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Rate of transmission: A major determinant of the cost of clinical mastitis

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ABSTRACT

The aim of this research was to use probabilistic sensitivity analysis to evaluate the relative importance of different components of a model designed to estimate the cost of clinical mastitis (CM). A particular focus was placed on the importance of pathogen transmission relative to other factors, such as milk price or treatment costs. A stochastic Monte Carlo model was developed to simulate a case of CM at the cow level and to calculate the associated costs for 5 defined treatment protocols. The 5 treatment protocols modeled were 3 d of antibiotic intramammary treatment, 5 d of antibiotic intramammary treatment, 3 d of intramammary and systemic antibiotic treatment, 3 d of intramammary and systemic antibiotic treatment plus 1 d of nonsteroidal antiinflammatory drug treatment, and 5 d of intramammary and systemic antibiotic treatment. Uniform distributions were used throughout the model to enable investigation of the cost of CM over a spectrum of clinically realistic scenarios without specifying which scenario was more or less likely. A risk of transmission parameter distribution, based on literature values, was included to model the effect of pathogen transmission to uninfected cows, from cows that remained subclinically infected after treatment for CM. Spearman rank correlation coefficients were used to evaluate the relationships between model input values and the estimated cost of CM. Linear regression models were used to explore the effect that changes to specific independent variables had on the cost of CM. Risk of transmission was found to have the strongest association with the cost of CM, followed by bacteriological cure rate, cost of culling, and yield loss. Other factors such as milk price, cost of labor, and cost of medicines were of minimal influence in comparison. The cost of CM was similar for all 5 treatment protocols. The results from this study suggest that, when seeking to minimize the economic impact of CM in dairy herds, great emphasis should be placed on the reduction of pathogen transmission from cows with CM to uninfected cows.

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INTRODUCTION

Mastitis remains one of the most common diseases of dairy cows and represents a large economic loss to the industry as well as a considerable welfare issue to the cows affected (Bradley, 2002; Halasa et al., 2007). Despite being an infectious disease, concentration is often focused on the individual animal with respect to treatment, cost, and management. The risk posed to the rest of the herd from infected individuals and the potential impact of disease transmission on the cost of a case of clinical mastitis (**CM**) is often overlooked.

The cost of CM is made up of direct costs (e.g., discarded milk, cost of medicines, and labor) and indirect costs (e.g., loss of future production and increased culling) and varies considerably between farms (Huijps et al., 2008). Although the direct costs are more apparent to the producer, they are reported to comprise only a small proportion of the overall cost of CM compared with the less-obvious indirect costs (Kossaibati and Esslemont, 2000; Huijps et al., 2008). Several studies have taken all of the direct and indirect costs into account and have produced average figures of $168 (Bar et al., 2008), $254 (Huijps et al., 2008), $266 (Kossaibati and Esslemont, 2000), and $518 (Hagnestam-Nielsen and Ostergaard, 2009) for the cost of a case of CM. Although this information is useful, such average figures are difficult to interpret for an individual producer unless they happen to have the average farm. Although some recent studies have investigated the impact of transmission on the overall cost of CM at herd level (Halasa et al., 2009; van den Borne et al., 2010; Halasa, 2012), most studies have not evaluated the impact that within-herd transmission may have on the cost of CM at the cow level, nor how important this may be relative to the other factors that make up the overall cost of a case of CM.

A technique now widely adopted by the human healthcare sector for analysis of the cost-effectiveness of new and existing treatments is probabilistic sensitivity analysis (**PSA**; Briggs et al., 2002; Brown et al., 2006). Indeed, the National Institute for Clinical Excellence

(NICE; London, UK) now requires all cost-effectiveness analyses submitted to the institute to use PSA (Claxton et al., 2005). The main feature of this technique is that all input parameters in a cost-effectiveness model are specified as full probability distributions (probabilistic), rather than point estimates (deterministic), to represent the uncertainty surrounding their values. This parameter uncertainty can then be propagated through the cost-effectiveness model so that imprecision in model outputs is transparent (Briggs et al., 2002). For example, rather than using a point estimate for the probability of clinical cure after the treatment of CM of, say, 60%, we might choose a probability distribution covering the range 40 to 80% instead, accepting that we don't know the precise figure, but being fairly confident that it lies somewhere within this range. The relative importance of different model parameter values on the outcome of interest can then be evaluated irrespective of model complexity. This form of analysis has widespread acceptance within the human healthcare sector, but the authors could find only 1 example of its use in the veterinary literature (Detilleux, 2004).

The purpose of this research was to use PSA to evaluate the relative importance of different components of a model designed to estimate the cost of CM. The model included the potential for pathogen transmission between cows and was an extension of a previously described model structure (Steeneveld et al., 2011). A particular aim was to assess the importance of the rate of transmission relative to other factors, such as milk price or the cost of therapeutic agents.

MATERIALS AND METHODS

Model Structure

A stochastic Monte Carlo model was developed using WinBUGS 1.4.3 software (Lunn et al., 2000). This was used to simulate an initial case of CM (**CM1**) at the cow level and to calculate the associated costs simultaneously for 5 treatment protocols as defined by Steeneveld et al. (2011). The 5 protocols used were 3 d of antibiotic intramammary treatment (treatment 1), 5 d of antibiotic intramammary treatment (treatment 2), 3 d of intramammary and systemic antibiotic treatment (treatment 3), 3 d of intramammary and systemic antibiotic treatment plus 1 d of nonsteroidal antiinflammatory drug treatment (treatment 4), and 5 d of intramammary and systemic antibiotic treatment (treatment 5). The initial probability that the cow was cured bacteriologically was defined by a probability distribution based on the maximal cure rates given by Steeneveld et al. (2011), but rather than being pathogen specific (e.g., *Staphylococcus aureus*, *Streptococcus dysgalactiae/uberis*, or *Escherichia coli*), a single distribution was used providing coverage of cure rates encompassing those for all of the pathogens modeled by Steeneveld et al. (2011). For example, for treatment 1 (3 d of intramammary treatment), the bacteriological cure rates given ranged from 0.80 for *E. coli* infections down to 0.40 for *Staph. aureus* infections, so the uniform distribution 0.40 to 0.80 was used for all treatment-1 cases. After an initial treatment, 3 outcomes were possible: complete cure (bacteriological plus clinical cure), clinical cure (with no bacteriological cure), or no cure (no clinical and no bacteriological cure), with probabilities based upon Steeneveld et al. (2011; Table 1). The probability that a case was cured bacteriologically was assumed to be further influenced by whether the cow was systemically ill, the SCC at the time of treatment, the DIM at the time of treatment, parity, and whether it was a repeat case or not (Steeneveld et al., 2011; Table 1). The cows that failed to cure bacteriologically were deemed to have an 80% chance of curing clinically (Steeneveld et al., 2011).

The model structure was adapted from the model described by Steeneveld et al. (2011; Figure 1), which models the sequelae following a case of CM within a single lactation, with the addition of a risk of transmission from cows that cured clinically but not bacteriologically. Cases that completely cured could either go on to finish the lactation or be culled within the remainder of the lactation. The probability of being culled was increased if the cow was systemically ill at the time of treatment. The cows that cured clinically but not bacteriologically could go on to finish the current lactation, be culled, or have a clinical recurrence of the original case (**CM2**). If a cow did not cure, it would receive a repeat course of the initial treatment protocol, resulting in the same 3 possible outcomes as previously outlined. Cows that failed to cure after a repeated course could either die or have the quarter dried off. If a quarter was dried off, the cow could then go on to finish the lactation at a reduced level of milk production, or be culled (Table 2). The same sequence of events was modeled for CM2, but after CM3 the options became narrower. The cows that cured completely after CM3 could either end the lactation or be culled. The clinical (but not bacteriological) cures and the "no cures" were culled as was the case in the model described by Steeneveld et al. (2011). The probabilities of a cow being culled varied according to whether the case was a first, second, or third case. The distributions used in the model are shown in Tables 1 and 2. Following each treatment for CM, the probability of a cow curing bacteriologically was selected from the specified distribution and of those cows that failed to cure, 80% were assumed to cure clinically but not bacteriologi-