

Investigating virulence factors of *Treponema* spp. with newly developed molecular tools

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Digital Dermatitis (DD) is the best known infectious claw disorder affecting dairy herds worldwide. DD is described as an ulcerative foot lesion, characterized by a complex pathology. DD results in cattle lameness and impairs animal welfare, this leads to significant economic losses worldwide. The suspected causative agent of DD is *Treponema* spp. They are anaerobic microbes that are difficult to study due to their fastidious nature and the lack of molecular genetic tools. This lack of knowledge hampers the understanding of disease pathogenesis and further limits effective, evidence-based treatment. In order to better understand the pathogenesis, we seek to understand the bacterial virulence factors underlying DD through genetic manipulation followed by animal infection experiments. To do this, we will create mutants of *Treponema* spp. and determine which mutants don't survive in the host by comparing to the original inoculum (sample containing microbes for infection). By identifying non-viable mutants, we can elucidate essential genes. With this genetic insight we will generate new mutants and compare their survival and pathogenicity to wildtype strains. This study will provide a wealth of knowledge about the genetic content of *Treponema* spp. and reveal details as to how those genes contribute to the establishment and survival of *Treponema* spp. in DD lesions. This information will serve as the foundation for the future development of novel drug targets and diagnostic tools for the prevention of DD. Take-Home Message: Through the identification of virulence genes, our approach to combating digital dermatitis becomes more direct and specific to limiting *Treponema* spp. survivability in lesions. Ultimately this will reduce economic loss and improve animal welfare.