

# **Johne's Disease Transmission: Investigating the Diversity of *Mycobacterium avium* subsp. *paratuberculosis* in the Canadian Dairy Industry**

Christina A Ahlstrom, Herman W Barkema, Jeroen De Buck

University of Calgary, 3330 Hospital Drive NW, HSC 2518 Calgary, T2N 4N1, Canada  
Email: [cahlstro@ucalgary.ca](mailto:cahlstro@ucalgary.ca), [barkema@ucalgary.ca](mailto:barkema@ucalgary.ca), [jdebuck@ucalgary.ca](mailto:jdebuck@ucalgary.ca)

**Background:** Johne's disease (JD) is a chronic enteritis in ruminants and is of particular concern to the dairy industry, as it causes significant economic losses. There is no cure for this disease, so the main strategy for control is to prevent infection with *Mycobacterium avium* subsp. *paratuberculosis* (*Map*), the causative agent of JD. While a number of herd management strategies have been implemented to reduce JD risk, the transmission of *Map* at both the inter- and intra-herd level is still not entirely understood. Without this knowledge, effective preventative measures remain out of reach. A thorough investigation of *Map* genotypes isolated from both high and low prevalence herds across Canada provides unprecedented insight into how this bacterium is transmitted and what genetic characteristics may influence the spread and severity of JD.

**Objectives:** With support from Alberta Milk, Dairy Farmers of Canada, and ALMA, we aim to understand the diversity and transmission patterns of *Map* in Canadian dairy herds. Additionally, we aim to correlate *Map* genotype to herd-level JD risk factors.

**Results:** More than one hundred *Map* isolates have been compared, originating from nine Canadian provinces. Sixteen different genotypes have been found based on ten distinct genetic loci. Two predominant genotypes exist in Canadian dairy herds regardless of geographical origin.

**Implications:** The control of JD in dairy herds is most effective by prevention; however, this is difficult without a thorough understanding of the transmission patterns and sources of *Map*. Identification of genetic loci that influence the virulence and transmission of *Map* will be essential in controlling JD. Further characterization of predominant genotypes will reveal strain specific differences in pathogenesis, detection by diagnostic tests and transmission of JD and should thus be considered in the design and evaluation of regional control programs. Additionally, association of specific genotypes with herd-level risk factors will allow the implementation of tailored control measures.