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CNS mastitis: Nothing to worry about?

Ynte H. Schukken *, Ruben N. González, Linda L. Tikofsky, Hal F. Schulte, Carlos G. Santisteban, Frank L. Welcome, Gary J. Bennett, Michael J. Zurakowski, Ruth N. Zadoks [1]

Quality Milk Production Services, Cornell University, 22 Thornwood Drive, Ithaca 14850, USA

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ABSTRACT

In this paper, we analyzed a very large field data set on intramammary infections (IMI) and the associated somatic cell count (SCC) in dairy cows. The objective of the study was to analyze the impact of coagulase-negative staphylococci (CNS) IMI on cow SCC, both mean and variability, and on the potential of these infections to have a major impact on the bulk milk SCC (BMSCC). Data and milk samples for bacterial culture were collected by Quality Milk Production Services (QMPS) between 1992 and March of 2007. The QMPS program services dairy farms in New York State and other states in the Northeastern USA and operates in conjunction with Cornell University. Only records from cows where SCC and milk production data were available, and where only one organism was isolated from bacterial cultures of milk samples (or where culture was negative) were used for this analysis. A total of 352,614 records from 4200 whole herd mastitis screening sampling qualified for this study.

Within herds an average of 15% (S.D. 12%) of cows sampled were infected with CNS, ranging between 0 and 100%. Average within herd prevalence of cows with a CNS IMI and an SCC over 200,000 cells/ml was 2% (S.D. 4%) with a minimum of 0% and a maximum of 50%. Results of linear mixed models showed three distinct populations of IMI statuses: negative cultures with the lowest SCC; CNS and *Corynebacterium bovis* with a moderate increase in SCC, and *Streptococcus agalactiae*, *Streptococcus* spp. and *Staphylococcus aureus* showing an important increase in SCC. Surprisingly, milk production was slightly but significantly higher in CNS infected cows compared to culture-negative cows, whereas it was strongly reduced in cows with a major pathogen IMI. The percentage contribution of CNS infections to the BMSCC was 17.9% in herds with a BMSCC less than 200,000 cells/ml. This value decreased to 11.9 and 7.9% in herds with bulk milk SCC between 200,000 and 400,000 and over 400,000 cells/ml, respectively. We concluded that very few herds with milk quality problems would have an important increase in BMSCC that could be mostly attributed to CNS infections. On the other hand, in herds with low BMSCC, CNS infections may be an important contributor to the total number of somatic cells in the bulk milk.

1. Introduction

Coagulase-negative staphylococci (CNS) intramammary infections (IMI) have been associated with an increase in somatic cell counts (SCC) of affected cows (Jarp, 1991). However, the importance of these IMI is debated. Classically, CNS were classified as minor pathogens and their importance as an independent cause of subclinical or clinical mastitis was judged to be limited.

* Corresponding author. Tel.: +1 607 255 8202; fax: +1 607 257 8485.
E-mail address: yhs2@cornell.edu (Y.H. Schukken).
[1] Moredun Research Institute, Pentlands Science Park, Bush Loan, Penicuik EH26 0PZ, Scotland, UK.

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These CNS infections are typically associated with only a moderate increase in cow SCC (Lam et al., 1997). Some studies would indicate that CNS infections are preventive for IMI by other major pathogens (White et al., 2001), although this is much debated and other observational studies did not find this protective effect (Zadoks et al., 2001). However, more recent studies propose that infections with CNS may cause a more serious harm than thought before (Taponen et al., 2006). CNS infections have been studied in pre-partum treatment trials in heifers and bacteriological cure was associated with a decrease in SCC (Borm et al., 2006). Most studies lacked a sufficient sample size to evaluate both the mean effect of CNS and the variability of the effect. A large variability would imply that in some cows and herds, CNS infections might play a major role in udder health and milk quality.

Even though individual CNS infections may only have a moderate impact on SCC (Lam et al., 1997), many cows infected with this family of organisms, in herds where the producer goal is to achieve a relatively low bulk milk SCC (BMSCC), would potentially lead to herd level SCC problems. No field studies on a large number of dairy farms exist to quantify this particular situation and to estimate its relative importance relative to other causal mastitis organisms.

In this manuscript, we analyzed a very large field data set on IMI and the associated SCC in dairy cows. The objective was to study the impact of CNS IMI on cow SCC, both mean and variability, and on the potential of these infections to have a major impact on the BMSCC.

2. Materials and methods

2.1. Data

Data and milk samples for bacterial culture were collected by Quality Milk Production Services (QMPS) between January 1992 and March of 2007. The QMPS program services dairy farms in New York State and other states in the Northeastern USA and operates in conjunction with Cornell University. Data included bacterial culture results from individual cow milk samples, individual cow data retrieved from Dairy Herd Improvement Association (DHIA) records, and herd management information obtained by questionnaires completed at the time of sampling. Herds with high BMSCC (>750,000 cells/ml) were required by New York state law to participate in the program; the same program was voluntary for other herds. Milk sample collection and isolate identification were performed by QMPS as described previously (Wilson et al., 1997). Composite milk samples were collected by QMPS personnel and cultured in one of the four regional QMPS laboratories. Collection of mammary secretion was done aseptically according to National Mastitis Council guidelines (Hogan et al., 1999). In brief, teat ends were scrubbed with cotton pads soaked in 70% isopropyl alcohol, and the first few streams of foremilk were discarded. Approximately equal amounts of milk were collected from each quarter into a composite milk sample. Milk samples were stored at 4–8 °C until cultured. An approximate 20-μl aliquot from each milk sample was spread onto blood agar plates containing 0.01% esculin using individual sterile cotton swabs and incubated for 48 h at 37 °C. After incubation, plates were observed and organisms identified presumptively as *Staphylococcus aureus*, CNS, *Streptococcus* spp., and coliform bacteria based on colony morphology on blood and MacConkey agar, CAMP reaction, Gram stain and catalase and coagulase test reactions (Hogan et al., 1999). *Streptococcus agalactiae* was identified using colony morphology and a positive CAMP reaction. A sample was considered contaminated when three or more dissimilar colony types were observed. SCC and milk production data were obtained from DHIA records and were matched to the culture results by closest test day relative to the day of milk sampling for bacteriology. Milk SCC was transformed to linear score (LS) using the formula: $LS = (LOGe(SCC)/0.6931) - 3.6439$, where SCC is the somatic cell count in thousands per ml.

Records were only included in the analysis from cows where SCC and milk production data were available and where only one organism was isolated in bacterial culture of the milk sample (or culture-negative). A total of 352,614 records from 4200 full herd samplings qualified for this study. Average herd size in these herds was 69 cows (S.D. 93) that average approximately 9330 kg milk (S.D. 3147) per 305 day standardized lactation. Throughout, a cow will be defined infected when a pathogen was detected in the composite milk sample. It is recognized that this definition of IMI is not uniformly accepted given our sampling method.

2.2. Statistical analyses

Descriptive analyses were performed. Means and standard deviations were calculated for each micro-organism. Analyses were performed separately for heifers and cows.

Herds of greater than or equal to 10 cows were used for further analysis on the impact of individual micro-organisms on estimated BMSCC. For each observation in these herds the percent contribution of the cow to the herd's estimated BMSCC was calculated. For each pathogen, total contribution to BMSCC during a whole herd mastitis screening sampling was calculated as the sum of contributions of all cows infected with this pathogen. The contribution of an individual cow was calculated as

$$\frac{\text{cow SCC} \times \text{cow milk (kg)}}{\text{sum over all cows of (cow SCC} \times \text{cow milk (kg))}} \times 100\% \quad (1)$$

Once the individual cow contribution to the bulk tank was estimated, contributions per organism were calculated by adding the individual contributions of all cows infected with each organism within a herd sampling. This provided the proportion of cells in the bulk tank attributed to a particular organism at a given sampling day.

A mixed model linear regression of LS and milk production was performed. Herd was treated as a random effect and forced into all models; days in milk (categorized by month in lactation), lactation number (heifers versus cows), pathogen code and all possible interactions were