Bovine digital dermatitis: Possible pathogenic consortium consisting of Dichelobacter nodosus and multiple Treponema species

Bovine digital dermatitis (DD) is a multifactorial disease involving at least one or more treponemal species. Virulent phylotypes of Treponema and other infectious agents contributing to disease etiology still remain to be identified. This study addressed these questions by analyzing the prevalence and distribution of seventeen phylotypes of Treponema in DD lesions by fluorescent in situ hybridization (FISH) applying species/phylotype-specific oligonucleotide probes. In situ hybridization for Dichelobacter nodosus, the cause of ovine footrot, was additionally performed. We sampled 90 biopsies of DD lesions originating from one Norwegian and six Danish dairy herds, and 24 tissue samples of healthy skin. All lesions revealed intermingled infections with multiple Treponema phylotypes (mean > 7). In six herds, the mean number of phylotypes identified varied between 12 and 15. D. nodosus was present in forty-nine (51%) of the lesions and in three of the apparently healthy skin samples. Two “healthy” samples also contained Treponema spp. and D. nodosus, and were histopathologically categorized as subclinical DD. Another eighteen of the “healthy” skin samples showed serious epidermal hyperplasia but were not colonized by bacteria while only four samples were found normal. We hypothesise that external noxious stimuli allow D. nodosus to break down the epidermal barrier creating a suitable environment for the secondary invaders, Treponema species, which gradually take over the infection site. The variety and different distribution of treponemes in the DD lesions observed in this study, suggests that most of the Treponema phylotypes have the potential to be pathogenic.

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