

Elk hoof disease likely causes systemic changes

September 28 2023



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Elk treponeme-associated hoof disease, previously thought to be limited to deformations in elks' hooves, appears to create molecular changes throughout the animal's system, according to epigenetic research from

Washington State University.

The findings, published in the journal [Scientific Reports](#), also suggest those changes may be heritable. It remains to be seen though whether this means subsequent generations of elk may be more, or less, prone to catching the devastating [disease](#) that severely impairs the elk's ability to find food and escape predators.

"It's not just the absence or presence of the infection. It's affecting the animal's entire physiology, all the cells," said senior author Michael Skinner, a WSU biologist. "It shows that there's a molecular impact by the presence of the disease organisms."

Epigenetics are stable molecular processes that can influence how genes behave independent of the DNA sequence itself. Changes in an organism's epigenetics can be caused by nutrition or [environmental factors](#)—and as this study shows, by an infectious disease.

Working with WSU wildlife veterinarian Margaret Wild, Skinner examined cells from leg tendons of 55 infected and uninfected Roosevelt and Rocky Mountain elk. The legs were donated by hunters and collected by wildlife agencies in Washington, Oregon, California, Idaho and South Dakota.

The researchers found [epigenetic alterations](#) that appeared associated with the disease only in the infected elk. Since the tendon cells were away from the infection in the elks' hooves, the researchers said it was likely that the changes from the treponeme-associated hoof disease were found systemwide.

"We're building foundational knowledge to understand this disease," said Wild. "By doing this epigenetic study, we can see apparent systemic impacts from the infection, even though we don't see those pathological

changes when we look at the elk."

This study is part of ongoing efforts by WSU researchers led by Wild to better understand elk treponeme-associated hoof disease. While the infectious disease is named after the treponeme bacteria, the researchers now believe it is likely caused by multiple bacteria. Wild's team is conducting studies in captive elk to see if they can pinpoint how it is transmitted. Then, they can start looking at factors such as diet that might change the animals' susceptibility to the disease.

So far, the disease has not been detected in any [wild species](#) except for elk, although the WSU researchers are investigating whether there is a connection to bovine digital dermatitis which is commonly found in cattle. They are also using computer modeling to look at environmental factors such as [soil type](#), moisture and geography to see if they can identify physical locations where elk are more likely to have the disease.

"This is a brand-new emerging disease that hardly anything is known about," Wild said. "We are taking a multi-pronged approach and conducting a broad range of exploratory studies. Our goal is to do as much research as we can to learn about all the impacts this disease is having on individuals and elk populations to help wildlife managers address the disease."

More information: Margaret A. Wild et al, Systemic epigenome-wide association study of elk treponeme-associated hoof disease, *Scientific Reports* (2023). [DOI: 10.1038/s41598-023-42546-8](https://doi.org/10.1038/s41598-023-42546-8)

Provided by Washington State University

Citation: Elk hoof disease likely causes systemic changes (2023, September 28) retrieved 28

April 2024 from <https://phys.org/news/2023-09-elk-hoof-disease.html>

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