Rabies on the Last Frontier: A Phylogeographical Look at Red (*Vulpus vulpus*) and Arctic (*Vulpus lagopus*) Fox with Respect to Mitochondrial DNA and the Spatial Diffusion of Rabies

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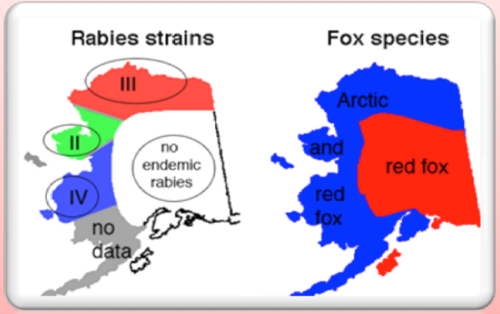
Introduction

- *Vulpus vulpus* and *Vulpus lagopus* are terrestrial animals that live in Alaska. They are also common carriers of the rabies virus.
- It has been determined that there are three different clades of rabies in Alaska being vectored by these two species of fox, but it is not clear why there are no endemic rabies in the Interior. See Figure 1.
- We are interested in the migration patterns of *Vulpus vulpus* and *Vulpus lagopus*, the spread and maintenance of the rabies virus as a function of climate warming.
- We hypothesize that there is some element, whether biological or geographical, that restricts the virus from spreading into the interior and maintaining itself as much as it does in the coastal regions of Alaska.
- This research provides a model for determining how the virus spreads under retreating Arctic conditions, as the globe warms.

Figure 1

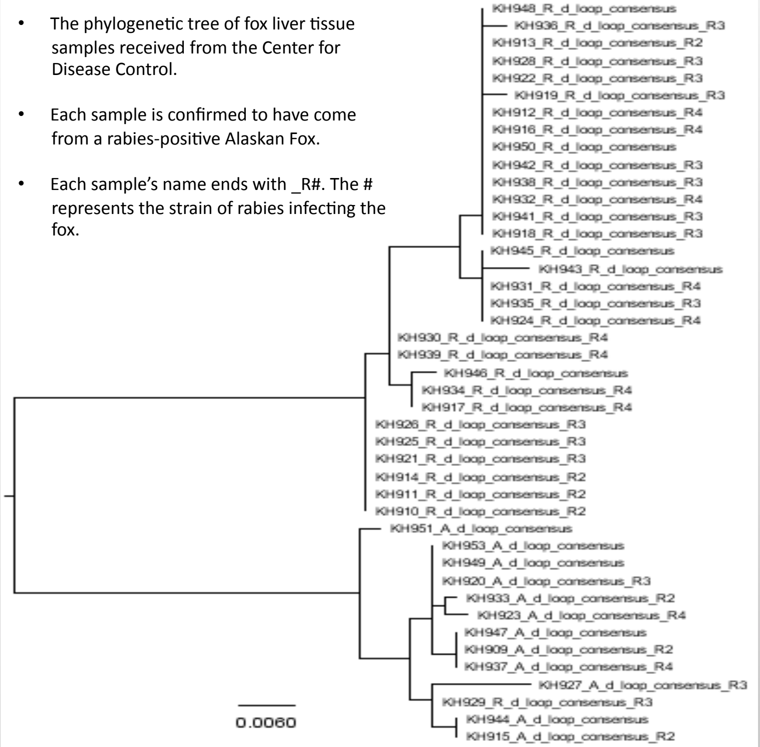


Methods

- We chose to conduct this research by using molecular genetics as a tool to understand the biology.
- We attained mitochondrial DNA from fox liver tissue samples received from the: 1) University of Alaska Museum of the North, 2) Center for Disease Control, 3) USDA fox control project, the 4) Alaska Department of Health and Human services, as well as 5) donations from trappers and the AK Department of Fish & Game.
- We chose a specific region of the DNA to compare. We amplified a 337-340 base pair region of the hyper variable D-loop of cytochrome C gene encoded in the mitochondrial genome using primers VVDL1 and VVDL6 in a PCR reaction.
- We cleaned up the PCR reactions using a standard purifying protocol and sent the samples to be sequenced by Elim Biopharmaceuticals.
- Sequenced results were fixed for discrepancies and aligned manually using Ridom TraceEdit.
- We created a phylogenetic tree using the computer software MEGA-4.

Results

- The phylogenetic tree of fox liver tissue samples received from the Center for Disease Control.
- Each sample is confirmed to have come from a rabies-positive Alaskan Fox.
- Each sample's name ends with _R#. The # represents the strain of rabies infecting the fox.



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Conclusions

- After viewing our results, we are reinforcing our belief that there are different clades of rabies in Alaska.
- Similar strains of rabies appear to be more likely located in animals that are related to one another in genetic coding. This suggests that the different clades of rabies are regional.
- Some rabies strains are found in different fox populations among different rabies strains. This suggests that the virus is spreading into a different region, but isn't endemic to that region.
- Future analyses of more samples is planned. More results and analysis techniques will be implemented to extract more information from the next stage of this research.