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Tracing transmission of Sin Nombre Virus and discovery of infection in multiple rodent species
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Orthohantaviruses are a family of negative-sense, single-stranded segmented RNA viruses that can cause hantavirus cardiopulmonary syndrome (HCPS) throughout North, Central and South America. Transmission of these viruses is primarily through exposure to droppings from infected rodents. Sin Nombre virus (SNV), found in North America, is primarily carried, and transmitted, by deer mice (*Peromyscus maniculatus*) and has a ~36% case fatality rate in humans. New Mexico has the highest number of human SNV cases in the United States making it important to understand the distribution and genetics of SNV within this region. In August 2020, amidst the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) pandemic, a patient entered the University of New Mexico Hospital for SNV infection while testing negative for SARS-CoV-2. Using a diagnostic tool established in the lab, we confirmed SNV infection through reverse-transcriptase quantitative polymerase chain reaction (RT-qPCR). However, it was uncertain exactly where the patient's exposure to SNV occurred, so we investigated two sites using trapping methods to capture rodents at both locations. We screened rodent lung samples for SNV infection and developed an in-house protocol for viral whole-genome sequencing for SNV. Using phylogenetic analysis, we found we could correlate the most likely site for patient transmission while also discovering SNV infection in multiple rodent species in addition to *Peromyscus maniculatus*. We propose using this method to increase the understanding of genetic variations of SNV and provide insight into hantavirus disease epidemiology within New Mexico.