

## Estimating bacterial cross-species transmission in Michigan

**Liliana C. M. Salvador**<sup>1</sup>, Daniel J. O'Brien<sup>2</sup>, Melinda K. Cosgrove<sup>2</sup>, Suelee Robbe-Austerman<sup>3</sup>, Tod P. Stubber<sup>3</sup>, Rowland R. Kao<sup>1</sup>, <sup>1</sup>University of Glasgow, Glasgow, United Kingdom; <sup>2</sup>Michigan Department of Natural Resources, Lansing, MI, <sup>3</sup>USDA/APHIS National Veterinary Services Laboratories, Ames, IA, Contact: liliana.salvador@glasgow.ac.uk

**Purpose:**Cross-species transmission of bacterial pathogens has major implications for livestock and wildlife management because of the implications for disease management and conservation. In recent years bovine Tuberculosis (bTB) has experienced an ecological shift in the US, with spillover from cattle leading to an endemically infected white tailed deer (WTD) population in Michigan that appears to serve as a reservoir of infection, with spillback to the sympatric elk population and cattle herds. Our objective is to better understand how the disease is maintained in WTD and how it is transmitted across species. Using epidemiological and Next Generation Sequencing data of *Mycobacterium bovis* isolates, we compare patterns of disease transmission with genetic similarity (based on SNP differences) between elk, deer and cattle.

**Methods:**BTB-positive deer that are spatially and temporally close to each positive elk are selected for inclusion from among the available archived isolates, as well as positive deer from the margins of the occupied elk range. Positive cattle herds in the same area are also selected. In total we identify isolates from 5 elk, 41 deer and 4 cattle herds. After verification of purity of isolates, DNA is collected and submitted for sequencing using Illumina NexteraXT 2x 250 chemistry and MiSeq instrument technology. Raw sequences are aligned to the reference AF2122 using BWA and SNPs are called using GATK. RAxML is used to build phylogenetic trees from the aligned SNPs.

**Results:**Preliminary results from analyses of discrete traits mapped into phylogenetic trees suggest that there may be highly variable evolutionary rates in sequences between the different species: there is little variability within outbreaks, but often large between outbreaks.

**Conclusions:**Further research on the role of each species on the maintenance and transmission of bTB In Michigan will be needed to determine the likely direction of the transmission and its evolutionary rate.

**Relevance:**With this study we will be better informed about the necessity of establishing new control programs in this area.