

Whole genome sequencing identifies cause of zoonotic epidemic

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For the first time, researchers have used whole genome sequencing to identify the cause of a zoonotic infection that sparked a national epidemic. In a study published this week in *mBio*, an open-access journal of the American Society for Microbiology, researchers describe their use of whole genome sequencing to determine the cause of a respiratory disease that ripped through a population of native horses in Iceland several years ago.

"Our study showed that you can use genomic sequencing to tell epidemic strains from endemic strains," said principal study investigator Andrew Waller, PhD, head of bacteriology, Animal Health Trust, Suffolk, United Kingdom.

The Icelandic horse [population](#) is geographically isolated, arising from animals introduced by settlers in the ninth and tenth centuries. Virtually no [horses](#) have been imported in the last thousand years. This isolation has kept Icelandic horses free from the most common contagious equine diseases. In 2010, a respiratory disease of unknown origin spread through almost the entire population of 77,000 native horses in Iceland. The disease involved coughing, nasal discharge, and high morbidity. "Iceland was so worried about what was causing it that they stopped exporting horses to the rest of the world," said Dr. Waller. "It had a big impact on their economy, as they breed and sell a lot of horses each year."

A team of scientists at the University of Reykjavik performed

microbiological investigations and ruled out known viral agents, but identified the gram-positive bacterium *Streptococcus zooepidemicus* from almost all of the nasal swabs taken from coughing horses and from the diseased tissues of occasional fatal cases. The bacteria is routinely isolated from healthy horses and widely considered to be commensal, but because it was so ubiquitous during the outbreak, the researchers began to think it could be the culprit.

Scientists at the Wellcome Trust Sanger Institute performed whole genome sequencing on 305 isolates of *S. zooepidemicus*: 257 from the epidemic including from 100 horses, two cats, one dog, and three people. They compared the recent isolates to ten archived Icelandic isolates of *S. zooepidemicus* from seven horses, two sheep and a dog to provide insight into the identity of historical isolates of *S. zooepidemicus* from Iceland, and to 38 isolates, which represented the wider population diversity of the bacteria beyond Iceland.

The majority of *S. zooepidemicus* isolates recovered during the epidemic fell into four distinct clades. "ST209 stood out as likely to be responsible for the epidemic," said Dr. Waller. The epidemic ST209 strain was also recovered from a cat and the blood sample of an Icelandic woman who had suffered a miscarriage.

Network analysis of affected farms identified a single common training yard as a primary center of transmission and demonstrated how a novel strain can spread rapidly through a susceptible population devoid of sufficient cross-protective immunity, despite a background of concomitant colonization with endemic strains. The most likely route of transmission of the [epidemic strain](#) at this yard, a water treadmill that horses used on a daily basis, did not contain disinfectant and was changed on a once- or twice-weekly basis. This provided ideal conditions for the transmission of *S. zooepidemicus* between visiting horses. Adding chlorine coupled with regular cleaning and disinfection of water

treadmills may minimize or eliminate the transmission of *S. zooepidemicus* or other infectious agents via this route.

Previously, researchers have used whole genome sequencing to determine how germs spread through a hospital, but this is the first time the technology has been used to track the outbreak of a zoonotic disease. "This study enabled us to identify which [strains](#) were normally present in the Icelandic horse population and which was the [epidemic](#) strain that was causing the problem and that is very new," said Dr. Waller. "It was great to be able to show that this particular strain had spread so quickly through the whole population, and as far as we are aware, that has not been done before using whole genome sequencing."

Provided by American Society for Microbiology

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