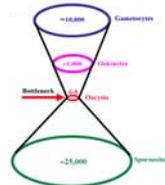


Past

- *Plasmodium falciparum* and *P. vivax* are co-endemic in Asia.
- We explored transmission of variants through the mosquito.
- Haplotypes were compared between patient blood and patient blood that was membrane fed to mosquitoes.

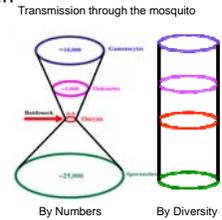


Wang and Jacobs-Lorena. Trends Biotechnol. 2013

UNC INFECTIOUS DISEASE EPIDEMIOLOGY AND ECOLOGY <https://www.med.unc.edu/infdis/ideel/>

Past

- *Plasmodium falciparum* and *P. vivax* are co-endemic in Asia.
- We explored transmission of variants through the mosquito.
- Haplotypes were compared between patient blood and patient blood that was membrane fed to mosquitoes.
- Bioinformatics pipeline SeekDeep\*



\*Hathaway NJ, Parobek CM, Juliano JJ and Bailey JA. (2018) Nucleic Acids Research, doi:10.1093/nar/gkx1201

Present

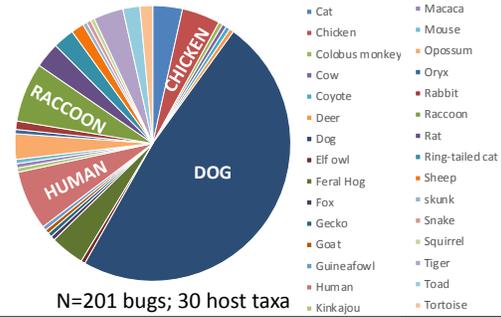
- Dr. Sarah Hamer's Lab focuses on ecology and epidemiology of disease at the interface of wildlife, domestic animal, and human populations.
- The vector of interest is *Triatoma*, which carries *Trypanosoma cruzi*
- We look at identifying bloodmeal hosts using a mitochondrial gene in Amplicon Deep Sequencing.
- Bioinformatics pipeline – SeekDeep\* + NCBI BLAST



\*Hathaway NJ, Parobek CM, Juliano JJ and Bailey JA. (2018) Nucleic Acids Research, doi:10.1093/nar/gkx1201

Present

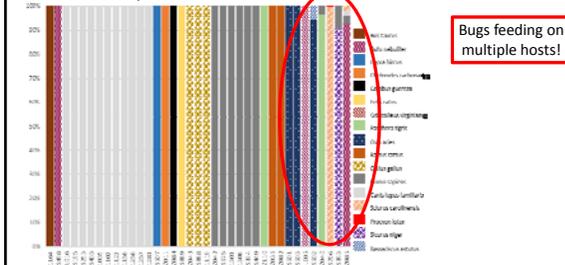
- Bloodmeal analysis of triatomines: status quo Sanger sequencing identifies only single host per bug



N=201 bugs; 30 host taxa

Present

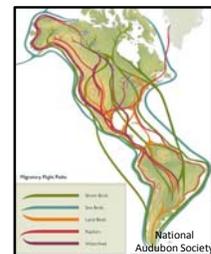
- Amplicon deep sequencing (Illumina MiSeq) reveals host community



N=38 bugs; 17 host taxa

Future

- Following our interest in spread of disease, we look at migratory birds and their ectoparasites.
- Applying NGS techniques to examine pathogen carriage.





Byron R. Buckley, M.S.  
 Genetic Assessment of Northern  
 Bobwhite Immune System  
 Texas Tech University

### Decline

- Range wide decline noted by 1940's
- Texas population
  - 5.8% decline 1999-2009
  - 2.8% decline in Texas panhandle region
- WHY?

BBS Trend Estimates 1966-2003

### We are still working on the causes

- Habitat?
- Human?
- Predation?
- Reproduction failure?
- Disease?\*

### Immune System Analysis

- Toll like receptors
  - Correlations in survival?
  - Population numbers?
- Population diversity
  - Microsats
  - Immune genes
- 2000 samples across 1.2 million acres

Ecological Regions of Texas

Map credit: <http://www.tpwd.state.tx.us/>

Stefano Catalano  
 Multi-host Spectrum of *Schistosoma* species/  
 hybrids and epidemiological role of  
 humans, livestock, wild mammals and  
 snails in West Africa  
 Royal Veterinary College

**PhD Student at the Royal Veterinary College**

**Multi-host spectrum of *Schistosoma* species/hybrids and epidemiological role of humans, livestock, wild mammals and snails in West Africa**

**Research Interests & Past Experiences**

**Parasitology & One Health applied to:**

1. Wildlife conservation and ecosystem health
2. Diseases at human-wildlife interface

**NGS Setup Protocols and RADseq Data**

**Box 2 | Ecological and evolutionary insights from RADseq data**

Restriction site associated DNA sequencing (RADseq) can be used to answer a wide variety of ecological, evolutionary and conservation-related questions.

**Genomics of adaptation**  
 Selection on colour patterns was found to be the most important factor maintaining butterfly hybrid zones by association mapping analyses (see the figure, part a and c). Similar tests can be conducted using RADseq data for two butterfly species (*Pieris napi* and *P. m. aeneus*). In part (b), these analyses revealed that  $F_{ST}$  outliers primarily occurred in genomic regions associated with colour pattern variation. In part c, association scans are colour-coded according to the phenotype. The results illustrated in part c, and only the top 20 associated SNPs for each phenotype are shown. In part d,  $F_{ST}$  values are shown for all SNPs, with significant outliers in red or orange. Unmapped sequence scaffolds that are not assigned to chromosomes in a reference genome assembly. Many pipelines have also used RADseq to identify the genomic architecture of adaptation in other study systems (for example, RFL 24.68.77).

**Island and genetic diversity**  
 A study investigating heterozygosity-fitness correlations in oak, *Quercus*, found a nearly fivefold higher correlation with a fitness-associated trait (d.d.2)

**Effective population size ( $N_e$ )**  
 Thousands of SNPs generated using RADseq were used to estimate  $N_e$  in salmon and smelt from western North America<sup>105</sup>.

**Population structure, phylogeography and conservation units**  
 RADseq was used to develop a population-informative SNP panel to monitor stock composition in salmon and to delineate population units in brown trout (see also RFL 22.48).

**Introgression**  
 Haldane et al.<sup>106</sup> used RADseq to identify 3,330 genomic diagnostic SNPs and to calculate admixture between a native and an invasive trout species; see also RFL 25.35.

**Phylogenomics**  
 RADseq data generated a highly resolved tree for 18 species of Lake Victoria cichlid fish, whereas previous analyses using amplified fragment length polymorphism (AFLP) microsatellites or a handful of sequence-based markers failed to resolve species-level relationships for these species<sup>107</sup>.

Andrews et al. 2016 *Nature Reviews*



UFRJ

## Liliane Cavalcante

### Characterization of wild felids Virome

### Federal University of Rio de Janeiro

#### Research - Virome

Leopardus Tigrinus  
(Northern leopard cat)Panthera Onca  
(Jaguar)Panthera Leo  
(Lion)Leopardus Pardalis  
(Civet)Puma Concolor  
(Mountain lion)Panthera Tigris  
(Tiger)

#### Methods

- Captive species (From Rio de Janeiro Zoo)
- Virus DNA/RNA extraction
- Illumina sequencing
- Data processing:
  - Filter low quality and small size reads (Sickle).
  - Filtering host reads (bwa/samtools)
  - Blastx against vertebrate virus data bank
  - Blastx against nr/nt data bank
  - Contigs assembling (Geneious)

BRAGGACACTATCAGCGGGCAGCAAAGACT  
Liliane Cavalcante - PhD Student  
Federal University of Rio de Janeiro, Brazil

#### Goals

- Identify the major circulating viruses in wild cat species.
- Characterize viruses by sequencing the entire genome.
- Check the correlation of the presence of viruses and clinical signs.

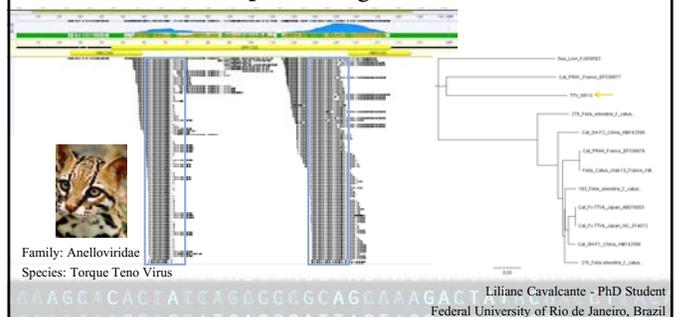


#### What we want is...

- Optimize the pipeline we already have

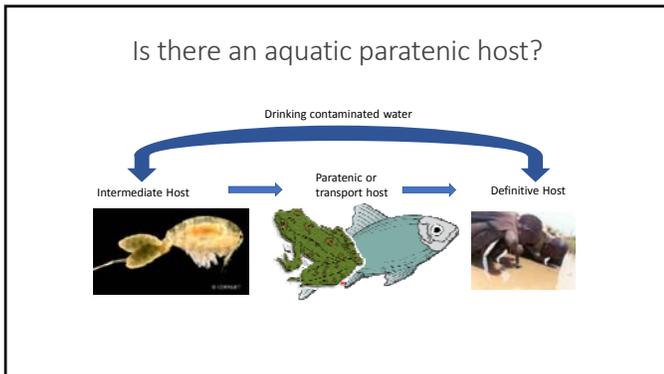
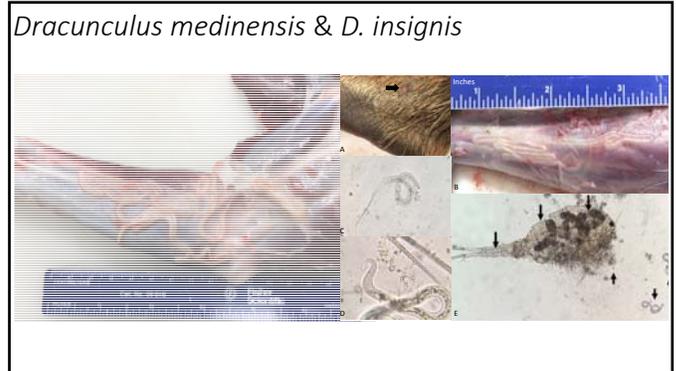
BRAGGACACTATCAGCGGGCAGCAAAGACT  
Liliane Cavalcante - PhD Student  
Federal University of Rio de Janeiro, Brazil

#### Interests - Data processing





Christopher Cleveland  
 Guinea Worm Eradication Program  
 University of Georgia



Guinea Worm Eradication Program  
 Chad, Africa

- Overall decrease in human cases
- Appearance and increase of dog infections since 2012.
- *Dracunculus medinensis* from humans and dogs genetically very closely related.
- Evidence of host switching among Dracunculids?
- Why are some Dracunculids host-specific vs. host generalists?
- How does this relate to the use of paratenic or transport hosts?

THE CARTER CENTER

Dr. Rick Gerhold  
 Wildlife Disease investigation and  
 classical and molecular parasitology  
 University of Tennessee



Training in wildlife disease investigations and classical and molecular parasitology

Investigating moose decline associated parasites

Working on developing ELISA tests for both parasites

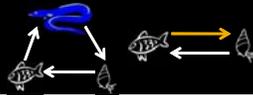
Detected emergence of *Elaeophora* both in moose from MN

Interested in utilizing NGS tools for future research projects



Dr. Kristin Herrmann  
 Evology and evolution of helminth parasites  
 and their hosts  
 Tarleton State University

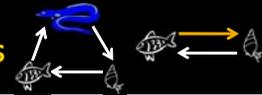
## Background



- B.S., University of Minnesota
- M.S., Minnesota State University Mankato
  - Thesis: Waterbird mortality associated with an invasive intermediate host of two trematodes
  - Advisor: Dr. Bob Sorensen
- Ph.D., University of Otago
  - Dissertation: Reproductive strategies of a trematode
  - Advisor: Prof. Robert Poulin
- Assistant Professor, Tarleton State University



## Research Interests



- Helminth parasites with complex life cycles
  - Ecology of host-parasite interactions
  - Communities and diversity
  - Cophylogeny of parasites and hosts
  - Cryptic species
  - Ecology and evolution of life history traits
- Other types of pathogens



BOISE STATE UNIVERSITY

Stephanie Hudon  
Parasite Load and Telomere  
Shortening in North American Raptors  
Boise State University

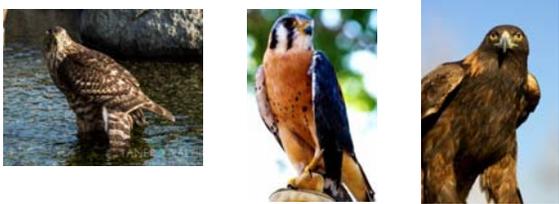


- The gut microbiome of mule deer is hypothesized to adapt to enable them to feed on sagebrush in the winter which contains toxic chemicals
- Captive deer were fed a sage-free pellet diet and then shifted to a sagebrush diet and then returned to a pellet diet
- Fecal samples were collected for microbial analysis
- Expand the study to other herbivore-sagebrush systems such as white-tailed deer and pygmy rabbits

© 2016 Boise State University 2



### Parasite Load and Telomere Shortening in North American Raptors



© 2016 Boise State University 3



### Avian Parasite Load and Telomere Senescence

Science, 2015, Jan 23;347(6220):436-8. doi: 10.1126/science.1261121

**Chronic infection. Hidden costs of infection: chronic malaria accelerates telomere degradation and senescence in wild birds.**

Alpar, M.<sup>1</sup>, Hasselquist, D.<sup>2</sup>, Hansson, B.<sup>3</sup>, Zentgraf, C.<sup>4</sup>, Nylin, S.<sup>1,4</sup>, Bensch, S.<sup>5</sup>



© 2016 Boise State University 4



THE UNIVERSITY  
OF QUEENSLAND  
AUSTRALIA

# Lyndal Hulse

## The Effect of Chlamydia on Koala Semen Quality

### The University of Queensland

#### Current status of South-East QLD Koalas

Conservation Status: Vulnerable (DEHP 2015)  
Population Estimate: 79,264 (53% decline over 20 years)  
(Adams-Hosking, McBride et al. 2016)

Threats to the species:

- Loss of habitat
- Trauma (car hits, dog attacks)
- Disease: Chlamydiosis



THE UNIVERSITY  
OF QUEENSLAND  
AUSTRALIA

#### Chlamydia and Koalas

- Koalas are infected with two chlamydial species:  
*C. pecorum* and *C. pneumoniae*
  - *C. pecorum* being the more pathogenic and widespread
- Clinical syndromes associated with *C. pecorum* in the koala:
- Ocular infection
  - Urinary tract infection
  - Reproductive tract infections



THE UNIVERSITY  
OF QUEENSLAND  
AUSTRALIA

**Objective:** Examine the effect of Chlamydia on koala semen quality with a view to developing methodologies to "clean-up" Chlamydia-infected semen for the purposes of artificial insemination and gamete recovery

#### Project Aims:

- Investigate the incidence of Chlamydia in semen of koalas in SEQ
- Detection of Chlamydia in semen and urogenital swabs correlated with clinical signs of chlamydiosis
- The effect of Chlamydia on sperm quality in koalas
- Transmission of Chlamydia using naturally-infected koala semen
- The effect of Chlamydia on spermatogenesis in the koala
- Antibiotic treatment of koalas and the effect on sperm quality: *in vivo* and *in vitro*

THE UNIVERSITY  
OF QUEENSLAND  
AUSTRALIA

#### Future Directions

- Koala genome released on NCBI May 2017
- Begin investigating whether there is genetic association between koalas and Chlamydial Disease



THE UNIVERSITY  
OF QUEENSLAND  
AUSTRALIA



Melanie LaCava  
Landscape Genomics of Wyoming Pronghorn and Mule Deer  
University of Wyoming

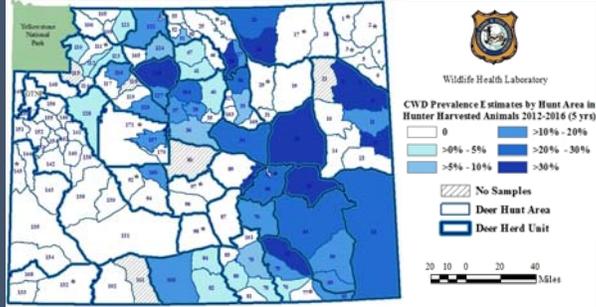
### Landscape genomics of Wyoming pronghorn and mule deer



Collaborators



### Genetic connectivity and chronic wasting disease in Wyoming mule deer



Wildlife Health Laboratory

CWD Prevalence Estimates by Hunt Area in Hunter Harvested Animals 2012-2016 (5 yrs)

- 0
- >0% - 5%
- >5% - 10%
- >10% - 20%
- >20% - 30%
- >30%
- No Samples
- Deer Hunt Area
- Deer Herd Unit

20 10 0 20 40 Miles

Parjwol Manandhar  
Carnivor Disease Research in Nepal  
University of Tampere



### Research studies on wildlife disease at CMDN

- Bengal tiger (*Panthera tigris*) gut microbiome research
- Carnivore disease project (Canine distemper virus)
- Fecal viral metagenomics in tigers, snow leopards
- Tuberculosis in elephants/rhinos/boars/deer
- Avian influenza and Newcastle disease viruses in chicken and wild birds

### Carnivore disease project

Project site

Kailhmandu valley

Bhaktapur

### Carnivore disease project

Project site

Canine distemper virus (CDV)

Felidae/JungleCat

Felidae/LeopardCat

Felidae/Leopard

Canidae/DomesticDog

Viverridae/Civet

Canidae/Jackal

Mustelidae/Marten

### Carnivore disease project

Lab Procedures

- RNA extraction and cDNA preparation
- PCR to screen for Paramyxoviridae virus family
- Gel electrophoresis to determine Positive results
- Hemagglutinin (H) & Phosphoprotein (P) gene PCR followed by sequencing

Phosphoprotein (P) gene

- Targeted fragment -> 450 bp
- Trimmed fragment -> 362 bp

Riley Mummah  
*Leptospira interrogans* in the  
 California Channel Island Ecosystem  
 The University of California

### *Leptospira interrogans* in the California Channel Island Ecosystem

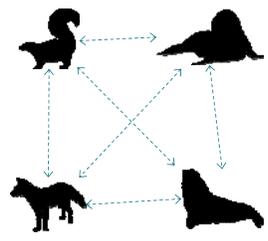
- *Leptospira interrogans* serovar Pomona was first detected in California sea lions (CSL) in 1970 and circulated continuously in sea lions from 1984-2013.
- *L. interrogans* serovar Pomona was discovered in 2009 on Santa Rosa Island in Channel Island foxes and spotted skunks.
- Subsequent serological studies have shown that it appears to have circulated in island foxes and other terrestrial mammals on Santa Rosa Island since at least the 1980s.
- The genetic profile (by VNTR analysis) of fox/skunk isolates from 2010 is nearly identical to isolates from CSL, raising questions about past transmission links.



 <p><b>Channel Island Fox</b></p> <ul style="list-style-type: none"> <li>• Endemic to California</li> <li>• Experienced a major population bottleneck in late 1990s</li> <li>• Underwent captive breeding and all releases were complete by 2008</li> </ul>	 <p><b>Leptospira interrogans</b></p> <ul style="list-style-type: none"> <li>• Generalist pathogenic spirochete bacteria</li> <li>• Infects mammals</li> <li>• Classified by serovar                             <ul style="list-style-type: none"> <li>• Does not map onto genetics</li> </ul> </li> <li>• 4.3 Mbp</li> </ul>
--	---

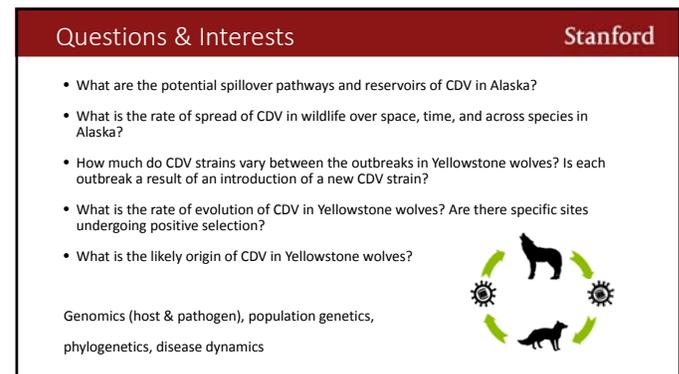
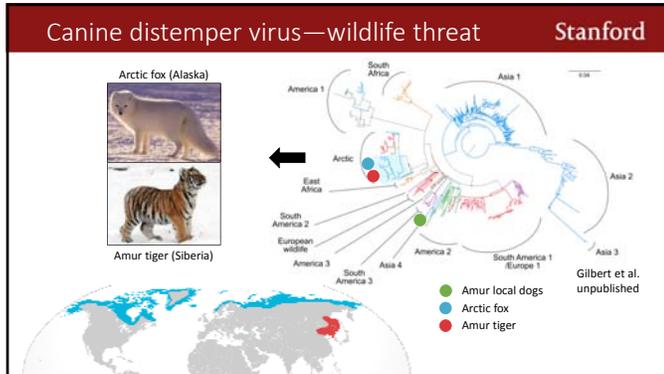
### A bit about me

- Lloyd-Smith lab at UCLA
- No background in genetics/genomics
- Using 48 isolates from 4 host species spanning 1988 to 2015




Nicole Nova

Phylogenetics and disease dynamics of canine distemper virus (CDV) in Neartic carnivores  
 Stanford University





Diana Prada  
 Pathogen Diversity and Host  
 Genetic Connectivity  
 Murdoch University



**Microbats of the South West Botanical Province of Western Australia: Pathogen diversity and host genetic connectivity**

Diana Prada, Mark O'Dea, Bethany Jackson & Peter Spencer, School of Veterinary and Life Sciences, Murdoch University, Perth, WA  
 Contact email: 32589004@student.murdoch.edu.au

Describe viruses in insectivorous bats within the region

- Do microbats of the SWBP carry viruses typical of this taxonomic group?

Genetic connectivity and diversity of four bat species

- Genetic diversity
- Level of connectivity amongst population
- Dispersal patterns

Associations by species, population or region

- Ecology of the host influences how pathogens move across populations
- Transmission routes





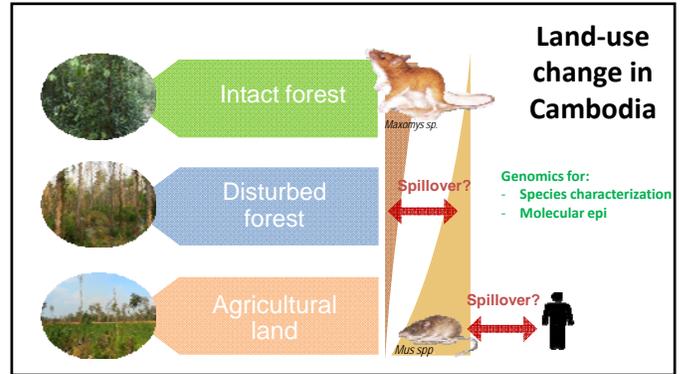
Dr. Mathieu Pruvot  
 Wildlife Health Surveillance  
 Wildlife Conservation Society



**LACANET**



- Building Wildlife Health Surveillance Networks
- Wildlife disease outbreak investigation – PPRV in Mongolian Saiga
- Drivers of zoonotic disease emergence
  - Land-use change
  - Wildlife trade



### Wildlife Trade In Lao PDR



- Conservation impact
- Zoonotic disease risk

**Genomics for:**

- Pathogen characterization
- Pop genetic to identify trade routes

### PPRV in Mongolia



**Genomics for:**

- Origin?
- How many spillover events?

Javier Sánchez Romano  
 Infectious Keratoconjunctivitis in semi-domesticated  
 reindeer  
 The Arctic University of Norway

**Infectious keratoconjunctivitis (IKC)**

- Contagious ocular disease of ruminants worldwide.
  - Norway: occurs in sporadic outbreaks.
- Acute, rapid progression, clinical signs vary in severity.
- Painful, can impact vision or cause blindness – Reduced survival.





Clinical symptom score = 0



Clinical symptom score = 1



Clinical symptom score = 1



Clinical symptom score = 1



Clinical symptom score = 2



Clinical symptom score = 2



Clinical symptom score = 2



Clinical symptom score = 2

**1. *Moraxella* spp. – Pathogenicity study**

Is the isolate pathogenic?

Two virulence factors:

- Type IV pili
- Cytotoxin A

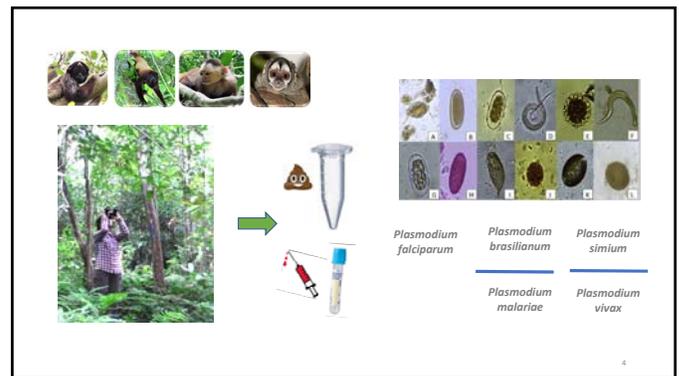
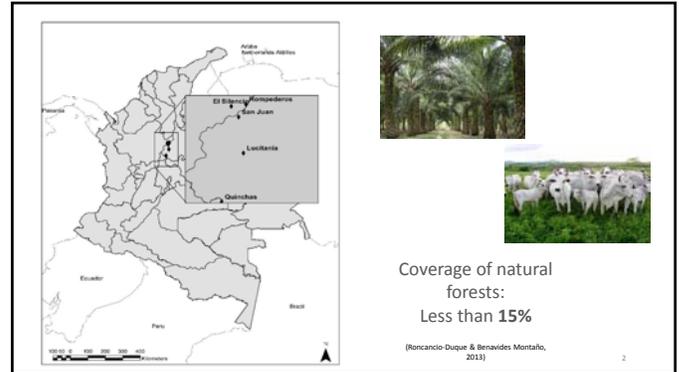
What about other isolates?

45 reindeer isolates from Norway, Sweden and Finland  
 16 cattle isolates from Denmark and Germany  
 36 isolates sequenced






Silvia Rondon  
Intestinal parasites and Plasmodium  
spp. in non-human primates  
Universidad de los Andes





Dr. Todd Shurry  
 Using genomic tools to advance understanding of host-pathogen dynamics for *B.abortus*/*M.bovis* to advance conservation of wood bison and apply to other wildlife reservoirs  
 University of Saskatchewan

**Title:** Wildlife Health Specialist  
**Employer:** Parks Canada Agency  
**Since:** Feb. 2004  
**No. of veterinarians employed full-time by Parks Canada:** 2  
**No. employees:** ~ 4,000  
**Job Description:** Constantly evolving – anything to do with wildlife health, veterinary medicine, One Health, zoonoses, wildlife disease, public health, ecohealth, animal care/welfare, epidemiology, wildlife policy.....

2015 PHD Thesis (U of Saskatchewan)  
 CHAPTER 5: SPATIAL AND MOLECULAR EPIDEMIOLOGY OF *MYCOBACTERIUM BOVIS* IN THE GREATER RIDING MOUNTAIN ECOSYSTEM

MIRU-VNTR and spoligotyping for *Mycobacterium bovis* isolates from elk, WT deer, cattle.

Recently WGSd 😊

Surveillance for *Echinococcus canadensis* genotypes in Canadian ungulates  
 Janna Schurer<sup>1,2\*</sup>, Todd Shury<sup>3,4\*</sup>, Frederick Leggett<sup>5,6</sup>, Emily Jenkins<sup>7,8</sup>

Molecular and morphological characterization of *Echinococcus* in cervids from North America  
 R. C. A. THOMPSON<sup>1</sup>, A. C. BOKELÉ<sup>1</sup>, B. J. BALATSONYI<sup>2</sup>, C. CONSTANTINE<sup>3</sup>, R. J. HERRICK<sup>4</sup>, T. SHU<sup>5</sup> AND B. J. HILTON<sup>6</sup>

Main interest: Using genomic tools to advance understanding of host-pathogen dynamics for *B. abortus*/*M. bovis* (*B. anthracis* also) to advance conservation of wood bison and apply to other wildlife reservoirs

As a result of recent tariffs imposed on our country by the Trump Administration.....Beer and Maple Syrup will cost you more. HA!!



# Dr. Kerry Sondergoth

## Determining "genotypes" of bacteria associated with pneumonia in Bighorn Sheep

University of Wyoming

### Background

**Bacterial Pathogens in BHS Pneumonia**

- Mannheimia haemolytica*
- Bibersteinia trehalosi*
- Pasteurella multocida*

**Focus**

- Isolates from 3 Wyoming herd units
- 2012-2018
- Diseased sheep samples
  - (Nebraska, Colorado, Wyoming)

	2012			2013			2014			2015			2016			2017			TOTAL		
	M	B	P	M	B	P	M	B	P	M	B	P	M	B	P	M	B	P	M	B	P
Absaroka	0	0	0	2	1	0	4	4	0	1	4	2	0	5	3	2	0	4	9	14	9
Jackson	5	0	0	0	0	0	4	0	0	0	0	0	2	0	0	2	0	1	13	0	1
Whiskey	3	3	0	0	0	0	2	2	0	1	1	0	0	0	2	1	1	1	7	7	3
																			29	21	13

### Project Overview

**Tools**

- Mass spectrometry
- Clin Pro Tools
- Whole genome sequencing

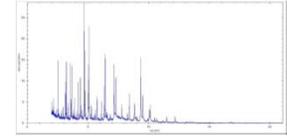
**Characterize isolates**

- Build bacterial ID database
- Compare isolates
  - Mass spec profiles vs sequencing

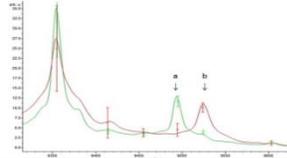
**Microbiome analysis**

- Tonsillar vs Nasal samples
- Sinus tumors

Mass spectrometry "protein fingerprint" for bacterial ID



*Mannheimia haemolytica* "genotypes" in cattle



### Expected Outputs and Goals

- Bighorn Sheep Bacterial Respiratory Pathogen database**
  - Differentiate species into genotypes
    - Requires WGS and Mass Spec data
  - Better diagnosis of bacterial isolates
    - *Learn how to handle and evaluate WGS for research AND diagnostics (workflow, choosing genes to generate comparisons, etc)*
- Microbiome analysis**
  - Tonsil vs Nasal swabs
    - Better inform wildlife biologists regarding sample collection and relocation
  - Predict sinus tumors based on microbiome?
  - Learn more about sinus tumor composition via tumor microbiome
    - *Become more competent with larger data sets and their manipulation/analysis for research*
    - *Learn how to effectively combine microbiome data (from individuals in herd) with overall health assessment data from the herd*



Dr. Nadine Vogt  
 Canadian Raptor Conservancy  
 Ontario Veterinary College



## Wildlife Interests

- Canadian Raptor Conservancy
- DVM (2014)
  - Mortality in the Eastern Loggerhead Shrike recovery program
  - Minnesota Raptor Centre
- MSc Epidemiology (2017)
  - Thesis: epidemiology of *Campylobacter*, *Salmonella* and *E. coli* among Canada geese in Ontario
  - Volunteer at Toronto Wildlife Centre




## Currently...

- PhD student in epidemiology at Ontario Veterinary College
- Advisors: Drs. David Pearl & Claire Jardine
- Thesis: Using whole genome sequencing to understand the ecology of *Salmonella* and antimicrobial resistance at the human, wildlife, environmental, and livestock interface in southern Ontario
- Research interests:
  - Zoonotic diseases
  - Evidence-based medicine
  - One Health research
  - Wildlife health



## Goals for the workshop

- Background knowledge of genomics: limited
- Goals
  - Technical introduction to WGS methods
  - Strengthen analytical skills

Dr. Tiffany Wolf  
Applied Infectious Disease  
University of Minnesota



## Applied Infectious Disease Research

- ◆ Moose health
  - ◆ *Parelaphostrongylus tenuis* epidemiology
- ◆ Primate health
  - ◆ At the interface with humans
- ◆ *Echinococcus* transmission
  - ◆ Domestic dog and human risk
- ◆ Tuberculosis transmission
  - ◆ Wildlife-livestock-human interface



Photo credit: Tiffany Wolf



credit: T

## Using Genomics to Understand Transmission

- ◆ Molecular epidemiology of *P. tenuis*
  - ◆ Landscape genetics
    - ◆ Genotyping of larvae from deer pellets
    - ◆ Examine transmission patterns across landscape
  - ◆ Metabarcoding of moose pellets
    - ◆ COX 1 marker gene
    - ◆ Exposure through the intermediate host

Adult Mortalities 2010-2015  
(n=22)

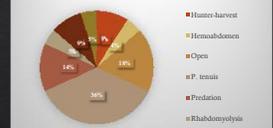


Photo credit: Seth Moore



Photo credit: Tiffany Wolf