

A Technical Update on *Mycoplasma Bovis*

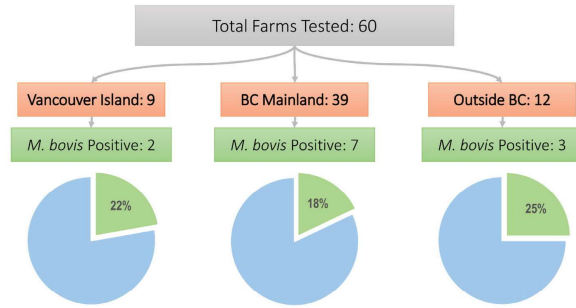
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Lyndsey received her Master's degree in Population Genetics from Dalhousie University in 2012. She has been working at the Applied Genomics Centre, which focuses on genomic solutions

to agricultural issues, since its inception in 2018. This article is based on the presentation she gave at Scotiabank's Lunch and Learn at the Pacific Ag Show in January.

Mycoplasma bovis (*M. bovis*) is a bacterium that lacks a cell wall, which makes it intrinsically resistant to many common antibiotics. *M. bovis* is found in cattle on many dairy and beef farms and has historically been thought to be responsible for causing significant disease symptoms, such as pneumonia, mastitis, arthritis, and ear infections. Such symptoms can be severe enough to interfere with overall animal welfare, reproduction and milk production. In many cases it is necessary to cull the infected animal. Moreover, *M. bovis* is highly communicable between cows and calves and can be carried asymptotically, which makes detection and control difficult. Consequently, *M. bovis* appears to be increasing in prevalence on farms around the world. However, the prevalence and the exact role of *M. bovis* in causing disease is still under debate.

The ability to test early and often, especially in calves and newly introduced animals, is critical to managing *M. bovis*. Such testing also allows a better understanding of the bacteria, the number of farms it affects, and its correlation with disease symptoms. For these reasons the Kwantlen Polytechnic University Applied Genomics Centre



Out of 60 farms tested, *Mycoplasma bovis* was detected on 20% of them. Prevalence appears to be similar throughout Western Canada.

(KPU AGC), in partnership with the WestGen Endowment Fund and the Natural Sciences and Engineering Research Council of Canada (NSERC), has developed a new DNA-based test for *M. bovis*. Over the past several years this test has been used to investigate the prevalence and patterns of infection in Western Canada.

Since developing the new test, members of the AGC have collected and screened

hundreds of samples from 60 farms in Western Canada. We have been able to detect *M. bovis* in milk, swabs from the ear or throat, and joint fluid samples, allowing testing of cows, calves, and bulk tank milk. Overall this has allowed us to determine that most farms fall into three categories – those without *M. bovis* on-farm, those with minor levels of *M. bovis*, and those with large-scale infection. Once present on a farm, *M. bovis* appears able

to spread readily, highlighting the need for a robust prevention and management strategy. Preliminary testing on BC dairy farms shows that on farms with low levels, about 10% of animals may test positive for *M. bovis*. However, on a farm with a known, widespread, *M. bovis* outbreak up to 90% of calves tested positive. In that case, the bacteria were more often detected in calves presenting either classic *M. bovis* symptoms or other clinical symptoms (e.g. lethargy, poor appetite) than it was in those that were asymptomatic.

In a larger scale epidemiology study, we tested individual cows and bulk tank milk from 60 farms across BC, Alberta, and Saskatchewan. Overall, we found that around 20% of farms had at least some *M. bovis* positive cattle. Interestingly, of the 12 farms with *M. bovis* positive cattle, only four of them had a positive bulk tank sample, while eight contained positive animals but had a negative bulk tank. This may be due to a low number of cows shedding into a large bulk tank, or infection in calves or other animals that are not contributing milk to the tank.

It has long been unclear whether or not *M. bovis* is directly causing the symptoms observed in some positive cattle, or if it is simply a natural part of the microbiome and other factors are responsible for the



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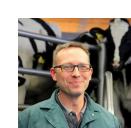
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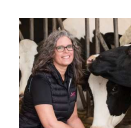
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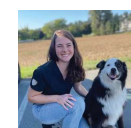
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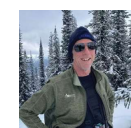
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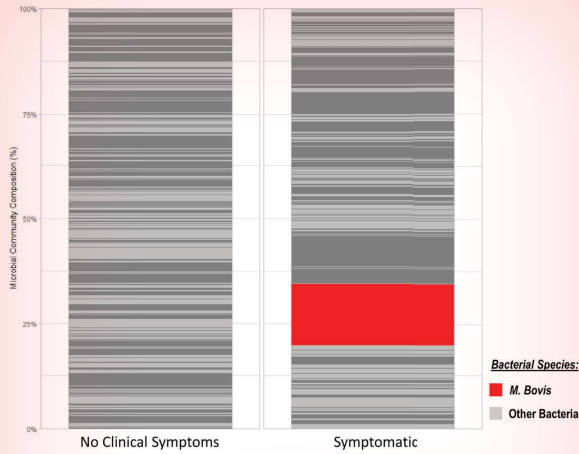


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Although many bacterial species are present in each sample, *Mycoplasma bovis* bacteria was more commonly found in animals presenting clinical disease symptoms. The 'other bacteria' species identified do not include any obvious candidates known to cause the observed symptoms.

presentation of disease. To explore the connection between the bacteria and disease further, the AGC performed 16S metagenomics Next-Generation Sequencing (NGS), which is able to identify almost all the different bacteria present in a sample and provide information on their relative abundance. Analysis of 80 animals shows that *M. bovis* is present in higher abundance in animals that are displaying clinical symptoms traditionally associated with the bacteria.

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Taken together, our data suggests that the presence of *M. bovis* is correlated with clinical disease symptoms. However, it is still possible that other factors are causing or worsening the observed symptoms, or that they are caused by a combination of multiple elements. What is clear is that worldwide concern about *M. bovis* is increasing, with countries like New Zealand now requiring a verified *M. bovis*-negative test for all imported animals, and animal products. Regular testing, especially beyond the bulk tank, and a plan to manage identified outbreaks are the best tools currently available to control spread on individual farms.

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