Advancing Integration of Museums into Undergraduate Programs (AIM-UP!)

Sin Nombre Hantavirus in the US

Educational Module

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Background

In the Spring of 1993, 10 people in the American Southwest died of a mysterious illness within an eight-week period, all with similar symptoms: fever, muscle aches, lethargy, followed by acute respiratory distress (Yates et al. 2002). To treat this new disease and potentially prevent future outbreaks, we needed to know what the disease was and where it was coming from, then determine the human, environmental, and wildlife factors that led to its emergence in humans and that has 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. Conveniently, an extensive frozen archive of tissues (biorepository) from wild mammals already existed at the Museum of Southwestern Biology that 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 of these pieces of information were critical to developing basic prevention and response measures by public health agencies.

Human epidemiology module

Learning outcomes

Skills:

- Computer search for relevant data

- Simple statistical analysis
- Develop hypotheses for observed patterns
- Design analyses to test hypotheses
- Role of public health agencies and biodiversity infrastructure in zoonotic pathogen mitigation

Students will 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. Understand the role of biorepositories in zoonotic pathogen research.

Investigating human hantavirus cases in the US
Go to the CDC Hantavirus page: https://www.cdc.gov/hantavirus/surveillance/index.html
Toggle between the map, bar chart, and table icons to get familiar with the data.

Teacher-guided or small group discussion questions:
Q: In 1993, when the disease emerged in the US, what states had the most cases?
A: NV, AZ, CO, NM (American Southwest/Four Corners region).
Q: What state had the highest number of deaths during the 1993 outbreak?
A: New Mexico (10).
Q: Since 1993, how many states have reported human hantavirus cases?
A: 40.

We want to look at the number of Hantavirus cases over time to see if there are any patterns. Click the “Download All Data” button *(or obtain csv file from instructor)* and open the csv file in Excel.
It should look like this:

Patient	IllnessOnsetDate	StateFIPS	Outcome
1	3/1/93	20	Alive
2	3/1/93	8	Dead
3	4/1/93	35	Alive
4	4/1/93	4	Alive

Tally (or sum) the number of cases that occurred in each year, starting in 1993 (regardless of the 'Outcome').

To do this in Excel:

1. Add a column and name it 'Year'
2. Split the IllnessOnsetDate value into 3 columns (day, month, year) using the formula "=YEAR(<DATE>)"
3. Double click the 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)

Q: What patterns do you see?

A: Not constant. Hanta is more prevalent in some years than others. Cyclic, boom/bust, repeating through time.

Q: What might explain such a pattern?

Suggestions: Environmental variation, changes in host population sizes, human behavior.

Q: What other data would you need to test your hypotheses?

Suggestions: Climate variables, estimates of host density.

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.

Patterns in New Mexico

Let's take a closer look at geographical and seasonal variation in the state with the largest number of hanta cases in the US to date: New Mexico.

Go to the NM Department of Health webpage on Hantavirus Pulmonary Syndrome:
https://www.nmhealth.org/about/erd/ideb/zdp/hps/
Scroll down to "New Mexico Case Data" to find an updated summary of NM's data by county, year, month, and demographics.

In the on-line presentation, find the number of cases that occur in each month across all years for NM.

Q: Which months have the highest prevalence or frequency of human infection?

A: April-July

Q: Why do you think human infection is not evenly spread across the year?

Suggestions: Environmental variation, host population sizes, human behavior (contact between humans and virus in the environment)

Q: What other variables do we have that could be used to assess human risk?

A: Demographic data (sex, age, race, ethnicity), socio-economic data, occupation, etc.

Q: 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 to explain the disproportionate impact on Native American communities?

A: Northwest New Mexico, in McKinley and San Juan counties. Location of the Navajo Nation.

Q: What age group(s) have the highest frequency of hantavirus infection in NM?

A: The highest number of cases occurs in the 20-29 years age group, but most cases occur in ages 20-59 years (88/119 = 74%).

Q: What are some factors that might explain this?

Suggestions: reflects NM demography, risk is higher for those who are most likely to be cleaning areas with rodent droppings.

Q: 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?

A: Proportion of the population that is ages 20-59 years.

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.

Acknowledgments

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Literature Citations and Background Reading

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