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Interdigital dermatitis, heel horn erosion, and digital dermatitis in 14 Norwegian dairy herds

M. Knappe-Poindecker,*[1] M. Gilhuus,† T. K. Jensen,‡ K. Klitgaard,‡ R. B. Larssen,* and T. Fjeldaas*
*Department of Production Animal Clinical Sciences, Norwegian School of Veterinary Science, PO Box 8146, 0033 Oslo, Norway
†Norwegian Veterinary Institute, PO Box 750, 0106 Oslo, Norway
‡National Veterinary Institute, Technical University of Denmark, Bülowsvej 27, 1870 Frederiksberg, Denmark

ABSTRACT

The aim of this study was to assess infectious foot diseases, including identification and characterization of *Dichelobacter nodosus* and *Treponema* spp., in herds having problems with interdigital dermatitis (ID) and heel horn erosion (E) and in control herds expected to have few problems. We also wanted to compare diseased and healthy cows in all herds. The study included 14 dairy herds with a total of 633 cows. Eight herds had a history of ID and E, and 6 were control herds. All cows were scored for lameness, and infectious foot diseases on the hind feet were recorded after trimming. Swabs and biopsies were taken from the skin of 10 cows in each herd for bacterial analyses. In total, samples were taken from 34 cows with ID, 11 with E, 40 with both ID and E, and 8 with digital dermatitis (DD), and from 47 cows with healthy feet. Swabs were analyzed for identification and characterization of *D. nodosus* by PCR, culture, virulence testing, and serotyping. Biopsies were analyzed by fluorescent in situ hybridization regarding histopathology, identification, and characterization of *Treponema* spp., and identification of *D. nodosus.* Interdigital dermatitis was the most frequent foot disease, with a prevalence of 50.4% in problem herds compared with 26.8% in control herds. Heel horn erosion was recorded in 34.8% of the cows in problem herds compared with 22.1% in control herds. *Dichelobacter nodosus* was detected in 97.1% of the cows with ID, in 36.4% with E, in all cows with both ID and E, in all cows with DD, and in 66.0% of cows with healthy feet. All serogroups of *D. nodosus* except F and M were detected, and all isolates were defined as benign by the gelatin gel test. *Treponema* spp. were detected in 50.0% of the cows with ID, in 9.1% with E, in 67.5% with ID and E, in all cows with DD, and in 6.4% of those with healthy feet. In total, 6 previously described phylotypes (PT) of *Treponema* were detected: PT1, PT3, PT6, PT13, and PT15 in cows with ID, PT1 in a cow with E, and PT1, PT2, PT3, PT6, and PT13 in cows with both ID and E. One new phylotype (PT19) was identified. The epidermal damage score was higher but the difference in inflammatory response of the dermis was minor in cows with ID versus those with healthy feet. Fisher's exact test revealed an association between ID and *D. nodosus,* and between ID and *Treponema* spp. Logistic regression revealed an association between both ID and E and dirty claws (odds ratios = 1.9 and 2.0, respectively). Our study indicates that *D. nodosus*, *Treponema* spp., and hygiene are involved in the pathogenesis of ID.

Key words: interdigital dermatitis, heel horn erosion, *Dichelobacter nodosus*, *Treponema* spp.

INTRODUCTION

Infectious foot diseases are common in dairy herds, causing reduced animal welfare and financial losses (Kossaibati and Esslemont, 1997; Bruijnis et al., 2012). Foot disorders are the cause of approximately 90% of lameness cases in dairy cattle, and infectious foot diseases are increasing in many countries (Murray et al., 1996). In recent years, Norway has experienced a shift from tiestall to freestall housing of cattle. Combined with larger herds and more frequent trade of cattle, this change has increased the occurrence of most infectious foot diseases, including interdigital dermatitis (**ID**), heel horn erosion (**E**), and, to some extent, digital dermatitis (**DD**) and interdigital phlegmon (Sogstad et al., 2005; Rogdo et al., 2011).

Interdigital dermatitis frequently occurs in wet, unhygienic environments (Hultgren and Bergsten, 2001). *Dichelobacter nodosus* is commonly isolated from the lesions, but its prevalence varies greatly between herds (Laing and Egerton, 1978). *Dichelobacter nodosus* is a gram-negative anaerobic bacterium known to cause footrot in sheep (Beveridge, 1941). The bacterium produces extracellular proteases that are assumed to be responsible for the associated tissue damage (Thomas, 1964). A few studies have virulence-tested *D. nodosus* isolates from cattle and all isolates were categorized as benign (Stewart, 1979; Richards et al., 1980; Gilhuus

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[1] Corresponding author: maren.knappe-poindecker@nvh.no

et al., 2013). *Dichelobacter nodosus* is divided into 10 serogroups (A to I and M) based on fimbrial antigens (Claxton, 1989; Ghimire et al., 1998; Bhat et al., 2012).

A survey from 2002 stated that E was the most common infectious foot disease in Norwegian dairy cattle with a prevalence of 38% in freestall herds (Sogstad et al., 2005). A wet, unhygienic environment reduces the hardness of the claw and predisposes for E (Enevoldsen et al., 1991; Borderas et al., 2004). A strong association exists between E and ID (Manske et al., 2002), and the prevalence of both diseases is reduced by grazing (Holzhauer et al., 2012).

Digital dermatitis is a multifactorial disease with a great impact on animal welfare and production (Argáez-Rodríguez et al., 1997; Bruijnis et al., 2012). Even though different bacteria such as *D. nodosus, Fusobacterium necrophorum*, *Bacteroides* spp., and *Campylobacter* spp. have been identified in the lesions (Blowey and Sharp, 1988; Cruz et al., 2005; Rasmussen et al., 2012), studies have indicated that *Treponema* spp. is the main causative agent (Walker et al., 1995; Evans et al., 2008). Several different phylotypes (**PT**) have been identified (Pringle et al., 2008; Evans et al., 2009; Yano et al., 2010). The PT isolated from DD lesions is categorized into 6 phylogenetic clusters (Evans et al., 2009; Yano et al., 2010). Digital dermatitis is considered endemic in many countries in Europe as well as in the United States (Rebhun et al., 1980; Blowey and Sharp, 1988; Holzhauer et al., 2006). Characteristic lesions are rare in Norway, but *Treponema* spp. have been detected and the prevalence seems to be increasing (Forshell et al., 2001; Rogdo et al., 2011). A study from 2009 identified PT1 and PT3 in Norwegian dairy cattle (Rasmussen et al., 2012), and hitherto unknown phylotypes were also discovered (Rogdo et al., 2011).

Infectious diseases of the bovine foot are often recorded in the same herd, and some authors have included all of them in "the bovine digital epidermitis syndrome" (Read and Walker, 1998; Cruz et al., 2005). Studies have shown that ID and E predispose for DD, and that these diseases have similar causative mechanisms (Manske et al., 2002; Holzhauer et al., 2006). It has recently been reported that *D. nodosus* may interact synergistically with treponemes to contribute to the development of DD in some regions (Rasmussen et al., 2012).

The aim of this study was to assess ID, E, and DD, as well as the prevalence of *D. nodosus* and *Treponema* spp., both in cows in herds expected to have problems with these diseases and in cows expected to have healthy feet (control herds). We also aimed to characterize the bacterial species with respect to genotypes, phylotypes, and virulence, and to analyze the association between ID and the bacterial traits, between ID and E, and between both ID and E and the cleanliness of the claws.

MATERIALS AND METHODS

Study Design

The study was a cross-sectional study of infectious foot diseases in herds with an expected high prevalence of such diseases and in herds assumed to have few such problems.

Study Population and Selection of Herds

We wanted the study population to include 8 herds with a high incidence of infectious foot diseases and an approximately equal number of herds with low incidence in the most recent years. We aimed for an equal number of freestall and tiestall herds. The herds were chosen from members of the Norwegian dairy herd recording system (**NDHRS**). Only freestall herds and tiestall herds with at least 30 and 20 dairy cows, respectively, were evaluated for eligibility.

All herds with 15 or more cases of foot disease registered in NDHRS between July 2009 and June 2010 received a questionnaire regarding general management, housing, claw trimming routines, and interest in participating in the study. Ninety-three out of 112 farmers replied, and 89 were willing to participate. After consultation with the local claw trimmer, local veterinarian, or both, 4 freestall and 4 tiestall herds were chosen that were expected to have problems with ID and E.

Only herds with 0 or 1 recorded foot disease were considered as control herds. Selecting such herds based solely on NDHRS recordings was not feasible because NDHRS does not differentiate between missing data and no reported cases. Therefore, claw trimmers were asked to recommend possible herds with previously good claw health. The owners of 8 farms were contacted by phone and answered a questionnaire, and finally 3 tiestall and 3 freestall control herds were included in the study.

Study Sample

The study sample consisted of 14 herds and 633 cows. Three herds were located in the western region, 10 in the east, and one in central Norway. Eleven herds had only Norwegian Red animals (n = 591), whereas 3 herds had a small percentage (2.5 to 17.5%) of Norwegian Red and Holstein crossbreeds (n = 14) and a few purebred Holstein (n = 7). Seven herds were housed in freestalls (444 cows), and 7 herds (189 cows) were housed in tiestalls. All heifers in the last 2 mo of gestation and all cows in each herd were examined. Cows that were in labor and cows that had most recently calved were not examined (n = 3).