Detailed Fingerprinting Of Map Bacteria Provides A New Perspective On Johne's Disease Control And Transmission

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Background: Johne's disease (JD) is a significant concern to the dairy industry from both a production-limiting and potentially human health perspective. JD is an incurable intestinal disease of ruminants and is extremely difficult to eradicate from a herd once the causative bacteria, *Mycobacterium avium* subsp. *paratuberculosis* (Map), is introduced. Therefore, the best control strategy for JD is to prevent infection with Map. An understanding of how Map spreads and where it comes from within the Canadian dairy industry can help pinpoint where our control efforts should be focused.

Methods and Results: Using innovative technology we are able to fingerprint individual Map bacteria with exceptional detail to identify the relationship of Map between herds and how different provinces are connected. Whole genome sequencing of nearly 90 Map bacteria originating from British Columbia, Alberta, Saskatchewan, Ontario, Quebec and the Atlantic provinces provides the first true picture of the diversity of Map in Canada and can be used to answer specific questions related to virulence and transmission both within and between herds across the country. There is a dominant strain that can be found in all provinces where samples were analyzed. Additional strains were identified, some of which are unique to specific provinces.

Implications: The different types of Map bacteria may have unique characteristics that influence the transmission and severity of JD in a dairy herd. Identification of the relationship between the dominant type and more unique types at different geographical scales is a critical step in adapting control measures that are specific to the Canadian dairy industry.