

A Comparison of Digital Dermatitis Associated Bacteria in Saskatchewan Dairy Herds

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Background: Digital Dermatitis (DD) is a polybacterial disease dominated by DD-associated treponemes in its clinical stages. This infectious disease is identified globally for causing lameness in dairy cattle and other ruminant species. As identified in a 2015 survey (unpublished data), 95% of Saskatchewan dairy producers that responded identified DD on their dairies. One dairy from this survey identified itself as being free of clinical DD. It was found that although this herd experienced no clinical, advanced lesions, irregular heel skin, similar to that of an early DD lesion, could be found on multiple animals at this location. However, these apparent early lesions never progressed nor caused lameness as verified by reviewing veterinary records.

Objectives: The objectives of this research were to 1) determine whether DD-associated treponemes are present in non-progressing apparent early lesions on a closed dairy free of clinical DD, and 2) determine whether DD-associated treponemes are present in early lesions on dairies with clinical DD.

Methods: Participants were selected with a survey sent to every registered dairy producer in SK in 2015. From the respondents that provided contact information, a convenience sample of 7 dairies were selected for a farm visit. From the 7 participant farms, 59 animals with lesions staged as A1, A2, B1, B2, or 3 using the Iowa DD scoring system were subjected to a 3 mm tissue biopsy. Bacterial gDNA was extracted from tissue specimens and subjected to targeted PCR, specific for DD-associated treponemes using published primers and methods.

Findings: *T. phagedenis*-like phylogroup was found in both healthy and diseased samples. Of the samples from the herd free of clinical DD, 6/10 tested positive for *T. phagedenis*-like, 0/10 tested positive for *T. medium*/*T. vincentii*-like, and 0/10 tested positive for *T. denticola*/*T. putidum*-like phylogroups.

Implications: Considering *T. phagedenis*-like bacteria was found in healthy, irregular, and diseased skin, it can be concluded that *T. phagedenis*-like bacteria alone is not sufficient for DD to progress to a clinical stage.