



Viral Tracking of Wildlife Corridors across the Rocky Mountains.

Background:

The ability of wildlife populations to respond to climate and land-use change depends upon connectivity and migration corridors. Predicting the spread of wildlife diseases also depends upon an understanding of the infected animal's (host) movement among populations. However, estimating the amount of connectivity among populations at a broad spatial scale is very challenging. Traditional radio-tracking and Global Positioning System (GPS) data from captured animals are applicable at the scale of wildlife management units (10-100 miles), but not at statewide or regional scales (100-1000 miles). Host genetics can be used to infer movement patterns at broad spatial scales, but the long generation times of many host species means that recent changes due to land-use change, roads, and climatic factors are undetectable.

Genetic information on parasites, however, may provide a better picture of host corridors and connectivity. In particular, some viruses have very high mutation rates, short generation times, and are highly host-specific, which are all beneficial properties for detecting genetic differences among populations.

Researchers at the USGS Northern Rocky Mountain Science Center (NOROCK) and their collaborators at Penn State University are using viral genetics to estimate contact patterns of mule deer and elk across several states in the Rocky Mountain region. By linking their

sampling efforts with chronic wasting disease (CWD) surveys in Montana, Wyoming, Idaho and Colorado they are looking at wildlife connectivity at an unprecedented scale. Field studies will be conducted around the Greater Yellowstone Ecosystem (GYE) and southeastern Montana, where researchers have ongoing GPS and virus tracking studies of elk and mule deer, respectively.



Figure1. Map illustrating the Greater Yellowstone Ecosystem. Adapted from the Mountain Prairie Information Node (MPIN) 2008.

Current Project Outcomes:

The two components of this study are 1) the analysis of host and retrovirus genetics at a broad spatial scale and 2) the collection of field tracking data, which will allow researchers to compare results from the genetic analyses with more traditional field techniques.

The first stage of this project was to determine which viruses would be the most useful. Ideally the virus should have a high mutation rate, widely distributed, and cause minimal host mortality. Retroviruses (those that replicate as part of the host's cellular DNA) like human immunodeficiency viruses have these characteristics, but few have been described for ungulates such as mule deer and elk.

To find new retroviruses the research team used new metagenomics technology based on genetic material from elk and mule deer lymph nodes. Partnering scientists at Penn State used a Roche 454 sequencer to find non-host DNA and RNA, a technique that is likely to be used more frequently in the future to identify unknown but emerging diseases. Using this technique, they have found three novel endogenous (non-infectious) gamma retroviruses and work is currently in progress on an exogenous (infectious) retrovirus.

In the next phase of the project, scientists will look at the landscape genetics of the retroviruses relative to the host genetics to define population boundaries and estimate the amount of movement among populations using the samples that NOROCK researchers have been compiling from across the Rocky Mountains (Figure 2).

These data will be useful in defining key connections between populations that will be important for understanding the spread of disease (e.g. chronic wasting disease and foot-and-mouth disease) as well the impacts of future development.

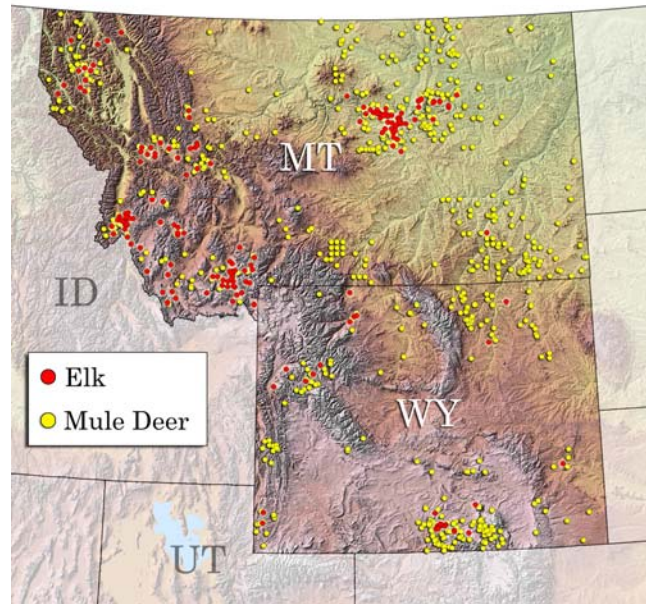


Figure 2. Map illustrating elk and mule deer lymph node samples taken at hunting check stations across Montana and Wyoming (Ebinger, 2008).

Deliverables:

Project outputs will include 1) manuscripts on the 454 sequence work and viral genetics; 2) collection of lymph nodes gathered at hunting check stations from multiple states in the region; 3) meta-analysis of home-range size and dispersal distances for mule deer and elk; and 4) map of host connectivity patterns, as indexed by both host and viral genetics, across the Rocky Mountains.

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The Northern Rocky Mountain Science Center is located in Bozeman, Montana and includes three field stations in Montana and one duty station in Wyoming. For more information on NOROCK's research, please visit <http://nrmsc.usgs.gov> or contact the Center Director: Jeff Kershner 406-994-5304 or jkershner@usgs.gov
