J. Dairy Sci. 90:4670–4678
doi:10.3168/jds.2006-900

Relationships Between Milk Culture Results and Milk Yield in Norwegian Dairy Cattle

O. Reksen,*[1] L. Sølverød,† and O. Østerås*†
*Norwegian School of Veterinary Science, Department of Production Animal Clinical Sciences, PO Box 8146, N-0033 Oslo, Norway
†TINE BA, PO Box 58, N-1430 Ås, Norway

ABSTRACT

Associations between test-day milk yield and positive milk cultures for *Staphylococcus aureus*, *Streptococcus* spp., and other mastitis pathogens or a negative milk culture for mastitis pathogens were assessed in quarter milk samples from randomly sampled cows selected without regard to current or previous udder health status. *Staphylococcus aureus* was dichotomized according to sparse (≤1,500 cfu/mL of milk) or rich (>1,500 cfu/mL of milk) growth of the bacteria. Quarter milk samples were obtained on 1 to 4 occasions from 2,740 cows in 354 Norwegian dairy herds, resulting in a total of 3,430 samplings. Measures of test-day milk yield were obtained monthly and related to 3,547 microbiological diagnoses at the cow level. Mixed model linear regression models incorporating an autoregressive covariance structure accounting for repeated test-day milk yields within cow and random effects at the herd and sample level were used to quantify the effect of positive milk cultures on test-day milk yields. Identical models were run separately for first-parity, second-parity, and third-parity or older cows. Fixed effects were days in milk, the natural logarithm of days in milk, sparse and rich growth of *Staph. aureus* (1/0), *Streptococcus* spp. (1/0), other mastitis pathogens (1/0), calving season, time of test-day milk yields relative to time of microbiological diagnosis (test day relative to time of diagnosis), and the interaction terms between microbiological diagnosis and test day relative to time of diagnosis. The models were run with the logarithmically transformed composite milk somatic cell count excluded and included. Rich growth of *Staph. aureus* was associated with decreased production levels in first-parity cows. An interaction between rich growth of *Staph. aureus* and test day relative to time of diagnosis also predicted a decline in milk production in third-parity or older cows. Interaction between sparse growth of *Staph. aureus* and test day relative to time of diagnosis predicted declining test-day milk yields in first-parity cows. Sparse growth of *Staph. aureus* was associated with high milk yields in third-parity or older cows after including the logarithmically transformed composite milk somatic cell count in the model, which illustrates that lower production levels are related to elevated somatic cell counts in high-producing cows. The same association with test-day milk yield was found among *Streptococcus* spp.-positive pluriparous cows.
Key words: subclinical, mastitis, cow, milk yield

INTRODUCTION

Bacterial culture is routinely used to diagnose mastitis, and culture results are often the basis for evaluating the quality and extent of a problem at the herd level. At the cow level, information about production potential following the isolation of mastitis pathogens is of importance in treatment and culling decisions. In the majority of studies, the focus has mainly been on clinical cases or cases with elevated cell counts when the relationship between mastitis pathogens and milk yield has been assessed (Rajala-Schultz et al., 1999; Gröhn et al., 2004; Wilson et al., 2004). However, a milk culture might test positive by microbiological analysis because of clinical or subclinical mastitis (Harmon, 1994) or because of colonization of the teat canal and cistern, with no major involvement of the mammary parenchyma (Persson et al., 1995). Clinical mastitis has been associated with marked losses in milk yield (Rajala-Schultz et al., 1999; Gröhn et al., 2004), and subclinical IMI, as defined by elevations in composite milk SCC (**CMSCC**), has been associated with losses in milk yield both during lactation (Miller et al., 2004) and from one lactation to the next (Fetrow et al., 1991). Relatively little is known about the relationship between milk yield and a positive culture of mastitis pathogens when sampling for bacteriological analyses is conducted, irrespective of cow-level characteristics. Mastitis pathogens isolated in milk cultures from clinically normal animals most likely originate from subclinical IMI or colonization of the udder.

Received December 28, 2006.
Accepted June 21, 2007.
[1]Corresponding author: Olav.Reksen@veths.no

Staphylococcus aureus is the most frequently isolated mastitis pathogen in Norway (Østerås et al., 2005), and the success in detecting infected cows is related to the number of colony-forming units found by microbiological analysis (Sears et al., 1990). Because isolates with a low number of colony-forming units of *Staph. aureus* per milliliter of milk are often not reported (Pitkala et al., 2004), there is reason to ask whether there are differences in milk yield between isolates with rich and sparse growths of *Staph. aureus* sufficient to justify this practice. A relevant question is whether this also applies to microbiological milk cultures obtained, irrespective of udder health characteristics.

The objectives of the present study were to assess milk yield before and after isolation of *Staph. aureus*, *Streptococcus* spp., or other mastitis pathogens in a random sample of the Norwegian cow population, and to compare differences in milk yield between cows isolated with sparse (≤1,500 cfu/mL of milk) and rich (>1,500 cfu/mL of milk) growths of *Staph. aureus*.

MATERIALS AND METHODS

A survey of quarter milk cultures obtained in 3,538 samplings at the cow level from 354 Norwegian dairy herds was conducted between January 19, 2000, and January 23, 2001. The study population, design of the survey, and laboratory procedures were discussed in detail previously (Østerås et al., 2006). Among all Norwegian dairy farms, 89.2% were enrolled in the Norwegian Dairy Herd Recording System (**NDHRS**) at the beginning of the investigation (Østerås, 2002), and the cows in this study were selected from these herds. Both herds and cows were subject to systematic random selection procedures such that every 50th Norwegian dairy herd was selected for sampling and culture from the files of the NDHRS. Cows were sorted according to their unique identity number within a herd, and every fifth cow was selected for microbiological sampling after drawing a starting number from 1 to 4. The random selection of cows was carried out 4 times (quarterly) during the investigation period to ensure a representative collection from all 4 seasons. Each cow had the same chance of being selected each season.

Quarter milk samples were collected aseptically by trained advisors from the dairy industry. The individual milk samples were analyzed for the growth of microorganisms in accordance with the official procedure in Norway (Aursjø et al., 1993), based on the procedures of the International Dairy Federation (1981, 1987), except that isolates of *Staph. aureus* were categorized according to the number of colony-forming units at the cow level. The amount of *Staph. aureus* was regarded as rich when >15 cfu was found in at least one sample of 0.01 mL of milk (>1,500 cfu/mL of milk) and was regarded as sparse when ≤15 cfu was found upon microbiological analysis in one or more quarters. The 1,500 cfu/mL threshold value between rich and sparse growths of *Staph. aureus* was chosen because of its use in the official Norwegian procedure of the National Veterinary Institute. Mastitis pathogens were regarded as present when the following microorganisms were isolated from the milk samples: *Staph. aureus*, *Streptococcus dysgalactiae*, *Streptococcus uberis*, other *Streptococcus* spp., coagulase-negative *Staphylococcus* spp., coliform bacteria (including *Escherichia coli*), *Enterococcus* spp., *Arcanobacter pyogenes*, and *Bacillus* spp. *Staphylococcus aureus* was regarded as present when a coagulase-positive *Staphylococcus* spp. was diagnosed. More than one diagnosis was assigned at the cow level when a microbiological diagnosis differed between quarters in the same cow.

For herds taking part in the NDHRS, records are maintained on calving date, parity, test-day monthly milk yield, test-day CMSCC (recorded bimonthly), culling, and disease history. Composite milk SCC was measured in milk samples collected from 2 successive milkings by Fossomatic 5000 equipment (Foss Electric, Hillerød, Denmark). This information was merged with data on the outcomes of the microbiological tests. To avoid interfering with management decisions, diagnoses resulting from the microbiological examinations were not reported to the farmer before the study ended. The median herd size in the study was 15.1 cows (range = 3 to 99). Purebred Norwegian Red cattle constituted 97.7% of the cow population in the study. The NDHRS lacked unique identification on 76 microbiological samples from 68 cows, and because of missing information for the covariates, the material included in the statistical analyses was reduced to a total of 27,665 test-day milk yield and 13,795 CMSCC observations, which were related to 3,547 microbiological analyses from 3,430 samplings in 2,740 cows. In total, 1,279 cows were sampled only once, 617 cows were sampled twice, 69 cows were sampled 3 times, and 5 cows were sampled 4 times.

Statistical Analyses

In the present investigation, multiple records on milk yield were used for each individual, and the relationships between the outcome variable (milk yield) and the explanatory variables were assessed by using the mixed model linear regression for repeated outcomes in PROC MIXED of SAS (Littell et al., 1996). Milk yield measurements within the same cow were correlated and accounted for by using a first-order autoregressive correlation structure. Other correlation structures were