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| **Sin Nombre Hantavirus****in the US** |  |

## Objectives

Upon completion of this module, each student should be able to:

1. Visualize human hantavirus cases in the US.
2. Describe geographic and temporal patterns in US hantavirus case data.
3. Examine demographic variables in NM hantavirus case data.
4. Explain the role of biorepositories in zoonotic pathogen research
5. Discuss the role of public health agencies and biodiversity infrastructure in zoonotic pathogen mitigation.
6. Develop hypotheses based on observed patterns.
7. Design analyses to test hypotheses.
8. Perform and interpret simple statistical analyses.

**Introduction**

In the Spring of 1993, 10 people in the American Southwest died of a mysterious illness within an eight-week period. All the affected individuals displayed similar symptoms: fever, muscle aches, and lethargy, followed by acute respiratory distress (Yates et al. 2002). To treat this new disease and potentially prevent future outbreaks, public health officials needed to know what the disease was and where it was coming from. They used a variety of data sources to determine the human, environmental, and wildlife factors that led to its emergence in humans and that have periodically triggered reemergence since then.

The Centers for Disease Control and University of New Mexico Health Sciences Center and Biology Department collaborated to identify the likely pathogen. Researchers scanned an extensive frozen archive (biorepository) of wild mammal tissues that existed at the Museum of Southwestern Biology to quickly identify this new pathogen as a hantavirus, identify its wild mammalian host(s), and determine where on the landscape the virus could be found.

The new virus was called “Sin Nombre” or “Without Name”. It is found in deer mice (*Peromyscus maniculatus*), which are extremely abundant and geographically widespread. The virus can pass to humans. Infections, like this one, that spread between people and animals, are called zoonotic diseases.

In this module, you will review different data sources to identify patterns in the distribution of this emerging pathogen.

**Activity 1: Investigating Human Hantavirus Cases in the US**

*Procedure:*

1. Go to the CDC Hantavirus page: <https://www.cdc.gov/hantavirus/surveillance/index.html>
2. Toggle between the map, chart, and table icons to get familiar with the data.



1. Use these data to answers to the questions below.

*Questions:*

1. In 1993, when the disease emerged in the US, what states had the most cases?
2. What state had the highest number of deaths during the 1993 outbreak?
3. Since 1993, how many states have reported human hantavirus cases?

**Activity 2: Identifying Patterns in the Data**

We want to look at the number of Hantavirus cases over time to see if there are any patterns.

*Procedure:*

1. On the CDC Hantavirus page (<https://www.cdc.gov/hantavirus/surveillance/index.html>), click on the chart icon, then click on the “download all data” button (or obtain the data file from your instructor).
2. Open the file in excel. It should look like this.



1. Copy all the data onto a second tab on the spreadsheet. Name the first tab “raw data”. You will be retaining this as an unchanged record of the original data. Name the new tab “cleaned data”.
2. Clean the data by deleting all records that do not have the onset date recorded.
3. Extract the year from each date into a separate “Year” column.
	1. Add a column and name it “Year”
	2. Split the IllnessOnsetDate value into 3 columns (day, month, year) using the formula “=YEAR(<DATE>)”. When entering this formula, replace <DATE> by selecting the cell with the date you are splitting.
	3. Double click the bottom right-hand corner of the first cell in the column to auto-fill all cells below it with the appropriate year
4. Highlight the “Year” column and create a histogram of the number of times the year occurs (i.e., the number of cases per year).
5. Paste your histogram below and use it to answer the questions.

PASTE YOUR GRAPH HERE

*Questions:*

1. What patterns do you see?
2. What might explain such a pattern?
3. What other data would you need to test your hypotheses?

**Activity 3: Geographical and Seasonal Variation**

We know that both climate and weather vary in predictable ways and the environment has cascading impacts on communities of plants, animals, and their symbionts (i.e., parasites and pathogens). This is one reason that cases of the flu (influenza) increase in the winter.

*Procedure:*

1. Go to the NM Department of Health webpage on Hantavirus Pulmonary Syndrome: <https://www.nmhealth.org/about/erd/ideb/zdp/hps/>
2. Scroll down to “New Mexico Case Data” to find an updated summary of NM's data by county, year, month, and demographics.
3. Use the data in the online slide presentation to answer the following questions.

Questions:

1. Which months have the highest prevalence or frequency of human infection?
2. Why do you think human infection is not evenly spread across the year?
3. What other variables do we have that could be used to assess human risk?
4. The majority of cases in New Mexico (63%) occurred in individuals who identify as American Indian. Which geographic region of NM has the largest number of hantavirus cases? How does this information help explain the disproportionate impact on Native American communities?
5. What age group(s) have the highest frequency of hantavirus infections in NM?
6. What other data should we consider if we want to assess whether there is an increased risk of infection for people ages 20-59 years?
7. Visit <https://censusreporter.org/profiles/04000US35-new-mexico/>. This website presents data from the US census. Consider the % population by age group. Ages 20-59 years account for 49% of the population, but the relative risk for this age group is equal to 74% divided by 49% or 1.5. That means that means people age 20-59 are 50% more likely to experience a hantavirus infection than if the risk was proportional to the age distribution of the population.

What are some factors that might explain this increased risk?

**Background Information**

In the Spring of 1993, 10 people in the American Southwest died of a mysterious illness within an eight-week period. All the affected individuals displayed similar symptoms: fever, muscle aches, and lethargy, followed by acute respiratory distress (Yates et al. 2002). To treat this new disease and potentially prevent future outbreaks, public health officials needed to know what the disease was and where it was coming from. They used a variety of data sources to determine the human, environmental, and wildlife factors that led to its emergence in humans and that have periodically triggered reemergence since then.

The 1993 outbreak originated in the Four Corners area (Arizona, Colorado, New Mexico, Utah) of the United States, on the ancestral homelands of the Navajo people. Native Americans accounted for nearly 20% of early cases (CDC Hantavirus, Case Information). As of 2021, hantavirus cases in North America have been documented in 40 states, Mexico, and western Canada. The states in the southwestern US (New Mexico, Arizona, California, Utah, Colorado) have the highest number of cases.

Early in the 1993 outbreak, it was unclear what was causing the sudden deaths in the Four Corners region. Many who died were young and in otherwise good physical condition. About 70% of early patients with the disease died. Because the pathogen was previously unknown, emergence revealed significant shortfalls in our understanding of potential zoonotic pathogens (pathogens that jump from wildlife species to humans and cause disease) in the environment, and in our ability to respond to disease crises. Local clinics and health care providers were unable to diagnose, treat, or in some cases even admit suspected cases into their health care facility (Yates et al. 2002).

Speculation about the origin of this “new” respiratory illness ranged wildly (Horgan 1993), much like the mysterious origin of SARS-CoV-2 the causal agent of COVID-19. The Centers for

Disease Control and University of New Mexico Health Sciences Center and Biology Department collaborated to determine that the likely pathogen was a new strain of hantavirus, a rodent- borne virus well known in Asia and Europe, but largely undocumented in the Americas. Previously, only one other hantavirus had been identified in North America, found in a vole species near the town of Prospect Hill in Maryland. That hantavirus apparently does not cause serious human health issues.

Fortunately, an extensive frozen archive of tissues (biorepository) from wild mammals already existed at the Museum of Southwestern Biology. The archive had been built to study mammal evolution and ecology, not viruses. This large archive of tissues allowed investigators to rapidly scan many specimens of potential host mammal species to quickly identify this new pathogen as a hantavirus, identify its wild mammalian host(s), and determine where on the landscape the virus could be found. The new virus was called “Sin Nombre” or “Without Name”. This particular hantavirus is found in deer mice (*Peromyscus maniculatus*) which are extremely abundant and geographically widespread. Museum samples of wild-caught rodents that were preserved in the 1980s crucially showed that this hantavirus was present in deer mice more than a decade before the 1993 outbreak (Yates et al. 2002). This was not a new pathogen, but simply a pathogen that had remained undetected by science or public health institutions until after the 1993 outbreak.

Biorepositories in natural history museums store the raw material necessary for many kinds of studies, including rapid genetic identification of pathogens. Biorepositories provide the key samples of hosts necessary for identifying the zoonotic source(s) of a disease and investigating the ecology and evolutionary history of the pathogen and its host(s). By connecting each host specimen to a particular place using locality information (GPS latitude/longitude) and date of collection in the wild (month/year), biorepository data can be used to identify fundamental characteristics of the host, pathogen, and their environment that provide an understanding of when conditions will promote future zoonotic emergence. This information is key to designing public health responses (Glass et al. 2005), such as public service announcements or safety guidelines.

How is the virus passing from the wild deer mice to humans? Public health scientists and mammalogists realized that when environmental conditions are right to cause deer mice populations to explode to high numbers, these mice are likely to invade homes, barns, garages, and other buildings in rural areas to find shelter and raise their young. Scientists hypothesized that rodents shed the virus in their feces and urine and humans were contacting the virus (perhaps through inhalation of dust) when they entered buildings that had mice living in them. All these pieces of information were critical to developing basic prevention and response measures by public health agencies.

**Literature Citations and Background Reading**

Glass, G. E., T. M. Shields, R. R. Parmenter, D. Goade, J. N. Mills, J. Cheek, J. Cook, and T. L. Yates. 2006. Hantavirus risk in 2006 for U. S. Southwest. Occasional Papers, Texas Tech University 255:1-16.

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Yates, T. L. et al. 2002. The ecology and evolutionary history of an emergent disease: Hantavirus Pulmonary Syndrome. Bioscience 52: 989-998.

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