

Johne's Disease In Canada: The Genetic Profile Of *Mycobacterium Avium* Subsp. *Paratuberculosis* In Ten Provinces.

Christina A Ahlstrom, Herman W Barkema, Jeroen De Buck

University of Calgary, 3330 Hospital Drive NW, HSC 2518, Calgary AB T2N 4N1

Email: cahlstro@ucalgary.ca, barkema@ucalgary.ca, jdebuck@ucalgary.ca

Background: *Mycobacterium avium* subsp. *paratuberculosis* (MAP) causes Johne's disease in cattle and is widespread in the Canadian dairy industry. An understanding of the diversity and distribution of MAP in Canadian provinces can help identify introduction events, improve control efforts, and target transmission pathways. Analysis of MAP genetics is revealing how the bacteria spread in Canada and which strains are more successful.

Methods and results: Whole genome sequencing was performed on 180 MAP bacteria from all ten Canadian provinces. The relatedness of MAP strains within provinces will be tested to identify whether MAP strains cluster predominately in a single province or if they are evenly distributed across the country. We determined that at least eight strain types currently exist in Canada, including a dominant type that represents more than 80% of MAP samples analyzed. The dominance of a single type in Canada will further be investigated to identify whether genetic changes make this strain more successful or if this was simply the first MAP strain introduced into the Canadian dairy industry over a century ago.

Implications: Different MAP strain types exist in Canada and the distribution of these strains can help identify where Johne's disease control efforts should be focused. The genetic differences between strains can influence the success and persistence of MAP and further studies are required to determine how these differences influence the burden of Johne's disease in Canada.