J. Dairy Sci. 96:7538–7549
http://dx.doi.org/10.3168/jds.2012-6078

Characterization of clinical mastitis occurring in cows on 50 large dairy herds in Wisconsin

L. Oliveira,[1] C. Hulland, and P. L. Ruegg
Department of Dairy Science, University of Wisconsin, Madison 53706

ABSTRACT

In recent years, the US dairy industry has experienced significant demographic changes, with an increase in the number of large herds. The objectives of the present study were to characterize clinical mastitis occurring in cows on large dairy herds in Wisconsin. Participating herds (n = 50) were required to have a minimum of 200 lactating animals, participate in monthly DHI testing (including monthly individual cow somatic cell count), use computerized herd records, use a milking routine that included fore-stripping quarters for detection of mastitis, and use antimicrobials to treat affected cows. After study personnel visited the farm, each herd was instructed to enroll the next 17 cows that experienced clinical mastitis, regardless of severity. At detection of clinical mastitis and 14 to 21 d after treatment ended, duplicate quarter milk samples were collected from all affected quarters and used for microbiological analysis. Treatments of affected cows were performed according to existing individual farm protocols. Cow level follow-up data was collected for 90 d after enrollment. Microbiological diagnoses at enrollment included gram-negative (35.6%), no growth (27.3%), gram-positive (27.5%), and other (9.6%). Of the 741 cases, the most prevalent pathogens were *Escherichia coli* (22.5%), followed by environmental streptococci (12.8%), *Klebsiella* spp. (6.9%), and coagulase-negative staphylococci (6.1%). Bacteriological cure was 75.0% for cases caused by gram-negative pathogens (n = 136), 50.8% for cases caused by gram-positive pathogens (n = 128), 47.5% for cases caused by other pathogens (n = 40), and 73.2% for cases which did not result in microbial growth (n = 123). Of the 583 cases with severity recorded, the distribution of mild, moderate, and severe symptoms was 47.8, 36.9, and 15.3%, respectively. The majority of cases presenting with severe symptoms were caused by gram-negative pathogens. Treatment cure was greater for gram-negative pathogens and cases for which no pathogens were recovered as compared with cases caused by other etiologies. Cows experiencing severe cases were more likely to receive multiple antimicrobial treatments.

Key words: large herd, clinical mastitis, characterization, severity score

INTRODUCTION

In recent years, the US dairy industry has experienced significant structural changes, with an increasing number of large herds responsible for a greater proportion of cow inventory and milk production as compared with small herds (USDA, 2009). Large herds differ from small herds in a variety of practices. Large herds have greater usage of computerized data records to track milk production, reproduction, and animal health as compared with small herds (USDA, 2009). Farmers with large herds also purchase more animals, are more likely to use diagnostic testing before purchase of animals, are more likely to vaccinate heifers, use more veterinary services, and have greater milk production per cow as compared with small herds (Hoe and Ruegg, 2006; USDA, 2007a). In addition, operators of large herds would be expected to observe more health problems in cattle due to the larger numbers of cows at risk for developing any health problem (USDA, 2007a).

Mastitis is the most prevalent health problem in dairy cows and one of the main reasons for permanently removing cows from herds (USDA, 2007b). Economic losses due to mastitis include reductions in milk production, increased cost of production, reduced milk quality, reduced longevity, increased labor and treatment costs, and transmission to other animals (Seegers et al., 2003; Gröhn et al., 2004; Pinzón-Sánchez and Ruegg, 2011). A variety of pathogens may cause mastitis in dairy cows; historically, the most common contagious mastitis pathogens have been *Streptococcus agalactiae* and *Staphylococcus aureus* (NMC, 1999). However, the adoption of modern milking practices has resulted in a considerable decline in the prevalence of these organisms in many modern US dairy herds (Makovec and Ruegg, 2003). Common environmental organisms include CNS, *Streptococcus uberis*, *Streptococcus dysgalactiae*, *Klebsiella* spp., and *Escherichia coli* (NMC, 1999). In the

Received August 23, 2012.
Accepted August 9, 2013.
[1]Corresponding author: leaneoliv@gmail.com

United States, several recent studies have shown that the most prevalent pathogens causing clinical mastitis in cows are usually organisms that originate from the environment (Lago et al., 2011; Pinzón-Sánchez and Ruegg, 2011; Schukken et al., 2011). Environmental mastitis pathogens are often associated with clinical mastitis, and few mastitis treatments have research that indicated efficacy against these organisms. Data that describe severity and treatment outcomes for clinical mastitis occurring on large, modern US dairy farms is sparse. The objective of this study was to characterize clinical mastitis occurring in cows on 50 large dairy herds in Wisconsin.

MATERIALS AND METHODS

Herd and Cow Enrollment Criteria

Wisconsin dairy herds (n = 50) were recruited by extension agents and practicing veterinarians. Herds were required to have a minimum of 200 lactating animals, participate in monthly DHI testing (including monthly individual cow SCC), use computerized herd records, use a milking routine that included fore-stripping quarters for detection of mastitis, and use antimicrobials to treat affected cows. Extension agents (n = 18) and veterinarians (n = 2) were trained by the study personnel on data collection protocols. Additional herd-level management data was collected during the visit. At least one farm visit per evaluator (extension agents or veterinarians) was supervised by the study personnel. During the visit, farm workers were trained to classify severity of clinical mastitis using a previously defined scoring system (Pinzón-Sánchez and Ruegg, 2011): mild (grade 1) when only the milk was abnormal; moderate (grade 2) when abnormal milk was accompanied by swelling or redness of mammary gland; or severe (grade 3) when the cow exhibited systemic signs of illness such as depression, anorexia, dehydration, or fever. After the farm visit, farmers were instructed to enroll the next 17 cows that experienced clinical mastitis. Each cow was eligible for enrollment only once. Sample size was estimated based on the expected distribution of mastitis pathogens.

Sampling and Data Collection

Cases were detected by trained farm personnel who collected duplicate quarter milk samples from only the clinically affected quarter(s) before treatment (**PRE**). After collection, cows were treated according to individual farm protocol. Farm personnel collected a second set of duplicate quarter milk samples from the enrolled quarter(s) approximately 14 to 21 d after the end of treatment (**POST**). Samples were frozen and mailed to University of Wisconsin-Madison's milk quality laboratory.

Farm personnel recorded data for each case including information about cow characteristics, the date the clinical mastitis case was detected, affected quarter(s), severity grade, drugs and doses used for treatment, number of days treated with each drug, the date milk returned to normal appearance (clinical cure), and the date milk was returned to the bulk tank. After enrollment, if a cow experienced an occurrence of a new clinical case in any quarter within 90 d, another set of duplicate quarter samples were collected before treatment from the affected quarter(s), frozen, and mailed to the laboratory. For repeated cases, study personnel collected the same data as described above for a PRE milk sample. Paperwork was left on the farm to collect information about events that occurred within 90 d after enrollment. Farmers were instructed to record information about removal (death or culling) of an enrolled cow from the herd, reason and date the cow was removed, date of the end of lactation (dry cows), if a cow lost a quarter (dried off naturally or therapeutically), any disease (such as pneumonia or foot problems), as well as drugs and doses used for treatment. The data from the forms were cross-checked with information from on-farm record-keeping systems. Milk production and SCC for each cow were obtained from the DHI monthly test occurring 14 to 52 d after treatment ended. Additional information collected included previous cases of clinical mastitis in the current lactation, quarter(s) affected, and drugs and doses used for treatment. Milk production and SCC before the clinical mastitis case for each cow were obtained from the DHI monthly test occurring 3 to 34 d before occurrence of the enrolled clinical mastitis case.

Microbiological Analysis

Upon arrival at the laboratory, all frozen samples were thawed at room temperature and 100 μL of milk from each duplicate sample were plated onto each half of a blood agar and 10 μL were plated onto a quarter of a MacConkey agar. Plates were incubated at 37°C for 24 to 48 h. Microbiologic procedures were conducted according to guidelines (NMC, 1999). *Staphylococcus aureus* were differentiated from other staphylococci by means of mannitol and tube coagulase reactions. Suspected *Streptococcus* spp. were identified as catalase negative, gram-positive cocci by the Christie, Atkins, Munch-Petersen test and esculin reaction. Gram-negative bacteria were identified using MacConkey agar, Gram stain, motility, indole, ornithine reactions, oxidase, and growth on triple sugar iron slants.