Genotyping of *Mycobacterium avium* subsp. *paratuberculosis* to understand the epidemiology of Johne's disease in Canadian dairy herds

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Background: Johne's disease 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 Johne's disease. While a number of herd management strategies have been developed, the transmission of *Map* 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 will provide unprecedented insight into how this bacterium is transmitted and what genetic characteristics may influence the spread and severity of Johne's disease. Preliminary results have revealed the presence of at least ten *Map* genotypes in 24 Alberta dairy herds, with as many as eight in a single herd.

With support from Alberta Milk, Dairy Farmers of Canada, NSERC and ALMA, we aim to understand the transmission patterns of *Map* in Canadian dairy herds. This will further our knowledge regarding the impact of genotype on a multiple epidemiologically relevant questions. To achieve our goals, we have developed a number of objectives, including:

‣ Develop a fast and reliable genotyping technique to characterize *Map* isolates
‣ Collect at least 500 *Map* isolates from dairy herds in all ten Canadian provinces
‣ Perform full genome sequencing on a number of isolates to capture the true diversity
‣ Link epidemiological data (ie geographic location, herd size, prevalence of *Map* infection and buying behaviour) to genotype.

Implications: The control of Johne's disease in dairy herds is most effective by prevention; however, this is difficult without a thorough understanding of the transmission patterns and sources of *Map*. Genotyping of *Map* isolates will provide valuable insight into the epidemiology of Johne's disease that can ultimately be used to design and evaluate regional control programs.