# Environmental Distribution of Mycobacterium avium ssp. paratuberculosis on Cow-Calf Farms with Clinical Johne's Disease in Western Canada

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## Introduction

Johne's disease, caused by Mycobacterium avium ssp. paratuberculosis (Map), is a progressive and debilitating disease of cattle. The main modes of transmission include direct contact with infectious manure or through exposure through colostrum. Calves from cow-calf herds cannot be isolated immediately after birth and so control efforts must reduce exposure to the bacteria from the environment. Environmental contamination on cow-calf farms is important to understand because if not adequately dealt with, disease control may not be achieved. Environmental testing could also reduce the cost of a herd test if it could replace animal testing in control programs. This study improves the understanding of environmental contamination of Map in cow-calf herds.

## Materials and Methods

30 beef cow-calf herds from Western Canada were identified as being actively infected with Johne's disease. Herds were recruited through local veterinarians. An actively infected herd was one that has had clinical cases of Johne's diagnosed by their veterinarian in the last 2 years confirmed by testing. The herd prevalence of Map was determined by collecting individual fecal samples from random cows at least 2 years of age. Fecal samples were pooled (5 per pool) and cultured using the modified BACTEC 12B method. All positives were confirmed with IS900 PCR. The environmental sampling was completed in the calving season. On each farm, approximately 15 samples were collected at the midpoint of their calving season by the local veterinarian. Detailed directions were given to standardize the samples collected. These samples were tested using the same methods described above. The herd prevalence was compared to the environmental results to find any potential relationship.

## Results

27/30 (90%) of herds selected completed all the required sampling and were included in the analysis. Of these 27 herds, 17 (63.0%; 95%CI 44.4-81.5) had at least one positive pooled fecal culture. Individual herds had between 0% and 60.0% of the pooled fecal cultures positive. 0/114 (0%) of the water samples including 54 samples from waterers, 26 biofilm samples, 21 dugout samples, and 13 farm drainage samples were positive for Map. 15/243 (6.2%; 95%CI 3.1-9.2) of the environmental samples (non-water) were positive for Map. Samples collected from within chutes were the most likely to be contaminated with Map with 4/26 (15.6%; 95%CI 1.2-29.5) positive. Other Map positive sites include: 3/21 (14.3%; 95%CI 0-29.6) of the samples from the ground outside of cow feeders, 2/21 (9.5%; 95%CI 0-22.4) of samples inside cow feeders, 2/13 (15.4%; 95%CI 0-35.8) of samples taken from mothering-up pens, 1/7 (14.3%; 95%CI 0-42.3) from bullpens, 1/10 (10.0%; 95%CI 0-29.6) from turnout pens, 1/18 (5.6%; 95%CI 0-16.4) from calf shelters, and 1/26 (3.8%; 95%CI 0-11.4) from calving pens. Map was not detected in the 101 samples from the remaining sites. 8 of the 27 (29.6%; 95%CI 12.1-47.2) herds had at least one environmental sample test positive for Map. Herds had between 0/15 (0%) and 3/9 (33.3%) of non-water environmental samples test positive for Map. Of the 17 herds identified as positive by pooled fecal culture, 6 (35.3%; 95%CI 11.9-58.7) were also positive on environmental sampling. Of the 10 herds that were negative on fecal pools, 2 (20%; 95%CI 0-46.1) were positive on environmental sampling. The agreement between the two testing methods had a calculated kappa of 0.13 which suggests only slight agreement.

## Significance

The level of environmental contamination on cow-calf farms in Western Canada is quite low as shown by only 8 of 27 herds in this study with any positive sites detected. A few sites were found positive on multiple farms suggesting that if environmental testing was to be used there should be a focus on these sites in order to reduce cost. While reducing the cost of testing, using environmental samples as done in this study is not sensitive enough as a herd test to be used in place of traditional herd test methods.