In the last Update, I described how and why we collect samples from hooves for disease surveillance and elk hoof disease research. We have shared the surveillance results and continue to update new detections on maps posted on our website.

Our results come from visual and microscopic examination of tissue samples by a WSU board certified veterinary pathologist. In addition to those results, we are now obtaining preliminary findings from a more advanced diagnostic approach called metagenomic analysis that uses DNA to identify the types of bacteria in a sample.

A metagenomic approach is powerful because it can identify all the bacteria in a sample (known as the microbiome) to allow analysis of which type of bacteria might be most important in causing disease. This is a great advancement over other methods in many circumstances including diagnosis of elk hoof disease.

Traditionally, we grew bacteria on laboratory culture plates to investigate what organisms are present and thus confirm diagnosis of a disease. But not all bacteria grow well in laboratories, including bacteria implicated in hoof disease.

More recently, advanced tests that look for specific bacteria known to cause a disease have been developed. For example, if you or your child has a sore throat, your physician can use a quick test for strep throat to provide results in minutes rather than the days needed for bacterial culture. However, if the test is negative, all that is known is that the one bacteria of interest, strep bacteria in this example, is not present. We have encountered similar challenges looking for specific bacteria thought to be associated with hoof disease. But metagenomics can detect all the bacteria in a sample in one test.

We used metagenomic analysis of samples collected from a relatively small number of elk (a total of 24) in Washington, Oregon, Idaho, and California as a preliminary test of this DNA sequencing approach with two questions in mind. First, we wanted to determine whether metagenomic analysis routinely detects Treponema bacteria in hoof lesions (and not normal hooves) thus supporting a diagnosis of treponeme-associated hoof disease (TAHD). And second, we are looking at all the bacteria present to search for others besides Treponema that are known to cause or contribute to infections in other places in the body or in other animals.

It is very important to emphasize that it is not possible to completely answer these questions with this initial investigation. Instead, the project was intended to provide cost-effective preliminary results to guide additional, larger investigations needed to obtain a high level of confidence in the results. Our research team, including one of our PhD students, Dr. Liz Goldsmith, is currently designing and planning those metagenomic investigations.

With that limitation in mind, I presented preliminary findings at two recent “virtual” scientific conferences, The Wildlife Society and the United States Animal Health Association, Committee on Wildlife Diseases. I also wanted to share these promising preliminary findings with you as interested stakeholders.

Preliminary results from this set of samples support previously published reports that lesions are associated with infection by known disease-causing bacteria. The majority, but not all, of the lesions contained DNA sequences identifying the presence of Treponema bacteria or as yet unidentified bacteria that are very similar to Treponema. The proportion of lesion samples with Treponema or Treponema-like bacteria was similar to studies that used other techniques.

Additionally, Treponema-like bacteria were also found in both of the samples collected from hooves that showed “pits” on the skin between the toes (see photos). These pitting lesions are not currently classified as TAHD, however, we speculate that they might indicate hooves that are damaged by bacteria and are therefore more...
susceptible to developing full-blown TAHD lesions. While these preliminary findings lend additional support to that speculation, more investigation is necessary. Like in previous studies, our approach using DNA sequences did not detect Treponema or Treponema-like bacteria in samples from elk with all normal-appearing hooves.

These preliminary results lend additional support for the involvement of Treponema or Treponema-like bacteria in elk hoof lesions. The findings go one step further to identify DNA sequences from an as yet unidentified Treponema-like bacteria in the vast majority of lesions. The identity and potential role of this currently unknown Treponema-like bacteria is intriguing and will be a focus in future studies.

In addition to Treponema-like bacteria, we also detected some other harmful bacteria in a high proportion of lesions but not in hooves from normal elk. Based on these results and similar findings in livestock hoof lesions, we speculate that multiple species of bacteria, including Treponema or Treponema-like bacteria, may be involved in creating the extensive hoof lesions observed in elk. More investigation is needed to fully understand the role of these bacteria to determine if they are required for the typical TAHD lesions to occur, or if they are simply taking advantage of damaged tissue as a suitable place to live.

Fortunately, studies with captive elk in the WSU research facility will allow us to closely monitor bacteria associated with hoof lesions. This, along with other metagenomic studies, provides a means to evaluate speculations such as those posed above using the scientific method to test hypotheses.

As is often the case, particularly in early investigations, this study raised more questions to investigate. We are making good progress but we are far from the end of the story. In addition to more studies focused on the bacteria, it is also important to keep in mind other factors that contribute to the occurrence of disease, most notably the host animal and the environment, including human-made changes.

Our approach is to first understand the infection, and then apply that knowledge to explore the potential role of alterations or abnormalities in the elk and in the environment where they live that may make the infection more or less likely to occur.

Every step takes us closer to these vital understandings. I sincerely appreciate the support and concern provided by all people who care about elk. And like you, I can’t wait for us to have COVID-19 under better control so we can return to more aggressive timelines for our studies.

The hoof on the left shows “pitting” lesions between the toes. Examination of tissues with a microscope did not reveal spiral-shaped bacteria required to diagnose TAHD. However, the very sensitive DNA sequencing analysis detected Treponema-like bacteria in this case, suggesting perhaps an early infection. The hoof on the right shows a typical TAHD lesion between the toes.