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An estimation of the clinical mastitis incidence per 100 cows per year based on routinely collected herd data

I. M. G. A. Santman-Berends,^{*1} T. J. G. M. Lam,^{*†} J. Keurentjes,^{*} and G. van Schaik^{*}

^{*}GD Animal Health, PO Box 9, 7400 AA Deventer, the Netherlands

[†]Department of Farm Animal Health, Faculty of Veterinary Medicine, Utrecht University, PO Box 80151, 3508 TD Utrecht, the Netherlands

ABSTRACT

The aim of this study was to evaluate whether it was possible to (1) estimate the clinical mastitis incidence rate (CMI) for all Dutch dairy herds and (2) to detect farms with a high CMI based on routinely collected herd data. For this study, 240 dairy farms with a conventional milking system that participated in the milk recording program every 4 to 6 wk were randomly selected and agreed to participate. From the initial 240 herds, data of clinical mastitis (CM) registrations and routinely collected herd data of 227 herds were complete and could be used for analysis. Routinely collected herd data consisted of identification and registration records, antimicrobial usage, test-day records from the milk recording program, bulk tank milk (BTM) somatic cell count data and results of diagnostic tests on BTM samples. For each of the 227 herds, the CMI per 100 cows per year was calculated per quarter of the year and was combined with the available herd data. Two models were developed to predict the CMI for all dairy herds and to detect individual herds that belonged to the 25% herds with the highest CMI. Records of 156 (67%) herds were used for development of the models and the remaining 71 (33%) were used for validation. The model that estimated the CMI in all herds consisted of 11 explanatory variables. The observed and predicted averages of the validation herds were not significantly different. The model estimated a CMI per 100 cows per year of 32.5 cases (95% confidence interval = 30.2–34.8), whereas the farmers registered 33.4 cases (95% confidence interval = 29.5–37.4). The model that aimed at detecting individual herds with a high CMI contained 6 explanatory variables and could correctly classify 77% of all validation herds at the quarter-year level. The most important variables in the model were antibiotic usage for treating CM and BTM somatic cell count. In conclusion, models based on routinely collected herd data gave an accurate prediction of CMI

for all Dutch dairy herds and could detect individual dairy herds with a high CMI. With these models it is possible to periodically monitor CMI both at the herd and at the national level, which is valuable for monitoring purposes and can motivate farmers to continuously improve udder health in their herds.

Key words: dairy cattle, clinical mastitis, predictive modeling, routinely collected herd data

INTRODUCTION

Clinical mastitis (CM) is a frequently occurring, economically important disease for dairy industries around the world (Olde Riekerink et al., 2008; Lam et al., 2013). Udder health is often monitored based on individual or bulk tank milk (BTM) SCC data. In some European countries, CM records are registered in disease-recording systems. However, these registrations underestimate the CM rates by 20 to 100% (Wolff et al., 2012). In the Netherlands, the clinical mastitis incidence (CMI) is an important indicator for both animal health and welfare, which is not uniformly registered on a routine basis for all dairy herds and, therefore, cannot easily be monitored. Monitoring CMI provides insight in the trend in time and enables early detection of unfavorable alterations. On the herd level, monitoring CMI provides farmers more insight in their own situation compared with other farms, which may motivate them to improve udder health. A decrease in CMI will have a positive effect on animal health, animal welfare, antimicrobial use (AMU), work pleasure, and net return of the farm (Huijps et al., 2008; Jansen et al., 2010; Trevisi et al., 2014).

In the Netherlands, the most recent CMI estimation was in 2009 and showed a slight decrease over the period January 1, 2005, and December 3, 2009, from 33.5 to 28.1 cases/100 cows per year, respectively (Lam et al., 2013). However, for these estimates of CMI farmers had to observe, register and communicate all cases of CM in the herd for a year, which is very labor intensive. Therefore, a need exists for an alternative method to estimate and monitor CMI. In previous studies, it has been shown that elevated SCC is indicative for IMI and

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¹Corresponding author: i.santman@gdanimalhealth.com

often results in CM (Berning and Shook, 1992; de Haas et al., 2005; van den Borne et al., 2010). Nevertheless, not all elevated SCC cases result in CM. In addition, in routinely collected data, such as BTM records and test-day milk recording, SCC records of cows with CM are generally excluded. Whether routine herd data has the ability to predict CMI on herd and national level has not previously been studied. Currently, besides SCC records, other routine herd data possibly associated with CM, such as AMU for intramammary and dry cow treatment, grazing management, milk production, herd size, animal movements, age, and parity, are also available.

The aim of the current study was to evaluate the possibility to use routine herd data to estimate the CMI on year and quarter-year level for the population of Dutch dairy herds. Further, we investigated the potential of routine herd data for comparing the CMI of individual herds to a benchmark of all dairy herds.

MATERIALS AND METHODS

Study Population

For our study, all dairy herds with a conventional milking system that participated in milk recording program on a 4- to 6-wk interval of the Dutch Royal Cattle Syndicate (CRV, Arnhem, the Netherlands) were eligible for inclusion (parameters that were available in the milk recording data are described in Appendix Table A1). Herds with an automatic milking system (AMS) were excluded because of the differences in detection of mastitis compared with herds with a conventional milking system. Farms that did not participate in the milk-recording program were excluded because of the lack of SCC data. Of the total population of 17,459 Dutch dairy herds, 12,490 met the inclusion criteria (18% of the herds were excluded because of the use of an AMS and 10% were excluded because they did not participate in the milk-control program). The study population was randomly split in 2 groups of dairy herds: one group for the development and one for the validation of the prediction models (split-validation method; Steyerberg, 2009). With the program Win-episcopy 2.0 (sample size to estimate a mean; Thrusfield et al., 2001), we estimated that at least 200 dairy herds had to be included to be able to obtain a precise estimation (accepted error in CMI <6) of the CMI in both subpopulations, assuming that the expected CMI would be 25 to 30 cases per 100 cows per year and the expected standard deviation would be 22 cases per 100 cows per year (Lam et al., 2013). In addition, with at least 70 herds in the validation group, it was possible to detect differences between observed and predicted

CMI of 7.5% or higher based on the previous mentioned assumptions. Based on previous experience (van den Borne et al., 2010; Lam et al., 2013), the drop-out percentage was expected to vary between 10 and 20%, and therefore 40 additional dairy herds had to be included. Assuming a response percentage of 15 to 20%, 1,350 randomly selected dairy herds were contacted by mail to participate in our study. The first 240 farmers that responded were included in the study. Participation meant that they were obliged to observe, register, and communicate all CM cases in their herd to GD Animal Health on a monthly basis from January 1 to December 31, 2013. They also gave consent for use of their routine herd data. In return, BTM was tested 10 times during the year on the presence of udder pathogens for free and, when the study had finished, participating herds received an overview of the udder health of their herds compared with the other participants.

Definitions and Collection of Herd Data

At the start of the study, all 240 farms were visited by an employee of GD Animal Health. During these visits, the aim and the methods of the study were explained. Farmers used a uniform definition of CM and used standard forms to register and report the CM cases. The definition of CM was every abnormality on udder or milk observed by the farmer (Lam et al., 2013). Abnormalities included alteration in color or consistency of the milk, swollen or red quarters, and clinical signs in cows such as depression, anorexia, dehydration, or fever (Lago et al., 2011). Analogous to previous studies evaluating CM in the Netherlands (Barkema et al., 1999; van den Borne et al., 2010, 2011), every CM case diagnosed by the farmer was considered a new case of CM, with the only exception that CM events occurring within 14 d in the same quarter were assumed to be the same case and were excluded from analysis. For each herd, the CMI was expressed as the number of quarter cases per 100 cows at risk per year and was calculated as the number of quarter cases of CM divided by the number of cow days at risk (DAR) multiplied by 365 d and 100 cows (equation 1):

$$\text{CMI} = (\text{CM}/\text{DAR}) \times 100 \times 365. \quad [1]$$

Based on the identification and registration data, DAR was calculated as the total sum of the number of days cows were present at the farm during at least 1 d in the study period, accounting for the moment of entrance and removal in the herd. An exception was made for primiparous cows, who became at risk at their first calving (and were assumed not at risk before this date). Cows were assumed to be always at risk for CM,

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