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Udder infections with *Staphylococcus aureus*, *Streptococcus dysgalactiae*, and *Streptococcus uberis* at calving in dairy herds with suboptimal udder health

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ABSTRACT

Udder infections with Staphylococcus aureus, Streptococcus dysgalactiae, and Streptococcus uberis are common causes of bovine mastitis. To study these pathogens in early lactation, a 12-mo longitudinal, observational study was carried out in 13 herds with suboptimal udder health. The aims of the study were to investigate the occurrence of these pathogens and to identify if presence of the 3 pathogens, and of genotypes within the pathogens, differed with respect to herd, season, and parity. Quarter milk samples, collected at calving and 4 d in milk (DIM), were cultured for the 3 pathogens. Genotyping of staphylococcal and streptococcal isolates was performed using spa typing and pulsed-field gel electrophoresis, respectively. For each of the 3 pathogens, cows with an udder infection at calving or 4 DIM were allocated to 1 of 4 infection types: cleared (pathogen present only at calving), persistent (pathogen present in the same quarter at calving and 4 DIM), new (pathogen present only at 4 DIM), or cleared/new (pathogen present in 1 quarter at calving and in another quarter at 4 DIM). Associations between season or parity and overall occurrence of pathogens or infection types were determined using univariable mixed-effect logistic-regression models and the Fisher's exact test, respectively. The most commonly occurring pathogen was *Staph. aureus*, followed by Strep. dysgalactiae and Strep. uberis. Persistent infections were the most common infection type among Staph. aureus-infected cows, whereas cleared infections were the most common among Strep. dysgalactiae- and Strep. uberis-positive cows. The proportion of cows with persistent Staph. aureus infections and the proportion of cows having a Strep. uberis infection at calving or

4 DIM were higher in the multiparous cows than in primiparous cows. Infections with Strep. dysgalactiae were less common during the early housing season than during the late housing or pasture seasons, whereas persistent Strep. uberis infections were less common during the pasture season than during the late housing season. The relative occurrence of the 3 pathogens, infection types of each pathogen, and genotype diversity of each pathogen throughout the year or in different seasons and parities varied among the herds, indicating that underlying factors predisposing for udder infections at calving differ between herds. Genotyping of bacterial isolates gave important insight into how such infection patterns differed within and between herds. These findings emphasize the need to choose preventive strategies for each individual herd.

Key words: dairy cow, mastitis, *Staphylococcus aureus*, *Streptococcus dysgalactiae*, *Streptococcus uberis*

INTRODUCTION

In dairy cows, both subclinical mastitis (SCM: Svensson et al., 2006; Madouasse et al., 2010; Archer et al., 2014) and clinical mastitis (CM; Valde et al., 2004; Svensson et al., 2006; McDougall et al., 2007) are common around calving and in early lactation. Most SCM and CM are caused by IMI. In a Swedish study, Staphylococcus aureus was the most common IMI causing CM during the first month of lactation in primiparous cows, followed by Streptococcus dysgalactiae and Streptococcus uberis (Persson Waller et al., 2009), which is largely in line with the overall distribution of IMI causing CM and SCM in Sweden (Ericsson Unnerstad et al., 2009; Persson et al., 2011); these results also coincide with Norwegian studies (Waage et al., 1999; Osterås et al., 2006). Staphylococcus aureus and Strep. uberis are also important IMI in many other countries (Gianneechini et al., 2002; McDougall et al., 2007; Olde Riekerink et al., 2008). The prevalence of different IMI or occurrence of CM may, however, vary between regions of the world

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(Bradley et al., 2007; Nam et al., 2010) and between herds (Myllys and Rautala, 1995; Barkema et al., 1998; Osterås et al., 2006; McDougall et al., 2007). Although, information on the distribution of IMI at calving and in early lactation within herds in the Scandinavian countries is not available.

Within-herd parity differences in distribution of IMI around calving have, to our knowledge, not been studied recently. Moreover, studies on seasonal variation of such IMI are scarce (Fox et al., 1995). When studying the whole lactation period, however, seasonal differences in prevalence of *Staph. aureus*, *Strep. dysgalactiae*, or *Strep. uberis* IMI in clinically healthy udders (Osterås et al., 2006) or in cases of CM (Waage et al., 1999; Olde Riekerink et al., 2007; Ericsson Unnerstad et al., 2009) have been described.

Staphylococcus aureus, Strep. dysgalactiae, and Strep. uberis have traditionally been categorized in different groups with regard to their major reservoirs. The recent introduction of genotyping has, however, contributed new information on the epidemiology of such IMI. Staphylococcus aureus is mainly considered a contagious pathogen, but the same genotypes of Staph. aureus can be found in milk, on body sites of calves, heifers, and cows, and in their immediate environment (Capurro et al., 2010). The presence of environmental reservoirs has also been suggested by others (Sommerhäuser et al., 2003), although the variation in Staph. aureus genotypes within- and between-herds is often small (Sabour et al., 2004; Mørk et al., 2005; Lundberg et al., 2014a).

Streptococcus uberis is mostly considered an environmental pathogen, and its risk factors for mastitis differ from those for *Staph. aureus* (Barkema et al., 1999). Studies also indicate that the genetic variation between *Strep. uberis* isolates is considerable both within- and between-herd (Baseggio et al., 1997; Douglas et al., 2000; Lundberg et al., 2014b). Within-herd spread of the same genotype of *Strep. uberis* has also been described (Zadoks et al., 2003).

Relatively few recent studies on *Strep. dysgalactiae* have been performed, and those that have indicate that it may act either as a contagious or environmental pathogen (Todhunter et al., 1995; Barkema et al., 1999). The genotype variation of *Strep. dysgalactiae* isolates from CM cases is larger than for *Staph. aureus* (Lundberg et al., 2014a), but smaller than for *Strep. uberis* (Lundberg et al., 2014b). Few recent studies have evaluated risk factors for *Strep. dysgalactiae* IMI, and none of those have been performed in the Scandinavian countries. A Dutch study on risk factors for CM indicate that *Staph. aureus* and *Strep. dysgalactiae* can have similar patterns of infection (Barkema et al., 1999).

To decrease the incidence of mastitis in early lactation, new IMI must be prevented. Today, preventive control measures are mainly based on the most common risk factors for the most common pathogens present in a herd. Staphylococcus aureus, Strep. dysga*lactiae*, and *Strep. uberis* are, however, probably able to spread both in a contagious and environmental way, and some farms experience long-term mastitis problems despite well-implemented preventive measures. To improve recommendations on preventive measures, a better understanding of variation within and among herds in Staph. aureus, Strep. dysgalactiae, and Strep. uberis infection patterns (i.e., occurrence of IMI close to calving in regards to bacterial species and genotypes within species) is needed. Therefore, the aims of the current study were to investigate (1) the presence of Staph. aureus, Strep. dysgalactiae, and Strep. uberis IMI and genotypes within species at and just after calving in large freestall barn-housed herds with suboptimal udder health (defined by the proportion of cows with SCM), and (2) whether the infection patterns identified differ with respect to herd, season (pasture, early housing, late housing), and parity.

MATERIALS AND METHODS

Herd Selection

Herds were selected on the basis of data from the Swedish Official Milk Recording Scheme (SOMRS; Växa Sverige, Stockholm, Sweden) in 2009 and 2010, a scheme in which approximately 80% of all Swedish dairy herds and dairy cows are enrolled. Criteria for inclusion in the study were to have (1) lactating cows in freestall barns, (2) a herd size of 75 to 250 cows, (3)conventional milking in a milking parlor, (4) a herd with at least 75% Swedish Holstein (SH) or Swedish Red (\mathbf{SR}) breeds, and (5) year-round calving. In addition, the herds should be among the 50% of the dairy herds enrolled in the SOMRS with the lowest average proportion of cows in udder health classes 0 to 2, corresponding to a cow composite SCC below 130,000 cells/ mL at 2 or 3 consecutive monthly milk recordings, during the selection year. Furthermore, the herds should have recorded cases of CM caused by Staph. aureus and streptococci. Due to practical reasons, only herds situated in the southern third of Sweden were contacted. The owners of eligible herds (n = 86) were contacted by letter in late 2010 or early 2011 and shortly thereafter by phone until 20 herds were recruited. Due to practical and economic reasons, it was not possible to include a larger number of herds in the study. The herd owners received in-depth information about the project and were informed that no results would be released until the end of the study unless Streptococcus agalactiae IMI was found. Farm visits were scheduled in January to Download English Version:

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