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Relationship between intramammary infection prevalence and somatic cell score in commercial dairy herds

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ABSTRACT

We examined consistency of the relationship between intramammary infection (IMI) and somatic cell score (SCS) across several classes of cow, herd, and sampling time variables. Microbial cultures of composite milk samples were performed by New York Quality Milk Production Services from 1992 to 2004. SCS was from the most recent Dairy Herd Improvement test before IMI sampling. Records were analyzed from 79,308 cows in 1,124 commercial dairy herds representing a broad range of production systems. Three binary dependent variables were presence or absence of contagious IMI, environmental IMI, and all IMI. Independent variables in the initial models were SCS, SCS^2, lactation number, days in milk, sample day milk yield, use of coliform mastitis vaccine, participant type (required by regulation or voluntary), production system (type of housing, milking system, and herd size), season of sampling, year of sampling, and herd; also the initial models included interactions of SCS and SCS^2 with other independent variables, except herd and milk yield. Interaction terms characterize differences in the IMI-SCS relationship across classes of the independent variables. Models were derived using the Glimmix macro in SAS (SAS Institute Inc., Cary, NC) with a logistic link function and employing backward elimination. The final model for each dependent variable included all significant independent variables and interactions. Simplified models omitted SCS^2 and all interactions with SCS. Interactions of SCS with days in milk, use of coliform mastitis vaccine, participant type, season, and year were not significant in any of the models. Interaction of SCS with production system was significant for the all IMI model, whereas interaction of SCS with lactation number was significant for the environmental and all IMI models. Each 1 point increase in SCS (or doubling of somatic cell count) was associated with a 2.3, 5.5%, and 9.1% increase in prevalence of contagious, environmental, and all IMI, respectively. Empirical receiver operator characteristic curves and areas under the curve were derived for final and simplified models. The areas under the curve for simplified and final models within each type of IMI differed by 0.009 or less. We concluded that the relationship of IMI with SCS was generally stable over time and consistent across seasons, production systems, and cow factors.
Key words: intramammary infection, somatic cell score, mastitis pathogens, udder health

INTRODUCTION

Mastitis is generally caused by IMI with pathogenic microorganisms and is recognized based on detection of the inflammatory response to that infection. Milk SCC, lactose percentage, lactate dehydrogenase, and N-acetyl-β-D-glucosaminidase have been evaluated as diagnostic indicators of IMI in dairy cows. Among these, a logarithmic transformation of SCC has been found to provide superior diagnostic performance (Berning and Shook, 1992; Nyman et al., 2014, 2016). Intramammary infections are the principal cause of subclinical and clinical mastitis and the predominant factor associated with variation in SCC (Harmon, 1994; Schepers et al., 1997). Somatic cell count is widely used by dairy producers and veterinarians to identify subclinical mastitis in individual cows (Schukken et al., 2003; Ruegg and Pantoja, 2013).

Many studies have documented effects of cow, herd, and sampling time variables on SCC, IMI, and clinical mastitis (**CM**). Milk SCC tends to be greatest in the first 10 d of lactation, drops to a low around the peak of lactation, then slowly increases with DIM (Laevens et al., 1997; Schepers et al., 1997; Reksen et al., 2008; Schukken et al., 2009). Average SCS increases with parity (Laevens et al., 1997; de Haas et al., 2004; Nyman et al., 2014), and this increase is greater for cows with

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CM or IMI (Laevens et al., 1997; Nyman et al., 2014). A decrease in milk yield is typically associated with an increase in SCC (Raubertas and Shook, 1982; Pantoja et al., 2009), or an increase in milk yield is associated with a decrease in SCC (Green et al., 2006).

Studies have reported associations between individual cow SCC and farm management practices (Barkema et al., 1999; Schreiner and Ruegg, 2003; Rowbotham and Ruegg, 2015). Although the very lowest SCC values have been found in small herds (Nightingale et al., 2008), smaller herds typically have higher SCC and average SCC decreases as herd size increases (Norman and Walton, 2014). Incidence rate of CM was greater in tiestall barns than freestall barns (Olde Riekerink et al., 2008). Efficacy of the J5 *Escherichia coli* vaccine has been demonstrated in commercial herds (González et al., 1989; Hogan et al., 1992; Wilson et al., 2007). Although these herd-level factors have been shown to influence udder health, it has not been demonstrated how they might influence the relationship of IMI with SCS.

The sampling time factors, season and year, are well known to be associated with differences in udder health (O'Connell et al., 2015). SCC and mastitis typically peak during seasons with hot and humid weather (Olde Riekerink et al., 2007; Norman and Walton, 2014; Nyman et al., 2014). Species of pathogens isolated from milk samples submitted to a state veterinary diagnostic laboratory differed among seasons, and seasonal differences varied among species (Makovec and Ruegg, 2003). Improvements in udder health management, partly driven by milk quality premium programs, have led to decreases in SCC across years (Nightingale et al., 2008; Norman and Walton, 2014). From 1994 to 2001, reductions of 40 to 60% in frequency of contagious pathogens were observed in samples submitted to the Wisconsin Veterinary Diagnostic Laboratory (Madison); little or no reduction was observed for environmental pathogens (Makovec and Ruegg, 2003).

Mastitis pathogens are generally classified as contagious or environmental based on the likely source of exposure. Contagious pathogens are generally considered to have longer subclinical states and are often gram-positive, whereas environmental pathogens are considered to be opportunistic pathogens (such as coliforms or environmental *Streptococcus* spp.) that may trigger a greater inflammatory response that results in obvious clinical signs. A survey in northeast United States spanning 1991 to 1995 found prevalences of contagious and environmental IMI were 26 and 22%, respectively (Wilson et al., 1997). A Wisconsin study spanning 1994 to 2001 found prevalences of contagious and environmental IMI were approximately 17 and 31%, respectively (Makovec and Ruegg, 2003).

Few large-scale studies in commercial dairy herds have determined the effect of these factors on the relationship of SCC with IMI (Steeneveld et al., 2008; Nyman et al., 2016). Nyman et al. (2016) examined performance of SCC as a diagnostic tool for IMI with or without adjustment for breed, parity, milk yield, fat percentage, and milk urea concentration. Steeneveld et al. (2008) examined consistency of the relationship of CM with composite milk SCS across categories of parity, month in lactation, and season. No studies have examined consistency of the IMI-SCS relationship across a range of years, production systems, or herd sizes.

The objective of our study was to characterize the relationship of IMI with SCS in composite milk samples in commercial herds representing the entire spectrum of management levels and production systems over a span of years. Further, we examined the effects on that relationship due to differences in lactation number, stage of lactation, production system, herd size, sampling year, sampling season, and certain herd management practices.

MATERIALS AND METHODS

Data

Herd data and milk samples for bacterial culture were collected by New York Quality Milk Production Services (**QMPS**) field personnel (Schukken et al., 2007) between 1992 and 2004. Data included results of bacterial culture of individual composite milk samples, matching individual cow data retrieved from DHIA records, and herd management information obtained by QMPS questionnaire at the time of sampling. Herds with bulk milk SCC greater than 750,000 cells/mL for 2 of a series of 4 consecutive official samples were required by New York State law to participate in the program; this standard was constant throughout the study period. Participation was voluntary for other herds. Milk sample collection and isolate identification were performed by QMPS laboratory personnel as described previously (Wilson et al., 1997; Schukken et al., 2009).

The IMI culture protocol at QMPS identified 18 microbial species. Pathogens were grouped as either contagious or environmental based on the presumed characteristic of transmission (Table 1). Cows with pathogens in both groups were classified as follows. If the contagious pathogen was not *Corynebacterium bovis*, the cow was classified as contagious; if *C. bovis* was paired with *Staphylococcus* spp., gram-positive *Bacillus*, or *Enterobacter* spp., the cow was classified as contagious; any other pairing with *C. bovis* was classified as environmental. These pairing decisions were made according to which pathogen had a higher aver-