

7. Summary

Biodiversity of bovine *Treponema* spp.

Dermatitis digitalis (DD) is an important disease of claws in cattle. It is a chronic infection mainly of the epidermis typically associated with several anaerobe bacteria like *Porphyromonas* spp. and *Prevotella* spp. Furthermore *Treponema* spp. can be detected in large numbers in affected samples so that they are assumed to play an important role in the pathogenesis of DD.

Therefore the aim of this study was to evaluate the high diversity and the influence of bacteria of this genus in causing DD on the one hand and to rule out one possible way of infection via the gastrointestinal tract on the other as the aetiology of this disease still remains unclear.

Beside standard cultivation techniques, culture-independent detection methods were applied utilizing DNA-DNA dot blot hybridisation and fluorescence *in situ* hybridisation (FISH). 58 biopsies from affected cows were examined as well as samples of feces and rumen fluid in order to point out the gastrointestinal tract as a possible source of treponemal infection.

By conventional cultivation most predominantly *Porphyromonas levii* could be detected in 80% of the biopsy samples, *Prevotella* spp. in 72%, *Porphyromonas* spp. in 52% as well as *Bacteroidaceae* spp. in 28% of the samples, bacteria that typically occur in DD. Furthermore seven identical *Treponema* isolates have been cultivated that are mostly related to *Treponema socranskii* based on 16S DNA analysis.

By DNA-DNA dot blot hybridisation techniques several different *Treponema* phylotypes could be detected in those biopsies. *Treponema* phylotype group TRE I could be detected in 47 biopsies, phylotype group TRE II in 45 and phylotype group TRE IV in 45 of the samples whereas 53 of the biopsies were positive for the phylotypes DDKL-4 and DDKL-12. The fact, that phylotype groups TRE I, II, IV, phylotypes DDKL-4 and DDKL-12 were diagnosed, as well as the occurrence of up to five different *Treponema* phylotypes in identical biopsy sample clearly points out the high diversity of this genus associated with DD. FISH also gave positive results for TRE I, II, IV and DDKL-4, identifying these bacteria not only superficially but also in deeper tissue of the epidermis. In addition *Treponema* spp. represent a large portion of the total microbiota in DD affected lesions. These results indicate that *Treponema* spp. are most probably involved in causing and maintaining DD.

Probably due to limited detection ranges of at least 3×10^6 cells/250 mg feces it was not possible to detect *Treponema* spp. in feces or rumen fluid samples. It therefore still remains

unclear whether the gastrointestinal tract of cattle serves as a possible source of infection with *Treponema* spp. Further examinations have to be performed to unravel the exact aetiology of DD.