

## How Many Types of *Mycobacterium avium* subsp. *paratuberculosis* are on Canadian Dairy Farms and How Do They Spread?

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### Why is this important?

1. *Mycobacterium avium* subsp. *paratuberculosis* (MAP) is the bacterial cause of Johne's disease (JD) in cattle, which is contagious and easily spreads among cattle. JD can result in reduced milk and beef production as well as increased involuntary culling. Several MAP strain types have been identified and each type varies genetically.
2. Understanding the transmission of MAP, or spread, between animals and between herds is important for controlling this disease. In order to do so, classifying different types of MAP strains as genetically "same" or "different" is essential. Strain typing can be used to track transmission of MAP through a variety of settings and animals. Studies looking at the spread of MAP infection, both within the herd and between herds, as well as the role of wildlife in spreading MAP, require molecular tools that can tell the difference between MAP types.
3. An understanding of MAP strains is also needed to accurately assess if there are different levels of virulence (ability to cause disease) between types. Vaccine development and effective management practices also rely on a full assessment of MAP types present and their distribution across different provinces.

### Summary Points

- Identifying different MAP strain types is important to track disease transmission and virulence
- All types of MAP identified were found in all 10 provinces sampled
- Cattle movement is likely a major driver of MAP transmission across Canada

### What did we do?

The objective of this study was to identify different MAP strain types across Canada and to determine the spread of these types through the provinces. Individual samples of MAP were isolated from environmental and individual cow fecal samples from regional JD control initiatives in all 10 Canadian provinces. A total of 602 samples from 264 herds were collected and analyzed. During our study we determined that the current methods of strain typing were unreliable in assessing the diversity and relatedness of MAP strain types. On the other hand, whole genome sequencing (WGS) provided great detail in determining the genetic profiles of different MAP types and was used to identify the relationship between hundreds of Canadian samples.



Cultures of MAP sampled from across Canada. It takes up to 2 months to grow bacterial colonies (left) which contributes to the difficulty in studying MAP strains.

### What did we find?

Nine different MAP strain types were identified in Canadian dairy herds. However, 80% of Canadian bovine MAP samples were found to belong to a single dominant type. Looking at the distribution of MAP strains at a national and provincial level, it was discovered that all types of MAP identified were found in each province. In addition to this, six samples of MAP were identified as “Bison type”, which was previously thought to be uncommon in dairy herds.

### What does this mean?

The presence of a dominant MAP strain type in Canada could be due to a variety of factors. If this type is more virulent, it causes disease more easily and will be transmitted more quickly than other types. This dominant type could also just be easier to grow and measure in the lab. Finally, there could also be a founder effect involved, where the dominant type was the first MAP strain type introduced into Canada. The overlap of MAP types across and within provinces suggests that cattle movement is the main driver of MAP transmission. This is further supported by no single MAP type being concentrated in one area or province.

The presence of six “Bison type” samples collected through routine JD control programs indicates this subtype is more common and widespread than previously recognized in Canadian dairy cattle. . The close similarity between the "Bison type" isolates from the USA and Canada also suggests a recent transmission event between bison and dairy cattle.

This study provided important insight into the transmission processes of MAP that can be targeted for improved herd management and JD control. This information can be used to evaluate links in the disease pattern and inform policy decisions and control strategies.

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The authors would like to thank ALMA and DFC for their financial support.