

# The Diversity of Bovine Digital Dermatitis Bacteria: How to Work Around the Complexity

Benjamin Caddey, Karin Orsel, Jeroen De Buck

Department of Production Animal Health, Faculty of Veterinary Medicine, University of Calgary, Calgary, Alberta, Canada. Emails: benjamin.caddey@ucalgary.ca; Karin.orsel@ucalgary.ca; jdebuck@ucalgary.ca

Digital dermatitis (DD) is common cause of lameness as it is a painful and chronic skin lesion of the foot. DD is polybacterial in nature, meaning that multiple types of bacteria are involved in the disease. Because of this, a thorough understanding of the most important bacteria remains a major gap in our ability to develop more effective DD prevention strategies. Our study aims to provide a better understanding of a 'core group' of bacteria consistently identified across DD lesions. We track bacterial populations and how dynamic they are throughout different stages of diseases as an effective strategy to investigate their potential roles in disease development. By using a deep sequencing methodology, it allows us to identify all bacteria present in DD lesions and quantify their abundance at all stages in the disease. We use this data to compare across cattle breeds and production systems, enabling us to observe a consistent group of potentially pathogenic bacteria in DD-positive cows. Historically, *Treponema* bacteria have been most commonly associated with a DD-causing role. In addition to *Treponema*, we identify an additional novel group of bacteria that appear consistently in DD lesions while absent in healthy skin. Through deep sequencing and culturing techniques, we observe the presence of multiple bacterial species that are potentially involved DD lesion development: *Porphyromonas levii*, *Fusobacterium* spp., and *Bacteroides pyogenes*. Implications: Establishing the 'core group' of DD-relevant bacteria is a significant step in progressing towards a confirmation of what causes DD and how. Current treatments may be ineffective at completely eliminating these pathogens, therefore future intervention strategies specifically for these bacteria may be beneficial in order to 1) completely heal lesions by clearing pathogens and returning to normal skin; and 2) reduce the reoccurrence of the disease.