Investigating different strains of *Mycobacterium avium* subsp. *paratuberculosis* causing Johne's disease in Canadian dairy cattle

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Why is *Mycobacterium avium* subsp. *paratuberculosis* bacteria important?

Mycobacterium avium subsp *paratuberculosis* (MAP) causes Johne's disease, which is responsible for substantial losses to the dairy industry. Specifically, it is associated with:

- Long-lasting diarrhea
- Progressive weight loss
- Decreased milk production
- Increased culling

- Increased cattle mortality
- Substantial annual economic burdens (\$90M)







Mixed strain infection

Researchers have found animals can be infected by multiple strains of the same bacteria at once.

An initially infecting strain can undergo a change after infecting an animal to give rise to a genetically different strain. This process is referred to as microevolution.

When an infected animal has the presence of multiple strains, whether from a mixed strain infection or from microevolution, it is called a **mixed genotype infection**.

Mixed genotype infections can influence:

- Progression and outcome of an infection
- ⊖ Diagnostic ability of tests to identify the bacteria
- ⊖ Response to preventive therapy using mycobacteriophage
- ⊖ Success of vaccination program against MAP

Johne's disease caused by many different strains of the same bacteria can be harder to detect and control.

Key Points

Cows can be infected with multiple strains of *Mycobacterium avium* subsp *paratuberculosis* (MAP) and the strain of MAP can evolve within the cow.

Substantial variability was found in the strains identified on different farms.

Whole genome sequencing is the epidemiological tool for monitoring inter-herd transmission of MAP strains.

This information can be used to explain differences observed between the spread of MAP and clinical signs associated with a MAP infection.

MAP is transmitted between cattle via the fecal-oral route, meaning that MAP is shed into the feces of infected cattle and those feces are consumed by a susceptible, often young, animal.



Researchers have identified multiple strains of MAP bacteria that are responsible for causing Johne's disease.

The challenges associated with Johne's disease detection and control could be influenced by the diversity of MAP strains that are causing the disease in herd.

Researchers collected samples from 20 dairy herds in the provinces of Quebec and Ontario and identified inter-herd transmission patterns using whole-genome-sequencing as an epidemiological tool to validate cow movement as the cause of inter-herd disease transmission.

They characterized MAP isolated from 67 cows from these herds. Within four dairy herds, further investigation of 14 cows shedding MAP into their feces allowed the researchers to identify if multiple MAP strains were infecting a single infected animal and if microevolution was occurring.



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20 dairy herds in the provinces of Quebec and Ontario



12/14 COWS (86%) HAD EVIDENCE OF MIXED STRAIN INFECTIONS AND MICROEVOLUTION

with independent co-infection from different strains.



MAP STRAINS DIFFERED SUBSTANTIALLY BETWEEN FARM

with the highest level of variability in strains from Quebec. This variability may explain differences in the severity of Johne's disease that may be present on farms and requires additional study.



MAP CAN SURVIVE IN THE ENVIRONMENT FOR LONG PERIODS OF TIME





ANIMALS CAN BE INFECTED BY MULTIPLE STRAINS

MAP CAN FURTHER EVOLVE WITHIN THE INFECTED HOST

This could have implications on the severity of clinical disease and how it transmits to other animals.



The major point to highlight from these studies is that there are many MAP strains moving around and between farms and that animals can pick up multiple strains. Understanding these components will be critical to controlling Johne's disease in the future.

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Therefore, it is important to practice **a high-level of biosecurity** to prevent these strains from gaining entry onto your farm.

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