and global stakeholders has led to significant strides in applied veterinary medicine for this critically endangered species. Successful campaigns to deliver preventative medicine in the form of vaccinations, to treat a serious infectious disease outbreak, and to save an individual gorilla from a life threatening ensnarement have all been accomplished in the past two years. These activities and interventions and their integration into the comprehensive gorilla conservation efforts in CAR will be the focus of this presentation.

116. PHYSIOLOGICAL EVALUATION OF MEDETOMIDINE-KETAMINE ANESTHESIA IN FREE-RANGING SVALBARD (*RANGIFER TARANDUS PLATYRHYNCHUS*) AND WILD NORWEGIAN REINDEER (*R. T. TARANDUS*)

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Previously published studies indicated that combinations of medetomidine and ketamine were effective for both Svalbard (*Rangifer tarandus platyrhynchus*) and wild Norwegian reindeer (*R. t. tarandus*). Both previous studies indicated that reindeer were hypoxemic, based on pulse-oximetry. We conducted a physiological evaluation of these two protocols using arterial blood-gasses. Medetomidine (10 mg) and ketamine (200mg) were administered by dart from the ground in Svalbard reindeer (October 2010) and from a helicopter for wild reindeer (March 2012). Of tested animals, all seven wild reindeer and five of seven Svalbard reindeer were hypoxemic before oxygen administration. Nasal oxygen insufflation (1 L/min for 5 Svalbard reindeer and 1 wild reindeer and 2 L/min for 4 Wild reindeer) corrected hypoxemia in all cases evaluated. For reversal, all animals received 5 mg atipamezole per mg medetomidine, intramuscularly.

SP1. PILOTING A TOOL FOR ASSESSING PUBLIC HEALTH RISKS FROM THE IMPORTATION OF WILDLIFE INTO THE UNITED STATES: THE CASE OF RODENT IMPORTATION FROM LATIN AMERICA

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An inherent risk of the wildlife trade – both formal and informal – is the risk of disease introduction and/or emergence into the United States. Numerous proposals have aimed to prevent or control this risk by banning importation of select species or by creating 'white lists' of species that are cleared for importation. These approaches could cause economic harm to certain private sectors, such as the pet industry, and would potentially place substantial burden on importers to provide proof of low risk for importation of individual species. Thus, there is a need for creation of an unbiased, scientifically-based, risk assessment tool that can be easily implemented by governmental agencies, NGOs and industry, in order to inform these critical policy and import decisions. As a feasibility study, we built a risk analysis framework following the general OIE guidelines and applied it to a specific group of animals (rodents), a specific geographical location of origin (Latin America), and a specific outcome (risk of zoonoses entering the United States). This subset was chosen for the pilot given the lack of any health requirements for rodents coming into the United States from South America and potentially the small number of traded species and zoonotic diseases to identify. This framework will be expanded to other taxa and geographic locations to ultimately inform policy.

SP2. SOCIO-ECONOMIC AND POLITICAL ASPECTS OF SPENT LEAD AMMUNITION

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Lead has been known to be toxic for humans and wildlife for thousands of years. Although lead shot was banned for waterfowl hunting on federal lands and on most state-owned hunting lands in the United States in 1991, lead ammunition is still used for hunting deer and other cervids, small game and upland birds. There is scientific evidence of the connection between lead intoxication in eagles and deer hunting in the Midwest, but any attempt to raise awareness of this issue has historically caused a negative response among the hunting shooting sports. An interdisciplinary team of experts met in 2012 to analyze this issue from different perspectives (economic, policy, epidemiology, public health, conservation, social, and cultural). Using a bottom-up approach, this team organized an event at an outdoor sporting goods retailer to create awareness about lead intoxication in eagles among the hunting community and discuss non-toxic ammunition alternatives. Although the event was carefully planned, an inaccurate media headline resulted in the event being significantly altered. Despite the disappointing outcome of the event, there has been huge progress on the issue of lead intoxication by using a holistic bottom-up approach. In addition, important lessons were learned about messaging and transparency in the communication with all stakeholders. Thanks to these initiatives, there is ongoing work with the goal of solving the issue of lead intoxication in wildlife.

SP3. WEIGHTS, HEMATOLOGY AND PLASMATIC CHEMISTRY OF 33 FREE-RANGING *Phaeton* TROPICAL SEABIRDS

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Red-billed tropicbirds (*Phaeton aethereus*) and white-tailed tropicbirds (*Phaeton lepturus*) are pelagic avian species found in tropical and sub-tropical seas. They breed in loose colonies, nesting in rocky crevices, cliffs or on the ground behind bushes at oceanic islands. No regular migration is undertaken, although individuals can undergo extensive dispersal out to sea for foraging purpose. Twenty-nine red-billed and four white-tailed tropicbirds that were reproducing at Santa Bárbara Island (Abrolhos Marine National Park, 17°20’ to 18°10’ South and 38°35’ to 39°20’ West, 65km away from the coast) in March 2013 were handled and examined. Hematological values were taken for clinical research on their health status. Data of mean, minimum, maximum and standard deviation values for weight, total red blood cells count, total and differential white blood cells counts, hematocrit, hemoglobin, mean corpuscular volume, mean corpuscular hemoglobin concentration and plasma concentration of total protein, albumin, uric acid and urea were analyzed. Baseline hematologic and plasma biochemical ranges were established, which may be useful as reference values for the species and/or clinicians working with these birds on the field or rehabilitation centers. We are grateful to the Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq), IBAMA and Abrolhos Marine National Park.

SP4. SURVEILLANCE FOR LYMPHOPROLIFERATIVE DISEASE VIRUS IN HUNTER-KILLED WILD TURKEYS (*Meleagris gallopavo*)

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Historically, the oncogenic avian retrovirus lymphoproliferative disease virus (LPDV) has been considered a poultry pathogen of minor importance with sporadic outbreaks in domestic turkeys in Europe and Israel. However, in 2009, LPDV was first detected in three Eastern wild turkeys (*Meleagris gallopavo*) with evidence of lymphotumoral disease. Subsequent testing of Eastern wild turkey diagnostic cases identified LPDV proviral DNA in clinically-ill turkeys from multiple eastern US states. In order to better understand the epidemiology of LPDV in wild turkeys, asymptomatic hunter-killed wild turkeys were tested for evidence of LPDV proviral DNA using primers targeting the gag gene. Based on sample availability, liver samples were tested from South Carolina, West Virginia, and Missouri and bone marrow from New York and New Jersey. Results of this testing indicate a high prevalence of LPDV proviral DNA in all states: SC 33/68 (49%), WV 21/42 (50%), NY 71/157 (45%), MO 8/33 (24%), NJ 13/35 (37%). Additional testing is currently underway to determine detection probability for different tissue types (liver, bone marrow, and spleen) in asymptomatic hunter-killed turkeys. These preliminary data suggest LPDV is widespread among apparently asymptomatic Eastern wild turkeys and provide insight for understanding the natural history of this virus, estimating potential risks for spill-over into domestic turkeys, and interpreting diagnostic results. In regards to the latter, although LPDV proviral DNA is present in a high proportion of Eastern wild turkeys, clinical disease (i.e. neoplasia) is uncommon.

SP5. MORPHOLOGICAL AND MOLECULAR CHARACTERIZATION OF HEMATOZOAN PARASITES OF AMERICAN BLACK DUCKS (*Anas rubripes*) IN THE EASTERN UNITED STATES.

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Avian hematozoan parasites have a near worldwide distribution, and although are frequently identified in dabbling ducks, molecular characterization of parasites from ducks is limited. For example, prevalences in the American black duck (ABDU) are high (>20%), but no hematozoa have been genetically characterized. In the current study, we aim to investigate the prevalence and genetic diversity of hematozoa in ABDU by combining partial cytochrome b sequences with morphological data from thin blood smear analysis. In 2010 we collected blood samples from 199 ABDU from January-February in six states, Connecticut (n=20), Maine (n=38), Maryland (n=43), Ohio (n=5), Rhode Island (n=5), and Virginia (n=5) and August from Maine (n=83). Two PCR assays were run for three hematozoan genera of interest. A total of 153 (77%) and 109 (55%) were positive for *Haemoproteus*/*Plasmodium* and *Leucocytozoon*, respectively. A subset of positive samples was sequenced and phylogenetic analysis of 41 *Haemoproteus*, 31 *Leucocytozoon*, and one *Plasmodium* revealed two monophyletic groups of *Haemoproteus* and extensive genetic variation among the *Leucocytozoon*. One *Haemoproteus* group, morphologically identified as *H. nettionis*, included most sequences (n=38) and two other *Haemoproteus* spp. from waterfowl while the other group, morphologically identified as *H. greineri*, included three sequences. Despite extensive variation among the *Leucocytozoon* sequences, all grouped into three monophyletic clades of other *Leucocytozoon* associated with waterfowl and were morphologically similar to *L. simondi*. However, because of high genetic variation, careful morphological examination may reveal that *L. simondi* is a species-complex. Further research is needed to carefully examine morphological characteristics among *Leucocytozoon* spp.

SP6. THE ROLE OF PASSERINES AND OTHER TERRESTRIAL BIRDS IN AVIAN INFLUENZA VIRUS EPIDEMIOLOGY

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Although passerines and peridomestic birds have been involved in influenza A virus (IAV) poultry outbreaks, there is little historic evidence for their involvement as reservoirs. However, recent reports of IAV detection by polymerase chain reaction (PCR) have challenged this paradigm and suggested additional research into the role of passerines as IAV hosts is warranted. To address this, we reviewed the published literature on IAV for 829 passerines and other terrestrial birds and conducted surveillance for IAV in 100 terrestrial avian species. In total, 3,868 serum samples and 901 swab samples were collected from four states, including Georgia, New Jersey, Delaware, and Minnesota. Of these, 310 of the Minnesota samples were collected on two domestic poultry farms that had recently experienced a H7N9 low pathogenic IAV outbreak. Serologic testing was performed with a commercial blocking ELISA (bELISA), and swab samples were tested using real-time reverse transcriptase polymerase chain reaction assay (RRT-PCR) and virus isolation in chicken eggs. Antibodies to IAV were detected in 4/3,868 serum samples (0.1%), including a Baltimore oriole (*Icterus galbula*), American robin (*Turdus migratorius*), American redstart (*Setophaga ruticilla*) and European starling (*Sturnus vulgaris*), all from Minnesota. The seropositive starling was the only bird sampled on the poultry farm that was seropositive, and H7 subtype hemagglutinin inhibition testing was negative. All 901 swab samples were virus isolation and RRT-PCR negative. Data from the literature review and prospective study provide no evidence to suggest that passerines or other terrestrial birds are important in IAV natural history.

SP7. HEMOPARASITE INFECTION AFFECTS WHITE BLOOD CELL PROFILES IN SONGBIRDS DURING FALL MIGRATION

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Migration is an energetically expensive life stage for many animals, including migratory songbirds. While much is known about the nature of bird migration, energetic investment into different physiological processes during migration is not well understood. During migration, birds may need to make trade-offs in allocating energy resources to different physiological functions like fat accumulation, which is important for successful migration, and disease defense. Here, we evaluate whether or not three species of long-distance migratory songbirds undergo trade-offs between infection with a blood parasite (*Haemoproteus* or *Plasmodium*) and fat accumulation, stress levels or immune condition. Birds were trapped at a stopover site in coastal Georgia during the peak of migration and blood samples obtained for analyses of hemoparasites and white blood cell counts. There was no detectable trade-off between infection with blood parasites and fat load or stress levels, which we estimated from counts of two white blood cells that co-vary with stress hormones (heterophils and lymphocytes). There was an increased level of immune investment (measured by total white blood cell count) in birds that are infected with hemoparasites, and this heightened immune investment may itself be costly during the migratory phase. Moreover, since prior studies conducted during non-migratory periods generally do not show immune responses to hemoparasites, our results emphasize how the energetic demands of long-distance migration can magnify effects of otherwise benign infections.

SP8. *OXYSPIRURA PETROWI* IN QUAIL FROM SOUTH TEXAS AND THE ROLLING PLAINS

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The northern bobwhite (*Colinus virginianus*) has experienced long-term population declines across their range, which has led to interest in studying parasites and diseases and their potential roles in these declines. *Oxyspirura petrowi* is an indirect lifecycle nematode found under the nictitating membrane and within the conjunctival sacs and nasolacrimal ducts of various gallinaceous birds. Recent observations suggest that *O. petrowi* infections in the northern bobwhite may negatively affect vision, supporting the hypothesis that this helminth parasite may reduce individual fitness within bobwhites. Historically, much of what is known about *O. petrowi* infections in northern bobwhites within Texas comes from the Rolling Plains, whereas little is known about the occurrence of this parasite in South Texas. Scaled quail (*Callipepla squamata*) in South Texas have never been surveyed for *O. petrowi*. The objective was to determine prevalence, intensity, and abundance of *O. petrowi* in northern bobwhites and scaled quail from South Texas and northern bobwhites from the Rolling Plains of Texas and western Oklahoma using hunter-shot samples collected in the winter 2012–2013. Findings are discussed in this presentation. Our research provides additional information about *O. petrowi* in northern bobwhites occurring in South Texas and the Rolling Plains eco-region, and some of the first data on *O. petrowi* infections in scaled quail from South Texas.

SP9. BIOGEOGRAPHY OF TRANSMISSION DYNAMICS FOR A VECTOR-BORNE PATHOGEN RECENTLY FOUND IN ARCTIC-BREEDING SHOREBIRDS

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Globally, shorebirds are declining at a precipitous rate; however the exact causes are unclear and likely complex. Recent evidence suggests that extinction risk is linked to migrations routes, and their extent of habitat loss and degradation. The change in land use patterns and degradation has been implicated in the rise of infectious diseases, which in turn increases the pathogen reservoir pool and provides novel routes of cross species transmission. Pathogen load may therefore be increased in shorebird species whose migration or wintering sites are undergoing anthropogenic changes, contributing to the process of population decline. Furthermore, shorebirds can be vectors of infectious disease and contribute to pandemic outbreaks. We screened 419 shorebird samples from the Arctic using PCR and found 10 (2.39%) positive for haematozoa. Although prevalence was variable across species, we did not find higher prevalence in species associated with degraded habitats. We detected infections by parasites from the genera *Plasmodium* and *Haemoproteus*. We found two *Plasmodium* lineages in this study, one lineage detected in the semi-palmated sandpiper was also found in the pectoral sandpiper and the white-tipped dove, a South American species. A new lineage (ASDN245116072) was detected in the pectoral sandpiper and was most similar to North American *Plasmodium* lineages retrieved from the American redstart, a New World migratory species, and the American robin, a migrant limited to the Nearctic. The presence of a previously reported lineage of *Plasmodium* and low lineage diversion between ASDN245116072 and previously reported lineages indicate that Plasmodium species may be distributed across the migratory route.

SP10. FERAL PERIL ON TROPICAL CHRISTMAS ISLAND.

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Christmas Island is a strategic surveillance site for Australian biosecurity given its proximity to South East Asia and Northern Australia. The tropical climate and rainforest environment of Christmas Island are conducive to the establishment and persistence of a wide range of parasites of zoonotic and conservation importance which may involve both feral and/or native wildlife and their respective ectoparasite communities. Pathogens previously reported from the island include *Bartonella* and *Trypanosoma*, both presumably introduced by black rats with the latter being attributed with the subsequent demise of two endemic rodent species (*R. macleari* and *R. nativitatis*). However little is known regarding the true prevalence of Trypanosomes on the island or which species it colonises. Additionally the island is a processing site for refugees from Middle Eastern origins which raises concerns for the introduction of *Leishmania* spp. In conjunction with these blood borne pathogens, feral cats and black rats are known to harbour many helminth parasites. This study investigates the parasite status of two competent host populations (feral cats and black rats) present on Christmas Island with particular emphasis on pathogens of zoonotic and conservation significance.

SP11. UTILITY OF TESTING BLOOD-FED AND QUESTING TICKS FOR PIROPLASMS FOR IDENTIFICATION OF NOVEL VERTEBRATE HOSTS OR VECTORS

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Worldwide, piroplasms in humans and animals are increasingly detected. For many piroplasms, the vector is unknown, but presumed to be an Ixodid tick. This study quantifies and characterizes piroplasms in Ixodid ticks from several US states. A piroplasm-specific PCR was used to screen 1,632 Ixodid ticks from Georgia (n=486), Kentucky (n=103), Tennessee (n=626) and Texas (n=416) that were questing (n=42), or collected from animals (n=627), and humans (n=963). The study focused on *Dermacentor variabilis* (n=702) and *Amblyomma americanum* (n=743), but other ticks were tested, including *A. maculatum* (n=16), *A. cajennense* (n=89), *Ixodes scapularis* (n=4), *I. woodi* (n=1) and unspeciated *Amblyomma* (n=77). Few ticks were infected, as 37 (2.3%), 36 (2.2%), and 9 (0.6%) were positive for *Theileria*, *Babesia*, or *Cytauxzoon*, respectively. Of the 36 *Babesia*-positives, 16 (44%) were from *A. americanum*, 19 (53%) were from *D. variabilis* and one (3%) was from an *I. scapularis*. Importantly, nine *Babesia*-positive ticks were removed from humans in Kentucky (n=1), Georgia (n=2), Texas (n=5) and Pennsylvania (n=1). Three *Babesia*-positive ticks were questing *A. americanum*, which is the first report of this in the U.S. Six of the *Babesia*-positive *A. americanum* (one from a dog, two from feral hogs, and three from humans) were *Babesia* sp. Coco, a *Babesia* found in immunocompromised dogs. These data suggest that *A. americanum* might vector *Babesia* sp. Coco, although studies are warranted. Finally, these data highlight the usefulness of screening questing and fed ticks so long as data interpretation stipulates that blood meals are present in non-questing ticks.

SP12. IMPACTS OF LONG-TERM PRESCRIBED BURNING ON TICK POPULATION DYNAMICS IN SOUTHWEST GEORGIA

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Incidence and emergence of tick-borne diseases has increased dramatically. Methods that can effectively reduce tick populations and tick-borne disease risk in wildlife, domestic animals, and humans are needed. One promising method is prescribed fire; however, the efficacy of long-term prescribed burning for tick control is unclear. This is primarily because past studies have not simulated typical operational management scenarios (i.e., frequent burns) and/or account for other predictors of tick abundance. Therefore, our study was conducted to investigate tick population dynamics relative to long-term prescribed fire management. Twenty-one sites in southwestern Georgia with varying burn regimes were sampled monthly for two years. Simultaneously, data on variables that can affect tick abundance (e.g., host abundance, vegetation structure, and micro- and macro-climatic conditions) were collected. In total, 47,185 ticks were collected, of which, 99% were *Amblyomma americanum* followed by *Ixodes scapularis* (0.7%), even fewer numbers of *A. maculatum*, *Dermacentor variabilis*, and two *I. brunneus*. Based on generalized estimating equation negative binomial regression models, long-term prescribed burning consistently and significantly reduced tick counts (overall tick abundance as well as specifically for *A. americanum* and *I. scapularis*) regardless of the burn regimes evaluated and all other variables as long as burning occurred in or around the site. Interestingly, tick species composition varied according to burn regime with *A. americanum* dominating at unburned sites and *A. maculatum* at burned sites. These data indicate that regular prescribed burning may be an effective tool for reducing tick populations and ultimately may reduce risk of tick-borne disease.

SP13. THE EFFECTS OF ENVIRONMENTAL STRESSORS ON DISEASE DYNAMICS IN AMPHIBIANS

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While factors influencing the emergence of diseases are likely multifaceted, many investigators suggest increased exposure to environmental stressors in animal populations is a key factor. A suite of stressors may be altering the physiological state of amphibians and affecting patterns of disease emergence. In this experiment, we have tested the effects of chronic copper exposure on Ranavirus susceptibility in green frog tadpoles. Ranaviruses (family: Iridoviridae) are double-stranded DNA viruses implicated in many amphibian die offs. Ranaviruses can infect amphibians indirectly, through water or sediment, or directly, via ingestion or contact. Copper is a naturally occurring, essential micronutrient; however, increased environmental concentrations can result in bioaccumulation and toxicity. Because they are confined to aquatic environments during larval development, copper disproportionately affects amphibian larvae at levels scarcely above normal physiological thresholds, levels now found in otherwise pristine ecosystems. Copper toxicity can decrease hatching success, embryonic survival, and survival during metamorphosis and chronic exposure to sub-lethal concentrations increases the incidence of deformities, delays embryonic development, alters escape behavior, reduces swimming performance, and decreases larval growth rate. We have tested the effects of three levels of environmental copper on tadpole survival, viral load, and lymphocyte proliferation.

SP14. THE MITIGATION OF AGRICULTURAL PESTICIDES BY AN AMPHIBIAN PATHOGEN IN AQUATIC COMMUNITIES

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Chytridiomycosis, an emerging infectious amphibian disease caused by the pathogenic fungus *Batrachochytrium dendrobatidis* (*Bd*), has played a major role in amphibian declines. Studies have also shown that widespread pesticide use contributes to declines in amphibian health. Because these causes are not mutually exclusive, studies must examine the effects of multiple concurrent perturbations on amphibian declines. We conducted field studies to determine the interactive effects of the fungicide thiophanate-methyl (TM; at 3 concentrations) and *Bd* in southern leopard frog (*Lithobates sphenocephalus*) tadpoles. In the field, we replicated similar treatments in aquatic mesocosms prepared to simulate aquatic communities. Tadpoles were added to the mesocosms after hatching, frogs were collected upon metamorphosis, and measures of survival or growth were assessed. We also recorded aquatic community measures to assess the effects of *Bd* and TM on aquatic community composition. Based on previous studies, we predicted that *Bd* and TM would act in opposition to directly affect amphibian health, while TM would alter aquatic community composition, possibly negating the direct effects of either pressure on the amphibians. Counter to our predictions, *Bd* mitigated the effects of TM by "protecting" tadpoles from TM-induced mortality, and both *Bd* and TM altered aquatic community composition. However, we conclude that alterations to the measured aquatic community variables were not the cause of tadpole mortality, as has been recorded in previous studies. Our research illustrates that interactions between pesticides and pathogens impact amphibian health and aquatic community composition.

SP15. A COMPARISON OF SPATIAL DISTRIBUTION MODELING METHODS FOR THE AFRICAN BUFFALO (*Syncerus cafer*) POPULATION IN THE KRUGER NATIONAL PARK

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Annual census data is collected on many mammalian species in the Kruger National Park (KNP), South Africa. Population data on the African buffalo (*Syncerus caffer*) is collected using a helicopter-based method which follows the major drainage lines. This is done during the late dry season (August/September) and is used to indicate more precise herd numbers rather than distribution patterns. By using the available *S. caffer* census data, three modeling methods were developed to estimate the spatial distribution of population. The modeling methods included disaggregation based on environmental variables, Poisson kriging, and conditional auto-regression. Two separate ground count data sets which were collected using a double randomized walk design, one during dry season (August 2012) and the other during wet season (January 2013). The ground count data will be used for model evaluation and comparison.

SP16. SURVEILLANCE FOR UPPER RESPIRATORY TRACT DISEASE AND *Mycoplasma* IN FREE-RANGING GOPHER TORTOISES IN GEORGIA

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Upper respiratory tract disease (URTD) in the gopher tortoise (*Gopherus polyphemus*) is highly contagious and has been implicated in the reduction of populations throughout their range. With the exception of a few limited studies, data on URTD in Georgia (USA) tortoise populations is largely lacking. In this study, we investigated the prevalence of antibodies to *Mycoplasma agassizii* and *M. testudineum*, two pathogens that can cause URTD, in 10 tortoise populations. Exposure to both *M. agassizii* and *M. testudineum* varied spatially. The prevalence of *M. agassizii* antibodies in individual populations was either very low (0-3%) or very high (96- 100%), whereas there was more variation in prevalence for *M. testudineum* among populations (38% to 61%), with only one site having 0% prevalence. Five sites were seropositive for both pathogens, and these were the only sites where we observed tortoises with clinical signs consistent with URTD. Interestingly, sites where no clinical signs of URTD were observed were only positive for *M. testudineum* supporting evidence that this organism may be of limited pathogencity for gopher tortoises. Collectively, our data indicate that both *M. agassizii* and *M. testudineum* are present in Georgia gopher tortoise populations and that clinical disease is more likely to occur in populations when both pathogens are present or possibly just *M. agassizii*. Continued surveillance is needed to better understand the role of these two pathogens, as well as other possible pathogens (e.g., iridioviruses), in the overall health of Georgia populations, especially if future conservation efforts involve the translocations of tortoises.

SP17. INVESTIGATING CHELONID FIBROPAPILLOMA-ASSOCIATED HERPESVIRUS IN SYMPTOMATIC AND ASYMPTOMATIC REHABILITATING SEA TURTLES

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Fibropapillomatosis (FP), a neoplastic disease characterized by cutaneous, conjunctival and visceral growths, is the most important infectious disease of sea turtles. The presumptive primary etiology of FP is chelonid fibropapilloma-associated herpesvirus (CFPHV). We conducted a retrospective case-series analysis of rehabilitating sea turtles and found FP in 7.6% (n=23), the majority of which were juvenile, female green turtles (*Chelonia mydas*). Compared to non-FP turtles, FP+ turtles were rehabilitated for longer periods of time and were more likely to be euthanized. Time to FP onset ranged from 0 to 40 weeks, suggesting that viral latency and recrudescence influences the timing of tumor development. We further investigated CFPHV latency and the subclinical carrier state using laser capture microdissection (LCM) and nested polymerase chain reaction (PCR). CFPHV DNA was identified in dermal and epidermal cells of a non-FP turtle, suggesting that an asymptomatic carrier is capable of shedding virus from normal skin. CFPHV DNA was also identified in pulmonary and gastrointestinal epithelial cells and spinal cord neurons, but not renal epithelium, of an FP+ turtle. Thus, specific cell types contain viral particles while others do not, and CFPHV transmission may occur via respiratory and/or fecal routes. Ongoing research includes utilizing quantitative PCR, LCM, and transcriptomic sequencing to compare tissues from FP+ and non-FP turtles. This research will help optimize detection and control strategies for FP, allow for better identification of factors leading to viral transmission and tumor formation, and provide a clear understanding of associated host and pathogen gene expression patterns.

SP18. EFFECTS OF BASKING BEHAVIOR ON PREVALENCE AND PARASITEMIA LEVELS OF HAEMOGREGARINES IN FRESHWATER TURTLES

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Haemogregarines are common intracellular blood parasites of freshwater turtles; however, the natural history of these parasites is poorly understood. This project was conducted to compare the prevalence and parasitemia rates of haemogregarines of freshwater turtles. We hypothesized that behavior (basking versus non-basking) would influence parasitemia levels, such that basking species would have lower parasitemias because of possible decreased leech exposure or enhanced immune response. During 2011-2012, 132 turtles of 10 species were sampled at numerous locations in Georgia, USA. Giemsa-stained blood smears were analyzed to determine prevalence of haemogregarines and parasitemias based on number of infected cells per 7,000 cells examined. To date, significantly higher prevalences were noted for nonbasking species (81%) compared with basking species (56%). Similarly, nonbasking species (0.26%) had significantly higher parasitemias compared with basking species (0.03%). These results indicate that basking behavior has a significant impact on the haemogregarine prevalence and parasitemia levels in turtles. Among the four most commonly sampled species, there was no difference in prevalence between the two nonbasking species (common snappers (*Chelydra serpentina*) [0.12%] and musk turtles (*Sternotherus odoratus*) [0.39%]) but parasitemias of the two basking species were different with sliders (*Trachemys scripta*) [0.05%] having significantly higher parasitemias compared with painted turtles (*Chrysemys picta*) [0.01%]. Lower parasitemias in basking species could be attributed to a reduction in leech exposure, an increase in the host immune response, biology of different haemogregarine species, or another unknown factor. Future studies will incorporate molecular characterization and additional sampling to better understand the ecology of these parasites.

SP19. PREVALENCE AND DIVERSITY OF *Babesia*, *Hepatozoon*, *Ehrlichia*, AND *Bartonella* IN WILD AND DOMESTIC CARNIVORES FROM ZAMBIA, AFRICA

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We conducted a molecular survey for several haemoparasites of domestic dogs (*Canis familiaris*) and three species of wild carnivore from two sites in Zambia. Three *Babesia* spp. were detected including *B. felis* and *B. leo* in lions (*Panthera leo*), and a *Babesia* sp. (similar to *B. lengau*) in spotted hyenas (*Crocuta crocuta*) and a single lion; whereas all wild dogs (*Lycaon pictus*) and domestic dogs were negative. High prevalence rates for *Hepatozoon* were noted in all three wild carnivores (38-61%) and in domestic dogs (13%). Significantly higher prevalence rates were noted in hyenas and wild dogs compared with domestic dogs and lions. All carnivores were PCR negative for *E. canis*, *E. ewingii*, and *Bartonella* spp. Overall, high prevalence rates and diversity of *Babesia* and *Hepatozoon* were noted in wild carnivores from Zambia. We report the first molecular characterization of *Babesia* from any species of hyena. We also report that lions and hyenas are infected with a *Babesia* species closely related to *B. lengau*, a parasite previously only reported from cheetahs (*Acinonyx jubatus*). Although usually benign, these haemoparasites can become pathogenic under certain circumstances for wild carnivores. Importantly, data on vectors for these parasites are lacking, so studies are needed to identify vectors as well as elucidate transmission routes, infection dynamics, and host specificity of these haemoparasites in wildlife in Africa and the risk of cross-transmission between domestic animals and wildlife.

SP20. PARASITOLOGY, VIROLOGY AND SEROLOGY FINDINGS IN FREE RANGING COYOTES FROM NORTH GEORGIA

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Thirty-one free-ranging coyotes from North Georgia were examined for selected parasites and viral agents. Fifty-one percent (n=16) of coyotes had adult heartworms on necropsy and 16% (n=5) had evidence of heartworm associated disease on histology. Antibodies were found against canine parvovirus (100%, n=27), canine distemper virus (48%, n=13), canine adenovirus (37%, n=10), *Trypanosoma cruzi* (7%, n=2), and *Toxoplasma gondii* (91%, n=22). No antibodies were detected against *Leishmania*. Real-time PCR of feces and mixed sections of tongue and intestines at the ileocecocolic junction showed 32% (n=10) of coyotes were shedding parvovirus. Sequence analysis indicated that three coyotes were infected with canine parvovirus type 2c and one coyote infected with canine parvovirus type 2b. One coyote that had parvovirus 2c also had pseudo-cytoplasmic inclusion bodies found within tongue tissue on histology, which is associated with a parvovirus infection. There is valid concern that coyotes could be a source of diseases for domestic dogs in the southeast and that coyotes could be a spillover host for canine parvovirus. Therefore, further population studies of coyotes in the Southeast should be conducted to screen for these diseases.

SP21. CHARACTERIZATION OF *Mycobacterium tuberculosis* ISOLATES FROM CAPTIVE ELEPHANTS OF NEPAL

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Tuberculosis with extensive lung lesions was detected from three Asian elephants of Nepal. *Mycobacterium tuberculosis* complex was isolated from all three elephants through the culture of lung tissue obtained at necropsy. Bacterial species was determined as *Mycobacterium tuberculosis* by a multiplex PCR assay and confirmed by gyrB sequencing. The gyrB sequencing of isolates had a single nucleotide polymorphism (SNP) which was revealed as lineage specific strains belonging to Indo-Oceanic lineage. gyrA sequence of Elephant-A had synonymous SNP while of other two elephants were wild type. Spoligotyping showed Elephant A and B isolates had new spoligotypes that were not found in the SpolDB4 database whereas Elephant C had a spoligotype belonging to the Indo-Oceanic Lineage (EAI5, SIT138). The drug resistance determination region sequences, rpoB, katG, inhA promoter region and rrs were wild type in all the isolates. Using multi-locus variable number of tandem repeat analysis (MLVA), Elephant B and C made a cluster with one locus difference while Elephant A formed a cluster with human isolates having the same gyrASNP, T231C which suggests that there was no direct transmission of a *M. tuberculosis* strain among those elephants, and the source of infection was different. The results strongly suggest the transmission of the bacteria from a human, most probably a handler, to an elephant. Since little information has been published on TB genotypes, further investigations should be needed to clarify the transmission route to protect this endangered animal species.

SP22. HOOKWORM DISEASE IN SOUTH AMERICAN FUR SEAL (*Arctophoca australis*) PUPS AT GUAFO ISLAND, CHILE

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Hookworms are highly pathogenic nematodes that parasitize a wide range of mammals, including several species of otariid seals. During the austral summers of 2012 and 2013 necropsies and captures of South American fur seal pups on Guafo Island, Southern Chile, were performed. Hookworm (*Uncinaria* sp.) infection was found in all pups necropsies (28/28). In at least 15 of those cases, *Uncinaria* sp. infection was considered as a primary cause or significant contributory factor in pup mortality. Common findings in these pups included severe hemorrhagic enteritis, with hookworms deeply embedded in the mucosa and occasionally free in the abdominal cavity, enteric and respiratory bacteria (*E. coli*, *Streptoccocus* sp.) in blood, lung, and liver, and Gram-positive or Gram-negative bacteria in hookworm feeding tracks and/or inside macrophages or the mesenteric lymph nodes and lungs. Based on necropsy examination, the bacterial infections were considered to be secondary infections relative to hookworm disease. Seventy live pups were also examined and many pups had varying degrees of weakness, pale mucous membranes, mucopurulent conjunctivitis, and bloody diarrhea. Sixteen pups with hookworm infection had a concurrent anemia (RBC < 3,000,000 µl). Hookworm disease associated with secondary bacterial infections is a significant cause of morbidity and mortality in this population.

SP23. UNDERSTANDING HOW TABANIDS INFLUENCE THE PREVALENCE OF *Elaeophora schneideri* IN MOOSE POPULATIONS AROUND WYOMING, USA

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In 2009, the Wyoming Game and Fish Department (WGFD) conducted statewide surveillance for the parasitic nematode, *Elaeophora schneideri*, by examining hunter-harvested moose (*Alces alces shirasi*). Prevalence was 48% statewide, the highest reported for moose, and ranged from 0-82.6% among moose herd units. To better understand what influences the prevalence of *E. schneideri* in moose, we collected tabanids using Manitoba fly traps around Wyoming in areas of high and low prevalence based on the WGFD surveillance. Tabanids, specifically those of the genera *Hybomitra* and *Tabanus*, are biological vectors for *E. schneideri*. Once collected, horse flies are identified and the relevant species are determined through dissection. Using species specific primers for moose, elk (*Cervus elaphus*), deer (*Odocoileus* spp.), cattle (*Bos taurus*), sheep (*Ovis* spp.), and horses (*Equus ferus caballus*), DNA from horse fly blood meal was quantified using real-time PCR. Using PCR to identify DNA in the blood meal of horse flies, interspecific transmission of the parasite, and host selection can be assessed. Horse fly species is also mapped across Wyoming to determine if a correlation exists between prevalence in moose and species composition of horse flies. These data will help managers to identify the factors that lead to high prevalence within moose herds. To date, nine species of horse flies have been recognized from three different genera, with two identified species are known to be carriers of *E. schneideri*.

SP24. ECHINOCOCCOSIS IN *Agouti paca* IN THE PERUVIAN AMAZON

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We report an unusual infection of *Echinococcus vogeli* in three pacas (*Agouti paca*) of free living from a forested region in Loreto, northeastern of Peru. The cycle of *E. vogeli* involves the paca as the main intermediate host and bush dog as definitive host, and humans probably obtain the infection by contamination from feces of infected hunting dogs. The macroscopic examination revealed that the liver of paca contained multiple spherical white or translucent lesions, relatively large and filled with fluid, which were isolated. The microscopic examination revealed cystic structures that contained abundant brood capsules and numerous protoscolices from the inner surface. The protoscolices possessed rostellar hooks (40.9 um in length), and a morphological characteristic of the blade was consistent with the metacestode *E. vogeli*. This case is the first reported in paca of Peru, suggesting the need to investigate the polycystic echinococcosis in pacas with hepatic cysts from areas of tropical forest and where the hunting habits are present.

SP25. THE POTENTIAL OF RACCOONS TO BIOLOGICALLY AND MECHANICALLY TRANSMIT *Salmonella*

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The potential role of raccoons in transmitting *Salmonella* biologically (through feces) and mechanically (on paws) is unknown. We isolated *Salmonella* from rectal and paw swabs of raccoons and from soil and livestock manure lagoon samples in areas where raccoons were trapped on swine farms and conservation areas in southern Ontario from June – October 2012. *Salmonella* was isolated from 26% (117/476) of raccoon rectal swabs, 18% (56/418) of raccoon paw swabs, 9% (36/497) of soil samples, and 35% (4/13) of livestock lagoon samples. The prevalence of *Salmonella* was significantly greater in raccoon rectal and paw swabs than in soil samples ($p < 0.001$ and $p = 0.006$, respectively); however, the prevalence of *Salmonella* from rectal swabs was significantly greater than paw swabs ($p < 0.001$). Of 418 raccoons, 40 (9.6%) tested positive for *Salmonella* from both paw and rectal swabs and 35 (8.4%) tested negative from rectal swabs but positive from paw swabs. Of 21 *Salmonella* serovars isolated, 9 were found only in rectal swabs, 4 only in paws, 1 only in manure, and none were unique to soil. Overall, serovars Oranienburg (68/236), Typhimurium (43/236), and Newport (38/236) were the most commonly detected and resistance was found in 4/236 *Salmonella* isolates. *Salmonella* serovars in raccoon rectal swabs did not always match what was found on paws from the same individual or from samples in their environment. Our results suggest that raccoons have the potential to transmit *Salmonella* biologically and mechanically, although the source of *Salmonella* exposure for raccoons was not clear.

P1. MORTALITY IN *TELMATOBIUS MARMORATUS* FROGS AFFECTED BY *BATRACHOCHYTRIUM DENDROBATIDIS* AND MYXOSPORIDIA INFECTION

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The marbled water frog, *Telmatobius marmoratus*, is an Andean frog classified by IUCN RedList as Vulnerable, because of population declines caused by several factors, such as chytridiomycosis. This disease is caused by the chytrid fungus *Batrachochytrium dendrobatidis* (Bd), which is negatively impacting frog populations worldwide. In 2012, we started a captive breeding program for rescued *T. marmoratus* in their home region, the highlands of Cusco, in southern of Peru. During the implementation of the program we identified individuals at early development stages (tadpoles, metamorphic, and juvenile post-metamorphic frogs) with lesions. Skin samples from toes, legs and ventral body surface were obtained from 20 metamorphic and juvenile frogs which died, and these were analyzed by standard histopathology procedures (hematoxylin-eosin and periodic acid-Shiff stains). Histopathology of these tissues showed Bd sporangia in different stages. In some individuals protozoa resembling Myxosporidia (Myxozoa) in were observed causing renal tubular necrosis. These findings suggest concomitant infections with Bd and myxosporidia are presumable causes of death in *T. marmoratus* specimens. This report confirms the presence of chytrid fungus in *T. marmoratus* in this region, as described by other authors, and warns about the role of this species as a potential disseminator of Bd to other frog species.

P2. SURVEY FOR *OXYSPIRURA PETROWI* IN NORTHERN BOBWHITES FROM THE ROLLING PLAINS ECOREGION OF TEXAS AND WESTERN OKLAHOMA

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Northern bobwhites (*Colinus virginianus*) have experienced long-term population declines and it is unclear what mechanisms are operative. Historically, the role parasites play is often overlooked or disregarded as inconsequential. *Oxyspirura petrowi* is an indirect lifecycle nematode that occurs under the nictitating membrane and within the conjunctival sacs and nasolacrimal ducts of gallinaceous birds. There is speculation that the vision of bobwhites may be impaired by *O. petrowi*, thereby decreasing the host's ability to survive. The present study was initiated to learn more about the occurrence of *O. petrowi* in bobwhites from the Rolling Plains of Texas and western Oklahoma, a region that has traditionally had an abundance of bobwhites. Examination of 510 bobwhites collected during 2011 and 2012 revealed 36% were infected with *O. petrowi* with a mean intensity of 7.5 ± 0.7 (SE) (range: 1–61). Discussion of *O. petrowi* relevance to bobwhites is expanded upon in this presentation. Our study provides additional information and insight about *O. petrowi* in bobwhites.

P3. CHESAPEAKE BAY 2012 AVIAN BOTULISM AND HARMFUL ALGAL BLOOM MORBIDITY AND MORTALITY EVENT

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The Paul S. Sarbanes Environmental Restoration Project at Poplar Island (PIERP), in Talbot County, Maryland is the site of dredge spoil deposition for the purpose of restoration of wildlife habitat in the Chesapeake Bay, Maryland. Multiple agencies are working together to rebuild this complex of islands creating upland and marshland habitat for migrating birds. Uncontaminated channel dredge material from the Bay has been deposited at PIERP since 2001. In 2001 the first documented wildlife mortality event occurred with approximately 100 birds found dead. Other small mortality events have been documented since that time. However, in 2012 777 shore birds, waterfowl, and several muskrats were affected and either found with neurologic signs and transported to Tri-State Bird Rescue and Research in Newark, DE for treatment, rehabilitation, and release or were found dead. Initial reports were received by the U.S. Fish and Wildlife Service, the Maryland Department of Natural Resources, and Tri-State Bird Rescue and Research. Live birds exhibited head bobbing, inability to fly, nictitans paralysis, limberneck, full body paralysis and seizures. Over the following fifteen weeks the 564 birds were found dead, and 82 out of 188 birds were treated and released by Tri-State Bird Rescue and Research. Species included Least and Semi-palmated Sandpipers, Blue-winged Teal, Green-winged Teal, Mallard, American Black Ducks and others.
The National Wildlife Health Center (Madison, WI) and Southeastern Cooperative Wildlife Disease Study (Athens, GA) received 15 carcasses for diagnostic testing and determined that avian botulism was the cause for some of the mortalities, but found some carcasses tested botulism negative. Blood, liver, gastrointestinal contents, and water were submitted for analysis by LC/MS for blue-green algae analysis by the University of Pennsylvania. Twelve out of sixteen liver samples submitted were positive for microcystin for levels equal to or exceeding those associated with other reported bird and mammalian mortalities in the United States. Water samples were also positive for microcystin. By November no further reports were received and the event was declared over. Disease and mortalities are part of the natural system at Poplar Island, and occur usually during summer and fall months, but can occur at any time of the year. Federal, state, university and private organizations work closely to monitor this island.

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P4. SEROPREVALENCE OF TWO ORTHOMYXOVIRUSES IN COMMON EIDERS

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The family Orthomyxoviridae includes a number of viruses, all with segmented, single-stranded, negative-sense RNA genomes. Avian influenza virus (AIV) is among the most studied of this group, and yet, very little is known about the ecology of AIV in sea duck populations. Alternatively, Wellfleet Bay virus (WFBV) is a newly described orthomyxovirus about which almost nothing is known. To date, WFBV has only been documented in the common eider (*Somateria mollissima*), an abundant and widely-distributed sea duck. Here we report the seroprevalence of AIV and WFBV in several common eider populations in North America. Antibodies against AIV were detected using a commercial blocking ELISA and antibodies against WFBV were detected using a microneutralization assay. Seroprevalances of AIV by location were: Nunavut 54% (300/551), Maine 71% (140/198), Massachusetts 61% (26/43), and Rhode Island 52% (71/137). Seroprevalences of WFBV by location were: Nova Scotia 3% (2/63), Maine 3% (2/65), Massachusetts 41% (28/69), and Rhode Island 4% (5/137). The respective ecology of these related viruses in sea duck communities is likely to be extremely divergent. Our findings indicate that common eiders are commonly exposed to both of these orthomyxoviruses, but additional research is needed to define the role of sea ducks in the ecology of each virus.

P5. INVESTIGATING THE POTENTIAL ROLE OF WILD BIRDS IN THE 2009 AND 2011 INTRODUCTIONS OF H7N9 INFLUENZA A VIRUS INTO DOMESTIC POULTRY IN THE UNITED STATES OF AMERICA

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Wild aquatic birds are the primordial source of influenza A viruses (IAV) detected in poultry, but the details surrounding these spillover events are often unknown. This represents a critical gap in our understanding; as such information is necessary to improve biosecurity and response efforts. During the winter and spring of 2009, antibodies to H7N9 IAV were identified in multiple poultry farms in four Midwestern states, and H7N9 (LP) LPIAV was isolated from multiple seropositive Minnesota farms. During the remainder of 2009-2010 there were no reports of H7N9 LPIAV in terrestrial poultry in the US; however during the spring of 2011, antibodies to H7N9 IAV were detected and H7N9 LPIAV was isolated from two poultry farms in Minnesota. To provide insights into the involvement of wild birds in these IAV introductions, serologic and virologic surveillance for IAV was conducted in peridomestic wild birds on both 2011 positive farms within approximately 6 weeks of the H7N9 LPIAV detections. No virus was isolated from 311 peridomestic birds. A single bird (0.3%; European starling) was seropositive to IAV nucleoprotein, but the antibodies were not directed against the H7 subtype based on hemagglutinin inhibition testing. Additionally, the complete hemagglutinin of the 2009 and 2011 H7N9 LPIAV turkey isolates was sequenced and compared to existing North American H7 sequences. Based on preliminary analysis, the origin of the turkey viruses is still unclear; however, the 2011 H7N9 IAV did not appear to result from a new wild bird introduction.

P6. A MODEL OF AN AVIAN-HUMAN INFLUENZA OUTBREAK AT LINCOLN PARK ZOO, CHICAGO

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Avian influenza virus (AI) is currently considered to be one of the most important global zoonotic diseases as it poses a pandemic threat to both animals and humans. AI viruses are susceptible to mutation and a few are considered to be highly pathogenic (HPAI) to many species including birds, humans, pigs, and several zoos species. Certain wild waterfowl and shorebirds are considered reservoirs of low-pathogenic AI (LPAI) and some have been found to carry HPAI strains asymptomatically in endemic countries. Addressing the interfaces between wildlife, livestock, zoo animals, and humans is essential in understanding AI disease dynamics. Due to the infeasibility of conducting large-scale studies on a sporadic and dangerous disease like HPAI, alternative research methods like mechanistic modeling can be employed to further explore HPAI disease dynamics and the risks for animal and human populations.
Lincoln Park Zoo (LPZ) of Chicago is a unique environment where wild birds, open-air collections of zoo specimens, and dense urban human populations can interact and coexist. Based on current knowledge of HPAI H5N1, LPZ's environmental setting, and observed species interaction at the zoo, there is considerable risk for extensive animal disease spread. With the goal of exploring disease dynamics in an urban zoo setting, a multi-agent modeling program is used to develop spatiotemporal models of H5N1 disease spread due to hypothetical wild avian introduction at LPZ. The model will also serve as a tool to analyze efficacy of various hazard control methods in the event of an HPAI outbreak at LPZ.

P7. ENVIRONMENTAL STABILITY OF SWINE AND PANDEMIC INFLUENZA VIRUSES IN WATER

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Although the movement of IAV from wild bird reservoirs to domestic animals and humans is well established, the transmission mechanisms that facilitate efficient movement across and within these host populations are not fully defined. Although predominant routes of transmission vary between host populations, the necessity or extent of IAV environmental stability needed for efficient transmission also may vary. Because of this, we hypothesized that viral stability would differ in response to varied host-related transmission mechanisms. If correct, such phenotypic variation could represent a potential marker for the emergence of novel animal or human influenza viruses. The objective of this work was to evaluate the ability of wild bird, swine, and human IAV isolates to remain infective under various pH, temperature, and salinity conditions using a pre-established distilled water system. As with the avian viruses, swine and human viruses persisted longest at near-neutral pH, cold temperatures, or under “fresh water” conditions. Our results indicate that though IAV persistence can be modulated by environmental variables, there has been no apparent change in the environmental stability of the viruses related to host adaptation.

P8. NOVEL H7N9 AVIAN INFLUENZA IN ASIA AND THE POTENTIAL ROLE OF WILD BIRDS

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In mid-February 2013 human cases of novel H7N9 emerged in China. We reviewed GenBank and 49 published studies where sample sizes could be ascertained to determine the distribution and prevalence of H7N9 in wild bird populations. We found that H7N9 is rare relative to other subtypes, globally distributed, and more often identified in wild birds than domestic birds. While still early in the epidemic curve, at this point the evidence suggests humans are infected from a domestic bird reservoir. Lastly we constructed phylogenetic trees to help determine the relationship of the novel H7N9 to viruses isolated from wild and domestic birds. The relationship suggests a spillover event from wild birds into domestic birds occurred recently within Southeast Asia, with subsequent reassortment in domestic birds.

P9. DETERMINATION OF TISSUE PERSISTENCE OF *MYCOBACTERIUM BOVIS* BCG IN TEXAS-ORIGIN FERAL SWINE ORALLY VACCINATED WITH *MYCOBACTERIUM BOVIS* BCG

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Bovine tuberculosis (bTB) is present in feral swine populations on Molokai, Hawaii, USA. *Mycobacterium bovis* BCG (BCG), an attenuated vaccine strain of *M. bovis*, used in humans, is being considered for use on Molokai to manage bTB in the feral swine population. Since BCG is a live bacterial vaccine and feral swine on Molokai are hunted year-round, it is important to know if and how long BCG persists in various tissues with the potential for transmission to humans and other hosts. Sixteen feral swine were hand fed 1 x 106 colony forming units BCG via an oral bait formulated for European wild boar. Four feral swine were each given bait without BCG. At 1, 3, 6, and 9 months post-vaccination, 4 vaccinated animals were randomly chosen for euthanasia and tissue collection to monitor persistence of BCG at the various time points. The nonvaccinated controls were euthanized at 9 months. Tissue were pooled and consisted of head pool, thoracic pool, abdominal pool, and muscle. Pools were cultured for *Mycobacterium* spp. Eighteen percent of the tissues were contaminated and could not be successfully cultured, the majority coming from three vaccinates. None of the remaining tissues grew any species of Mycobacterium. Based on our data, it is likely that BCG does not persist in feral swine tissues after one month post oral vaccination. However, further work needs to be performed on a larger sample size and testing needs to be expanded to determining the presence of BCG within the first month after vaccination.

P10. PARASITES IN MAINE MOOSE 2010-13: COLLABORATIVE STUDIES

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During 2010-13, the University of Maine Animal Health lab provided necropsy services as needed for the Maine Department of Inland Fisheries and Wildlife. Of approximately 25 moose necropsies, a large proportion was affected with lungworms, winter ticks, and lung cysts. A student project to sequence the ITS2 gene of these worms indicated that it may be a unique Dictyocaulus species. A followup survey of Maine moose during the 2012 hunt was coordinated between IFW and UMAHL, yielding an additional 62 lung sets of which 13% were lungworm positive, and 34% were found to be positive for lung cysts, consistent with *Echinococcus granulosus*. Several cysts were analyzed using PCR and identified as the G8 strain, *E. granulosus canadensis*. In this interaction, collaboration with the university, the state wildlife agency, the state Center for Disease Control, and the new Northeast Wildlife Disease Cooperative yielded new information about Maine's moose population, notified the public about diseases with potential zoonotic potential, and created learning opportunities for undergraduate students.

P11. DETECTION OF CHRONIC WASTING DISEASE PRIONS FROM ENVIRONMENTAL SOURCES BY PROTEIN MISFOLDING CYCLIC AMPLIFICATION

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Chronic wasting disease (CWD) is an emerging prion disease affecting free-ranging and captive North American cervids. Prions have been detected in the saliva, urine, and feces of infected animals. In captive settings, transmission can take place both via direct contact or environmental contamination from infectious secretions or from decomposed infected carcasses. However, the role of environmental reservoirs of disease transmission in free-ranging cervid populations is unknown. Suspected environmental reservoirs include areas such as mineral licks, scrape sites, and other concentration areas where both prion deposition from infected animals and exposure of susceptible animals is likely to occur. Protein misfolding cyclic amplification (PMCA) is a method >1000 fold more sensitive in the detection of CWD prions than bioassay. Currently, highly sensitive PMCA methods of prion detection in environmental samples–soil, organic matter, and excreta–are lacking due to inhibitory compounds present in both the sample and the extraction buffer selected. We have been developing methods of efficient prion extraction and amplification from environmental samples by PMCA.

P12. POTENTIAL CONTAMINATION OF ENDANGERED FLORIDA KEY DEER HABITAT WITH *MYCOBACTERIUM AVIUM* SUBSPECIES *PARATUBERCULOSIS*

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Mycobacterium avium subspecies *paratuberculosis* (MAP) is the causative agent of Johne's disease, a progressive wasting disease of domestic ruminants that has also been found in wild ruminants. Johne's disease was first reported in the endangered Key deer (*Odocoileus virginianus clavium*) in 1996 on Big Pine Key (BPK), Florida. This study was conducted to determine the current distribution of MAP in Key deer and whether natural or man-made freshwater sources and artificial feeding sites are contaminated with MAP. Between 11/2009-09/2012, MAP was isolated from 36/369 (10%) fecal samples collected throughout the Key deer range on BPK and the Newfound Harbor Keys. All positives were from Little Palm Island (36/142 (25%)). Only 1/729 (0.1%) environmental samples were positive which was from Little Palm Island (1/81 (1%)). In addition, MAP was isolated from 3/43 (7%) necropsied deer, all from Little Palm Island (3/3 (100%)), and of these, samples from the ileum, cecum, and ileocecal lymph node from two were MAP-culture positive and feces from one of these was culture positive. The third deer was only PCR-positive. Results indicate that Johne's disease was restricted to Key deer from Little Palm Island during this sampling and that if MAP transmission occurs through environmental contamination, it is likely intermittent or at a very low rate. The apparent decreased distribution of MAP on BPK may indicate that management plans are working to decrease the incidence of MAP infections. However, the continued presence of MAP on Little Palm Island remains a threat to the remaining Key deer population.

P13. TRANSECT SAMPLING METHOD FOR DETECTING WINTER TICKS ON ELK HIDES IN YUKON, CANADA

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Winter ticks (*Dermacentor albipictus*) were first collected from Yukon wildlife in southeast Yukon in 1994. In 2007, winter ticks were found on free-ranging elk (*Cervus elaphus*) in south-central Yukon, indicating that ticks were established despite the harsh northern climate. Between 2008 and 2011, ticks were quantified on 117 ungulate hides from road-killed or hunter-harvested animals using a hide digestion technique. While this method provided high-quality data on abundance of ticks of all life-stages, it was cumbersome, time-consuming, and destructive. The objective of this study was to validate a hair transect method of classifying hides from hunter-harvested elk into categories of tick burden based on examination of a targeted section of the hide. Hides from 13 female and 4 male elk were collected between September 2010 and January 2012. A target area was identified over the dorsal neck and shoulder region of each hide, and 4-8 232 cm 2 sections were removed from each hide. Five equidistant transects were made in each section by parting the hair to expose the skin and ticks observed on transects were counted using 10X magnification. Subsequently, hide sections were digested by NaOH and recovered ticks were counted. The hair transect method detected 13% (range 6-23) of ticks found using the digestion technique. Overall, there was a significant positive relationship between tick counts from hair transects and tick counts from digestion ($p < 0.001$, $R2 = 0.9$). This method can quantify relative winter tick burdens in elk and will be used for ongoing tick monitoring in Yukon.

P14. PHYSIOLOGIC EFFECTS OF HUMAN ENCOUNTERS AND HUNTING ON THE SCANDINAVIAN BROWN BEAR (*URSUS ARCTOS*)

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Very few studies have evaluated the physiologic effects of human disturbance on wild animals, yet the effects could have significant animal welfare concerns. Using temperature and movement as an indicator of stress, we evaluated the effect of experimental approach by humans on six bears and hunting with dogs on six legally shot bears. All bears were fitted with GPS collars and implanted with abdominal biologgers to record temperature every one or three minutes. Temperature and distance moved were evaluated for the day of approach and the day of hunting, as well as the week before and after approach and before hunting. A physiologically significant increase in temperature was defined as ≥38.50C. More bears reached a maximum temperature of ≥38.50C during the hunting season (4/6 pre-hunt, 3/6 during hunt) than during experimental human approach (1/6 pre-approach, 1/6 during approach). Two hunted bears had critically high temperatures of 40.71C and 42.00C near death. Although not statistically significant ($p=0.1117$), the average maximum temperature during hunting (39.35 ± 1.69, $n=6$) was more than a degree higher than the average maximum during approach (37.96 ± 0.83, $n=6$). No significant differences were noted between distances moved before and during hunting; similarly for experimental approaches. These preliminary results suggest that not just the act of being hunted, but the hunting season itself could be a significant stressor for the brown bear. Further analysis should incorporate more sophisticated movement and activity analysis with temperature analysis to provide a more complete description of the physiologic effects of these disturbances on the brown bear.

P15. SEEKING ADDITIONAL BIOLOGICAL CONTROL AGENTS TO AUGMENT RABBIT HAEMORRHAGIC DISEASE (RHD) AND MYXOMATOSIS: MANAGING AUSTRALIA'S RECOVERING PEST RABBIT POPULATION

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The release of myxoma virus in 1950 and rabbit haemorrhagic diseases virus (RHDV) in 1995 reduced Australia's pest rabbit (*Oryctolagus cuniculus*) population providing c.$70 billion in agricultural economic returns, and major environmental benefits. Both viruses initially reduced rabbit numbers in many areas by up to 95% however, as expected with pathogen/host relationships, the viruses changed and genetic resistance developed in the rabbits allowing their numbers to recover, albeit to levels lower than those before the virus releases. With seedling recruitment in native vegetation being prevented at rabbit densities as low as 0.5/ha, and increasing agricultural and pastoral impacts, further rabbit control is still necessary. This could be achieved economically in arable lands using poisons and rabbit burrow destruction but in the remote, vast (>1 million km2) and sparsely populated semi-arid and arid parts of Australia where management of rabbits is problematic, biocontrol agents are the only realistic solution. Agents additional to myxoma and RHDV have been suggested though not as yet assessed. In conjunction with expert review of these agents, we are developing wildlife and commercial rabbit industry disease networks to detect other control agents that might assist Australia in its continuing battle with the rabbit.

P16. EVALUATING MANAGEMENT ALTERNATIVES FOR FREE-ROAMING CAT POPULATIONS ACROSS A RANGE OF LANDSCAPES: AN INDIVIDUAL-BASED, DEMOGRAPHIC SIMULATING MODELING APPROACH

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Challenges surrounding management of free-roaming cat populations continue to receive considerable attention in scientific and popular literature. We used VORTEX simulation modeling software to evaluate the effects of removal, sterilization, and temporary contraception on large urban, small urban, and rural free-roaming cat populations.
Nearly 550 unique model scenarios were constructed and projected for fifty years. Output data on population growth rate, final abundance, and extinction risk were tabulated and interpreted to detect trends and important relationships. Results include the following:
• population dynamics may be more sensitive to changes in age-specific survival than to age-specific reproduction;
• demographic connectivity, through dispersal between surrounding free-roaming cat population and litter abandonment, can dramatically reduce the effectiveness of population management efforts;
• a removal or sterilization program focused on adults, targeting at least 30% of the untreated individuals every six months, can decrease cat numbers. This is in line with other analytical efforts suggesting that 70% of a free-roaming cat population must be neutered annually to achieve negative growth;
• treatment protocols targeting females can be considerably more effective in reducing population growth than a gender-independent treatment protocol;
This information must be applied within the broader context of the real and emotionally-charged issue of free-roaming cat population management. Responsible decision-making requires the explicit consideration of an array of objectives: reduction or elimination of the free-roaming cat population, minimizing risks to potential prey and other impacted species, minimizing costs, securing individual animal welfare, decreasing nuisance complaints, optimizing public health, and maximizing public support.

P17. WILDLIFE DISEASE AND ECOSYSTEM HEALTH IN NICARAGUA AND EL SALVADOR

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Cūra Earth is identifying specific health and disease risks in Central America in order to develop a comprehensive program in ecosystem health. Pilot research projects are initially focusing on key indicator species in aquatic health, marine health, and zoonotic diseases. Cūra Earth is collaborating with government, academic, and non-governmental organizations active in Central America. We are also working with veterinary schools in country to provide training and expand their current curricula. Nicaragua is one of our main field sites and is the second poorest country in the western hemisphere with poor public health and veterinary medical infrastructure. Few major conservation nonprofits are active in the country, despite the fact that Nicaragua has the second largest intact rain forest in the western hemisphere, second only to the Amazon rain forest. Many threatened and endangered species reside in the country or along the coastal shores. Nicaragua is also a hotspot for such diseases as leptosporosis, dengue fever, malaria, and encephalitis viruses. Extensive literature reviews have revealed no published wildlife health studies in Nicaragua and few in El Salvador. Cūra Earth is developing country wide Sea Turtle Health Networks, which will hopefully extend to cover all of Central America, involving numerous nonprofits and governmental programs to provide standardized data collection, trainings in sea turtle sample collection, necropsies, and response to mass strandings or die offs. This program also includes pilot studies in sea turtle health in northwestern Nicaragua and southwestern El Salvador collecting baseline health data on the endangered hawksbill sea turtle.

P18. A WEB BASED PHARMACEUTICAL MANAGEMENT SYSTEM

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The objective of this project was to develop a better system for managing pharmaceuticals. Such a system should result in greater accuracy, security, transparency, and control of these substances than was currently possible with a paper record method, thereby assuring their continued availability and effective use in field operations. In order to maximize ease of use and timeliness of entries a web based system was developed. The system assigns levels of access and permissions to assure appropriate responsibility and timely identification of problems associated with the use of all classes of drugs. Changes in personnel, supervisory roles, pharmaceuticals needed, and vendors can be easily made. The life of a vial of drug begins with the application of a barcode and ends when it is scanned into an annual report reflecting returned vials. The vials location and the history of use of its contents can be accessed at any time. While some changes and adaptations have been made during the first year of use, the system has met our expectations and has been well received by field personnel.

P19. USING THE HEALTH OF AMPHIBIAN POPULATIONS TO EVALUATE ECOSYSTEM HEALTH IN THE OIL SANDS REGION OF CANADA

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Although substantial economic benefits are derived from extracting Alberta's oil sands deposits, the poorly understood ecological costs of mining and upgrading operations have drawn scrutiny. We are examining the health of wild amphibian populations at varying distances from oil sands mining operations as a way to evaluate overall ecosystem health. Amphibians link terrestrial and aquatic food webs as a result of their complex lifecycles. Further, developing eggs and young tadpoles may be exposed to particularly high levels of organic contaminants and heavy metals because these substances accumulate with snowfall during the winter and then wash into breeding ponds in a pulse in the spring. Key parameters we are investigating include population biology, rates of malformations, infectious disease dynamics (ranaviruses, chytrid fungus), and levels of metals, naphthenic acids and polycyclic aromatic hydrocarbons in amphibian breeding ponds and amphibian tissues. Ranaviruses and chytrid fungus have been detected in several populations across the study region, including recurrent ranavirus-related die-offs at some wetlands. Levels of several substances in pond water are highest within 65 km of upgraders, with some substances exceeding levels deemed safe for aquatic life (e.g., total mercury). Abnormalities found thus far involve hind limb abnormalities and asymmetrical eye placement, but rates of malformations are generally low in the study region. Work is ongoing to examine the spatio-temporal patterns of these indicators of amphibian health with one of our goals being the development of tractable parameters that can be measured and interpreted by regulators and other groups responsible for monitoring ecosystem health.

P20. MULTIPLE HOST TRANSFERS BUT ONLY ONE SUCCESSFUL LINEAGE OF *MYCOPLASMA GALLISEPTICUM* IN HOUSE FINCHES

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Emergence of a new disease in a novel host is thought to be a rare outcome following frequent pathogen transfers between host species. We examined the successful host transfer and subsequent evolution of the bacterial pathogen *Mycoplasma gallisepticum* (MG) an emergent pathogen of house finches (*Haemorhous mexicanus*). Principal goals were to assess whether host transfer has been a repeated event between the original poultry hosts and house finches, whether only a single host transfer was ultimately responsible for the emergence of MG in songbirds, and whether the spread of the pathogen from east to west across North America resulted in spatial structuring in the pathogen. Phylogeny of 107 MG isolates from songbirds (mainly house finches) and domestic poultry showed that the house finch epidemic was derived from a much more diverse set of MG pathogens circulating in poultry, and confirmed that the first house finch isolate made in1994 was ancestral to other songbird isolates. However, we infer that MG has repeatedly jumped between these two groups of hosts but that to date only a single lineage of MG has persisted and evolved in songbirds. All house finch isolates from western North America were derived and slightly differentiated from a single colonization of that region by an eastern North America source. Phylogeny also indicated that genetic diversity of MG in a geographic area increases with the length of time that MG has been established in a population, and that the house finch epidemic now consists of eastern and western MG clades.

P21. FOR A BETTER UNDESTANDING OF THE ENVIRONMENTAL CONTAMINATION BY *TOXOPLASMA GONDII* IN RURAL AREA: SPATIAL ANALYSIS OF HOST INFECTION AND SOIL CONTAMINATION.

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Toxoplasmosis is a zoonosis with increasing concern from a public health perspective. All mammals, including humans, can become infected through ingestion of contaminated meat or oocysts. During its epidemiological cycle, the parasite *Toxoplasma gondii* circulates between rodents and cats through predation and rodents become infected by ingesting oocysts dispersed in the environment through feces of infected cats. Our aim was to analyze the spatial distribution of the parasite at a local scale, in the populations of definitive hosts (cats), intermediate hosts (rodents), and in the soil, simultaneously. Demographic and epidemiological surveys of cats (since 2008) and rodents (since 2010) were implemented in a rural village in France, and in 2011 a random soil sampling was performed.
The parasite *T. gondii* is strongly present in this rural site: 64.7% of samples of cats, 4.1% of rodents and 30.5% of soil sample showed presence of the parasite. The spatial distribution of toxoplasmosis in rodents and soil samples shows the same geographical trends with the infection level decreasing as the distance to the nearest cat feeding sites increases. However, the spatial distribution of soil contamination was more evenly spread than the distribution in rodents. These results could be explained by the behaviour of cats who defecates away from their home range, and after issuance, by oocysts being widely dispersed in the environment. These results about the spatial distribution of oocysts highlight the existence of a wide rural contamination by *T. gondii* that can represent a risk for veterinary and human health.

P22. SPATIAL RISK FOR TUBERCULOSIS IN RELATION TO DOMESTIC AND WILD UNGULATE DISTRIBUTION ASSESSED BY UNMANNED AERIAL SYSTEMS

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The study of host aggregation is relevant in the study of the transmission of diseases in ungulates, both from epidemiological andmanagement perspectives. Ungulates in South Spain are frequently exposed to mycobacteria. Population demography and behavior, as well as environmental exposure may play an important role for intra- and inter-specific pathogen transmission. We hypothesized that Mycobacterium bovis infection prevalence in wild ungulates depends on host ecology and variations in prevalence will reflect variation in the interaction between hosts and environmental aggregation risk factors, namely water points during the dry season.We aimed to study the role of water sources (water holes and marsh-shrub ecotone) relative to natural resources and other hosts in ungulate distribution and environmental TB infection risk in Doñana National Park (DNP, South western Spain). For this purpose, and by using a novel approach (unmanned aerial systems), we mapped the spatial distribution and aggregation pattern of ungulates respect to potential environmental risk factors (environmental water sources) and the distribution of other hosts during the period of the year when water resources becomes more limiting, i.e., drought. Drought severely reduces foodavailability,and therefore aggregation around water resources is expected to be maximal This study revealed that spatial aggregation is significant risk factor for mycobacterial infection in wild ungulates, reflecting both interspecific and intraspecific transmission. Modeling revealed that environmental water sources could act not only as important environmental sources ofmycobacteria, but also by favoring closer contactbetween the species in DNP. This could promote the transmission of M. bovis by close contact and/or indirecttransmission.

P23. MALFORMATIONS FOUND IN WOOD FROGS, *LITHOBATES SYLVATICUS*, FROM NORTHEAST ALBERTA AND THE NORTHWEST TERRITORIES, CANADA

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Amphibian physical abnormalities, reported in multiple species from three continents including several locations in North America, have been ascribed to one or more causes, such as increased UV-B radiation, predation, exposure to pesticides and other environmental contaminants, and eutrophication-associated infection with the trematode *Ribeiroia ondantrae*. Our objective is to document the presence and characteristics of malformations (defective development) and deformities (acquired alteration of a normally-developed structure) in wood frogs, *Lithobates sylvaticus*, from areas in the Canadian boreal forest greatly altered by human activity including oil sands and base metal mining, forestry, and rapid urban expansion. Recent metamorphs (n=25) and adult (n=6) wood frogs with obvious anatomical abnormalities were collected from northeast Alberta and the South Slave region of the Northwest Territories during 2010, 2011 and 2012, as part of a program that uses amphibian health to monitor ecosystem health in the boreal forest. The frogs were fixed in formalin and examined through radiography (Sound-Eklin RapidStart with a flat panel detector, exposure 50kV and 1.2mAs), histology (routine processing and staining with hematoxylin/eosin) and differential staining of the skeleton (alcian blue and alizarin red S stains). Malformations encountered involved the limbs and eyes. Limb abnormalities included amelia, hemimelia, micromelia and ectromelia; eye abnormalities were microophthalmia and anophthalmia. Malformations were more frequently encountered in recent metamorphs and prevalence rates were greater than 10% at some sites. This is the first report that characterizes malformations in frogs from the Canadian boreal forest using radiographic and histological descriptions.

P24. VIABILITY OF *BAYLISASCARIS PROCYONIS* EGGS EXPOSED TO FLUCTUATING TEMPERATURES AT RACCOON LATRINE SITES

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Baylisascaris procyonis is a large zoonotic nematode that occurs in the small intestine of raccoons (*Procyon lotor*), and the larvae can cause visceral, ocular, and neural larva migrans within intermediate hosts. However, eggs of Baylisascaris procyonis dessicate and die at 65 C (150 F). Humans, especially children, have become infected through contact with raccoon latrines, which commonly include tree crevices, woodpiles, barns, and attics. Therefore, we placed temperature and humidity data loggers on the ground in full sun and in the shade, in attics with and without exhaust fans, in woodpiles, in barns, and in closed cars parked in the sun in southern Texas. Data loggers recorded temperature and humidity every 30 minutes during 2012 to determine the likelihood of survival of *Baylisascaris procyonis* eggs at the various potential latrine sites. The hottest month during 2012 was August with a maximum temperature of 42 C (107 F) and 15 days where temperatures exceeded 38 C (100 F; $\bar{x}$ = 2.2 hrs/day; range 0.5 – 6 hrs/day). However, no potential latrine site exceeded 65 C at any time throughout the year. A car parked in the sun came the closest to the lethal limit (i.e., 62 C, 144 F) but only for 1 hour. Southern Texas is one of the furthest southern locations in the contiguous United States and has one of the warmest known climates. Unfortunately it is not hot enough for an extended period to kill eggs of *Baylisascaris procyonis*, making it possible for such eggs to accumulate within an environment.

P25. THIAMINE DEFICIENCY AFFECTING WILDLIFE HEALTH IN THE BALTIC SEA AREA

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Thiamine (vitamin B1) is synthesized in plants, fungi, and bacteria and is essential for all fish and bird species. Thiamine deficiency causes metabolic disorders in several subcellular compartments, such as the cytosol, mitochondria, and peroxisomes. Clinical symptoms include ataxia, convulsions, paralysis, immune suppression, behavioral and memory disorders, reduced feeding, and anorexia. In the Baltic Sea salmon (*Salmo salar*), thiamine deficiency has been observed since 1974. This disorder has been named the M74 syndrome. It occurs in episodes affecting the reproduction in 10–90% of the females, depending on year and river. The disorder causes neurological disturbances and histopathological changes in the brain, muscles and kidneys, both in the yolk-sac fry and in the adults.

Recently, thiamine deficiency has also been demonstrated in adults, newly hatched young, and eggs of herring gulls (*Larus argentatus*), and common eider (*Somateria mollissima*) in connection with extensive paralysis and mortality in bird colonies in the Baltic Sea area. We have observed in these colonies reproductive disorders, with a reduced number of laid eggs, and high mortality (> 90 percent) in eider ducklings during their first week of life. The many observations of advanced thiamine deficiency in adult birds imply that a varying degree of moderate thiamine deficiency occurs among the affected species. This might be an explanation for the observed increased occurrence of incomplete nest building and misplaced eggs in nests of other bird species. The thiamine deficiency may be induced either by a causative agent(s) acting directly on the affected individual, by reduced uptake of thiamine, and/or by insufficient transfer of thiamine between the trophic levels in the food web. Further studies will focus on thiamine levels in the food for these birds, as well as factors involved in the high mortality of juvenile eider ducklings.

P26. BIGHORN SHEEP SINUS TUMORS ARE ASSOCIATED WITH COINFECTIONS BY PNEUMONIA-CAUSING BACTERIAL AGENTS IN THE UPPER RESPIRATORY TRACT

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Recently, we described a novel disease in bighorn sheep characterized by tumors (predominantly fibromyxomas) of the paranasal sinuses, and we have proposed a retroviral etiology for this disease. Grossly, bighorn sheep sinus tumors expand the sinus lining, obstruct the sinus cavities, and exude abundant mucus. We suspect that these features may interfere with the normal clearance of bacterial pathogens from the upper respiratory tract. Proliferation of bacteria in the upper respiratory tract may lead to bronchopneumonia, which is the leading infectious cause of death in bighorn sheep. The purpose of this project was to determine whether or not bighorn sheep sinus tumors are associated with the presence of pneumonia-causing bacteria in the upper respiratory tract. We found that tissues from the upper respiratory sinuses of bighorn sheep with sinus tumors were more likely to harbor potentially pathogenic bacteria than tissues from bighorn sheep lacking sinus tumors. These findings may have implications for understanding the development of bacterial bronchopneumonia in bighorn sheep herds affected by sinus tumors.

P27. PREVALENCE OF ENDOPARASITES RELATED TO DIFFERENT FEEDING SITES OF RODENT IN KIRTIPUR, NEPAL

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Rodents are found in wide range of habitat and play an important role in many zoonotic cycles. Rodents of local houses, vegetable markets, departmental stores, agricultural fields, and garbage disposal place were studied to understand, where they are highly infected? Also, we aimed to identify the most prevalent endoparasites. For this a total of 32 rodents (Rodentia: Muridae) belonging to seven species (12 *Rattus turkestanicus*, 6 *Rattus nitidus*, 6 *Rattus rattus*, 3 *Niviventer fulvescens*, 3 *Bandicota bengalensis*, 1 *Bandicota indica* and 1 *Mus cervicolar*) were trapped from five different sites and endoparasites were collected. Salt (NaCl(aq)) flotation technique was followed to extract parasitic eggs and larvae from the gut contents. Overall infection rate of endoparasites (96.8%) was found. Ten different endoparasites were identified: 1 trematode, 2 cestodes, 6 nematodes and 1 acanthocephalan species. Among the ten species of identified helminthes, six species (60%) have been incriminated as zoonotic. The most prevalent helmith type was the cestode *Taenia taeniaeformis* (strobilocercus larva) (62.5%) followed by nematode *Syphacia* sp. (53.1%) and cestode *Hymenolepis diminuta* (12.5%). Prevalance of infected liver by the eggs of *Capillaria* sp. was 43.7%. The highest prevalence of parasitic infection was found in household areas (28.1%), followed by agricultural field (25%), departmental stores (21.8%), vegetable market (15.6%) and garbage site (6.2%). The diversity and prevalence of parasites were statistically [$F(cal) = 7.8$ and $F(tab) = 2.447$,(for $v1=4$ and $v2=56$), $P < 0.05$] found to be affected by the type of sites, with household area being at high risk area for zoonotic disease transmission.

P28. HYDROCEPHALUS IN FOUR BEARS

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Hydrocephalus is an increase of cerebrospinal fluid within the ventricular system of the brain, occurring secondary to congenital or acquired causes of obstruction. Occasionally in severe cases, periventricular clefting and tearing occur. Hydrocephalus has been reported in a wide variety of animal species, including the American black bear (Ursus americanus). In this report, four cases of hydrocephalus in American black bears are described. Three wild bears were 3 to 10 months of age; one captive bear was 20 years old. Clinical signs varied from none to seizures, cortical blindness, and ataxia. At necropsy, the main gross findings were doming of the calvarium, compression and flattening of the gyri, and dilatation of the lateral ventricles. One case had severe bilateral ventricular dilatation with loss of the septum pellucidum, atrophy of the surrounding corpus callosum, and bilateral periventricular tears. Histologically, the mild cases had lesions varying from none to moderate cortical necrosis and edema. In the severe case, there was grossly visible tearing in the area involving the caudate nucleus, internal capsule and adjacent cerebrum. Histologically, this area was characterized by axonal loss and degeneration, necrosis, hemorrhage, and astrocytosis. All four cases are likely congenital given that an acquired obstruction was not found grossly or histologically. This is the first report of periventricular changes associated with hydrocephalus in a black bear.

P29. TRANSMISSION OF *TOXOPLASMA GONDII* IN WILDLIFE IN THE SOUTHEASTERN US

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Toxoplasmosis, caused by *Toxoplasma gondii*, is one of the most common infections of humans and animals worldwide. Toxoplasmosis is considered one of the Neglected Parasitic Infections, which is a group of parasitic diseases that has been targeted by the Centers of Disease Control and Prevention for public health action. Infection of *T. gondii* can occur by ingestion of microscopic oocysts in contaminated food or water or by ingestion of tissue cysts in undercooked meat. Genotyping has disclosed that *T. gondii* isolates can be divided into six different groups that are associated with varying degrees of virulence, with some being highly virulent. *Toxoplasma gondii* infection occurs in many wild birds and mammals; however, genotype data for isolates from these hosts are lacking. Previous studies of isolates from US wildlife suggest that wild species maintain a greater diversity of *T. gondii* genotypes than is found in agricultural animals – suggesting a wild/feral animal diversity model. To further understand the diversity of *T. gondii* in southeastern US wildlife, we screened sera from multiple wild bird and mammal species for *T. gondii* exposure via the modified agglutination test. Heart or tongue from select seropositive animals was digested and inoculated into mice to propagate *T. gondii* tachyzoites. Tachyzoites were genotyped by multiplex multilocus nested PCR-RFLP method employing 10 genetic markers. Of the 204 sampled wild animals, 74 (36.3%) were seropositive. Genotyping results of nine white-tailed deer and one mink disclosed five distinct strains, including the type 12 and type III lineages common in US wildlife, two other previously identified genotypes, and one novel genotype. We conclude that *T. gondii* is prevalent in wildlife from the southeastern US and that further research is needed to understand *T. gondii* diversity, transmission dynamics among wildlife, and the associated potential for human infection with these wild/feral animal genotypes.

P30. PREVALENCE OF SEXUALLY TRANSMITTED DISEASES IN TWO WILD CHIMPANZEE POPULATIONS

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Sexually transmitted diseases (STDs) can persist endemically and are known to cause sterility and increased infant mortality in humans. African apes (i.e., chimpanzees, bonobos and to a lesser extent gorillas) show promiscuous mating behavior that could offer opportunities for STD transmission, yet little is known about the prevalence and impact of STDs for this endangered primate group. In this study, we tested 111 wild chimpanzees from two habituated communities in Uganda for *Chlamydia* and *Trichomonas* spp., both of which are common human STDs. Voided urine samples (N=394) were screened with nested PCR. All chimpanzees were negative for *Chlamydia*, whereas 38% were positive by *Trichomonas* PCR. Females were significantly more likely to be infected than males, and that individuals were more likely to be infected during the dry versus rainy season. A subset of positive samples (N=29) were cloned and sequenced, and the resulting sequences formed two main groups, one group (N= 23) was most similar to *Tetratrichomonas* spp. from several mammals, reptiles, and birds whereas the other group was a sister group to the tetratrichomonads. Notably, *tetratrichomonads* have fecal-oral transmission rather than sexual transmission. Interestingly, some chimpanzees appear to be co-infected with both types of trichomonads. To investigate transmission routes for the two tetratrichomonad groups found in this study, we will screen fecal samples collected from the same individuals. Despite lack of STDs, we encourage investigations for great ape STDs, as this work could offer insights for the management of endangered great apes and for our understanding human STD origins.

P31. INVESTIGATING THE EFFECTS OF MERCURY AND PCB EXPOSURE ON HEALTH AND REPRODUCTION OF A PISCIVOROUS BIRD

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We investigated concentrations and effects on health/reproductive success of Hg and the unique PCB mixture Aroclor 1268 in least terns (Sternula antillarum) at a highly-contaminated estuary in coastal Georgia (LCP Superfund) where until 1994 industrial enterprises dumped effluent containing these contaminants. High concentrations of Aroclor 1268 and Hg are found in local biota, but no studies examine impacts on piscivorous birds. We compared nesting success, clutch size, egg volume and fresh weight, eggshell thickness, prevalence of congenital deformities, fluctuating asymmetry in offspring, growth rate in chicks, lymphocyte estimates, and hemoparasite load, between the LCP least tern breeding colony and other colonies. We correlated these parameters with concentrations of PCBs and Hg found in eggs, chick feathers, feces, and whole bodies. Mean Aroclor 1268 concentrations of eggs were highest at colonies in and just outside LCP when compared to other colonies. Mean Hg concentrations of eggs varied little among sites, with highest concentrations closest to LCP. Concentrations of Aroclor 1268 in eggs, Hg in chick feathers and Hg sediment samples were highest at the site closest to LCP. However, fecal Hg was highly variable within each colony, and did not differ significantly among colonies—thus, chick samples best reflect contamination than eggs, as chicks are fed local fish until fledging, while adults accumulate contaminants over time. Lastly, we report the transport of Aroclor 1268 ~110 km north, and ~70 km south from its point source (LCP)—transport of this unique PCB mixture > 40 km has not previously been documented.

P32. RODENTICIDES IN BIRDS OF PREY IN MASSACHUSETTS, USA: A COMPARISON OF DATA BEFORE AND AFTER EPA RISK MITIGATION ACTION

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In response to the threat posed by second generation anticoagulant rodenticides (SGARs) to children, domestic animals, and wildlife, the EPA issued a Risk Mitigation Decision in 2008 prohibiting the sale of SGARs on the general consumer market. Under this decision, SGARs were to be removed from these markets by June 2011, and these products were to be replaced by first generation anticoagulants (FGARs) or the neurotoxin bromethalin, both of which are required to be used in tamper-resistant bait stations. Although not all manufacturers complied with the EPA decision by June 2011, most manufacturers did comply and introduced new these new products to the general consumer market. Data collected on four species of birds of prey in Massachusetts, USA, prior to June 2011 revealed a high level of exposure to SGARs, particularly brodifacoum. This report details results of follow-up screening on these same four species from the same geographic area. Both FGARs and SGARs were screened for, as well as bromethalin. Results will be presented and comparisons to pre-June 2011 data will be made.

P33. OCCURRENCE OF EXTENDED-SPECTRUM β-LACTAMASE PRODUCING E. COLI IN WILD BIRDS FROM THE NETHERLANDS

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Objectives: The occurrence of extended-spectrum β-lactamases (ESBL's) has been studied extensively in Dutch Enterobacteriaceae from humans and livestock, however information on ESBL's in Dutch wild life is lacking. In this study, we screened for the presence of ESBL-producing E. coli obtained from Dutch wild birds. ESBL-genes and plasmids were further characterized to reveal the genetic background.

Methods: Cloacal swabs were obtained and selectively cultured in media with cefotaxime. All cefotaxime resistant E. coli were screened for beta-lactamase gene families using a microarray. The ESBL-genes were identified by PCR and sequencing. To determine the size of plasmids and the location of ESBL-genes S1-PFGE was performed on transformants followed by Southern hybridization. Plasmids were typed with PCR based replicon typing.

Results: The study included 414 cloacal swabs originating from 55 different bird species. Cefotaxime resistant E. coli isolates were identified in 65 samples (15.7%) from 21 different bird species. The presence of ESBL-genes was confirmed in all 65 cefotaxime resistant E. coli predominately consisting of blaCMY-2 and variants of blaCTX-M. Replicon typing of the ESBL-carrying plasmids revealed the predominant presence of IncI1 plasmids and variants of IncF plasmids.

Conclusions: Our results indicate a wide dissemination of ESBL-genes in wild birds especially among waterfowl, gulls and waders. The identified genes and plasmids reflect those predominant in livestock animals as well as in humans.

P34. *CHLAMYDIA PSITTACI* IN WILD BIRDS IN THE NETHERLANDS

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Chlamydia psittaci is the causative agent of the zoonosis psittacosis (or ornithosis). Birds, especially psittacine birds and pigeons, are the main source of infection of the bacterium for humans. In birds *C. psittaci* can cause disease with symptoms like conjunctivitis, inactivity and weight loss, but most of the time birds are symptomless carriers. *C. psittaci* can be excreted via excreta including faeces. For each species, the number of samples ranged from one to 148 (mallard). From the swab DNA was extracted and tested in a real time Polymerase Chain Reaction (PCR) targeting the OmpA gene. In 2010, 90 samples were tested from 14 bird species. In 2011, 112 samples were tested from 19 bird species. In 2012, 394 samples were tested from 46 bird species. DNA of *C. psittaci* could be detected in 5 mute swans, 2 mallards, 1 eurasian coot, 3 northern gannets, 1 great black-backed gull, 2 common buzzards and 5 herring gulls. In total eighteen (3.0%) of the 596 tested birds were positive for C. psittaci DNA. *Chlamydia psittaci* was detected in a wide variety of wild birds in the Netherlands with an overall rate of positive birds of 3.0%. The number of animals that were sampled for each species varied greatly, and no information on the prevalence in different bird species is available. Further research is needed to value these results and its implications for public health

P35. PARALYTIC SHELLFISH POISONING IN KITTLITZ'S MURRELET NESTLINGS

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Paralytic shellfish poisoning (PSP) in humans is caused by eating shellfish contaminated with a suite of neurotoxins (saxitoxins) produced by marine dinoflagellates, most commonly *Alexandrium* sp.. Saxitoxin binds to and blocks sodium channels in nerve cell membranes, stopping the flow of nerve impulses; severe cases may result in respiratory paralysis that is fatal if untreated. PSP is well documented in humans, but has been rarely reported in wild birds. Shellfish accumulate saxitoxin through direct ingestion of toxic algae. Zooplankton also ingest toxic algae, and in turn may be ingested by marine organisms at higher trophic levels. The majority of documented bird deaths from PSP appear due to consumption of planktivorous fish. During 2011 and 2012, several apparently healthy Kittlitz's murrelet (*Brachyramphus brevirostris*) nestlings on Kodiak Island died. Most of these nestlings were being monitored by remote cameras. Nestlings were being fed regularly by adults and died during mild weather conditions. High levels of saxitoxin were documented in crop content and/or liver in 87% of nestling carcasses (ELISA), and it was determined that exposure to saxitoxin was likely the cause of death. Camera data indicated that nestlings died shortly after consuming sand lance (*Ammodytes hexapterous*), which is the fish species most commonly associated with the biomagnification of saxitoxin. Marine bird deaths from PSP may be under-reported.

P36. ASSOCIATION OF HAEMOGREGARINES INFECTION OF GOPHER TORTOISES (*GOPHERUS POLYPHEMUS*) WITH THE GOPHER TORTOISE TICK (*AMBLYOMMA TUBERCULATUM*)

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Haemogregarines (genera *Haemogregarina, Hepatazoon*, and *Hemolivia*) are common intraerythrocytic parasites of reptiles, although they are relatively rare in tortoises. Because haemogregarines of African and European tortoises are transmitted by ticks, this study was conducted to investigate the potential role of the gopher tortoise tick (*Ambylomma tuberculatum*) as a vector of a recently detected haemogregarine in gopher tortoises (*Gopherus polyphemus*). Two sites were included in this study; one was the Jones Ecological Research Center (JERC) at Ichauway in Newton, GA where ticks have a patchy distribution across the property. A second site, St Catherines Island in Liberty, GA, is included because it is part of a translocation event that moved tortoises from the mainland where they were infested with ticks to the island where ticks are rare/absent. Tortoises were captured from 1994-2011 on St. Catherines island and from 2009-2012 at the Jones Center. Blood smears were prepared, stained with modified Giemsa, and examined for parasites. Positive samples were further analyzed to calculate a parasitemia. At the JERC, data show that the majority of haemogregarine-infected tortoises were trapped from three areas known to have tick infestations. Additionally, preliminary data from St. Catherines Island shows that tortoises hatched on the island are all negative and that parasitemias in adult tortoise (that were infected prior to translocation) declined over time. These preliminary data suggest that haemogregarine infections in gopher tortoises are correlated with the tick species A. tuberculatum, but further research is necessary to confirm that haemogregarine parasites are transmitted by this tick species.

P37. TIME … AND CWD … MARCHES ON

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Alberta began surveillance for CWD in wild deer in 1998. Cumulatively, we tested over 48,000 wild cervids and detected the disease in 161 deer and one moose. Ongoing surveillance relies largely on hunter harvest samples, supplemented with clinical emaciated cervids (and antelope) across the province and opportunistic road-kills within CWD risk areas. Management included increased harvest opportunities and aggressive winter disease control applied by way of government-directed herd reduction in the vicinity of known CWD cases from 2006 to 2008, inclusive. Since 2008 the program focused on disease surveillance only. Consistent patterns in the data indicate: recent invasion from adjacent areas of Saskatchewan, disease occurrence in two primary watersheds, predominance of infection in mule deer, and higher incidence in adult males. Targeted winter disease control appeared to limit the rate at which CWD spread geographically and numerically (although, as with most field data, the evidence is not definitive). After the control activities were discontinued, the rate of geographical and numerical spread appeared to increase. With the current management approach, we predict CWD will continue to increase its occurrence in local deer populations within the enzootic area and expand further westward in Alberta.

P38. BLOOD SERUM CHEMISTRY AND HEMATOLOGY IN FIELD-FRESH RACCOONS (*PROCYON LOTOR*) IN NORTHWEST MISSOURI DURING SUMMER.

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Blood serum chemistry and hematology profiles are basic diagnostic tools for assessing and monitoring health conditions in individuals and populations, whether human or wildlife sources. The purpose of this study was to 1) establish normal reference profiles for hematological characteristics and serum chemistry for healthy, field-fresh raccoons from an urban habitat in NW Missouri while chemically restrained, and 2) determine if there were any gender differences in serum chemistry and/or hematological values. Nineteen male and 21 female raccoons were live trapped then chemically restrained. We took standard morphometric measurements, noted their reproduction condition, checked them for ectoparasites, and then marked them with a metal ear tag and a PIT tag. We took up to 5 mL of blood from the jugular vein; 3 mL of the sample was put in a sterile red top Vacutainer allowed to clot, centrifuged to separate serum, and then transferred to a fresh red top Vacutainer. The remaining blood was put into a sterile purple top Vacutainer@ containing EDTA as an anticoagulant. Both samples were shipped to the lab to be analyzed for 26 serum chemistry characteristics, and 14 hematological characteristics. We found significant gender differences for the albumin, and in four hematological values: erythrocytes; MCHC; platelet count; and eosinophils. We know of no other published literature on blood chemistry and hematology values for field-fresh raccoons. Preliminary comparisons with the International Species Information System (ISIS.org, Apple Valley, MN) database resulted in significant differences for 15 blood chemistry and 8 hematological values.

P39. DETECTION OF mecC-POSITIVE METHICILLIN-RESISTANT *STAPHYLOCOCCUS AUREUS* (MRSA) (CC130-MRSA-XI) IN DISEASED EUROPEAN HEDGEHOGS (*ERINACEUS EUROPAEUS*) IN SWEDEN

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Methicillin-resistant *Staphylococcus aureus* (MRSA) are a major problem for infection prevention and control and antibiotic treatment worldwide. The resistance of MRSA against almost all beta-lactam compounds in clinical use is mediated by the expression of an alternate penicillin-binding protein (PBP2a), which is encoded by the mecA gene. Recently, a novel mec gene termed mecC mediating beta-lactam resistance in *S. aureus* has been described. This gene is encoded on a staphylococcal cassette chromosome-mec XI (SCCmec XI) element that has to date been identified in clonal complexes (CCs) 49, 130, 425, 599 and 1943. Because the sequence of mecC is highly divergent, it cannot be detected by routinely used molecular tests designed to identify mecA. Some of the currently known mecC isolates have been identified from humans and various animal species in Europe. In this study we describe mecC-positive *S. aureus* (CC130-MRSA-XI) recovered from two diseased free-ranging European hedgehogs (Erinaceus *europaeus*) and the lesions related to the infections. One hedgehog was found dead in a garden in 2003 in central Sweden. It was diagnosed with acute *S. aureus* septicaemia. It showed multiple foci of necrosis and inflammatory infiltration in the kidneys, spleen, lungs, meninges and brain parenchyma, with numerous Gram-positive cocci. The other hedgehog was found alive on the island of Gotland in 2011. It was taken care of in a wildlife rehabilitation centre, but did not recover and was euthanized. It had a severe dermatitis, with ulcerations and dense infiltration of neutrophils. CC130-MRSA-XI isolates were cultured from lesions from both hedgehogs and were essentially identical to previously described isolates from humans. To the best of our knowledge, this is the first report of CC130-MRSA-XI in hedgehogs. CC130 might be a zoonotic lineage of *S. aureus* and SCCmec XI/mecC may have originated from animal pathogens

P40. DEVELOPMENT AND IMPLEMENTATION OF A BROAD-BASED PCR SURVEILLANCE METHOD FOR BACTERIAL DNA IN ALASKAN WILDLIFE TISSUES

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Current methods of bacterial disease surveillance include antibody detection, culture, and agent-specific PCR. These methods are agent-specific and an organism or disease must be suspected to be present before diagnostic tests or surveys are conducted. Additionally, these methods can be difficult to interpret and are often cost prohibitive when conducting large surveys in wildlife populations. Here we discuss the development and implementation of PCR protocols to survey for the 16s rRNA gene in tissue samples of Alaskan wildlife. Between June 2011 and October 2012, quantitative real-time PCR (qPCR) was used in two large surveys of presumed healthy trapped red fox (*Vulpes vulpes*) tissue samples (n=680) and harbor seal (*Phoca vitulina*) blood samples (n=144). End-point PCR (n=454) was used on smaller sets of blood and tissue samples received from necropsy specimens from the Alaska Department of Fish and Game. Of all samples (n=1298), 108 had detectable PCR product. Upon sequencing, 65 revealed interpretable sequences, 47 of which are known or potential pathogens. Only a few potentially pathogenic species were detected during large surveillance efforts of presumed healthy animals. Relatively more potentially pathogenic and known pathogenic species were detected in tissues collected during necropsy of diseased animals. These results show that 16s rRNA gene-based PCR methods are useful tools able to perform large-scale surveillance for bacterial pathogens.

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