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A Cow- and Herd-specific Bio-Economic Model of Intramammary Infections in Dairy Cows

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Introduction

Mastitis, or intramammary infection (IMI), is one of the most significant diseases in dairy herds worldwide (Seegers et al. 2003). It is caused by environmental and contagious bacteria. Simulation models have proven useful for evaluating the effect of different control strategies (e.g. Down et al. 2016). However, previous published models are not cow-specific and therefore not so detailed in the simulation of host-pathogen interactions. If a simulation model is to be used by dairy farmers as a decision-making tool, it needs to be cow-specific because daily management decisions are made on cow level. Furthermore, as IMI is often caused by more than one pathogen in the same herd, such a simulation model should also be pathogen-specific to account for different transmission characteristics and treatment effects. Moreover, as different strains of pathogens can have different transmission routes (i.e. environmental, contagious or mixed), the model should be able to reflect this diversity. Our objective was thus to create a pathogen-, cow- and herd-specific bio-economic simulation model that could simulate multiple pathogens and strains at the same time within a dairy herd. This model should be able to simulate realistic scenarios for specific herds, thus being a tool for decision-making for individual farmers.

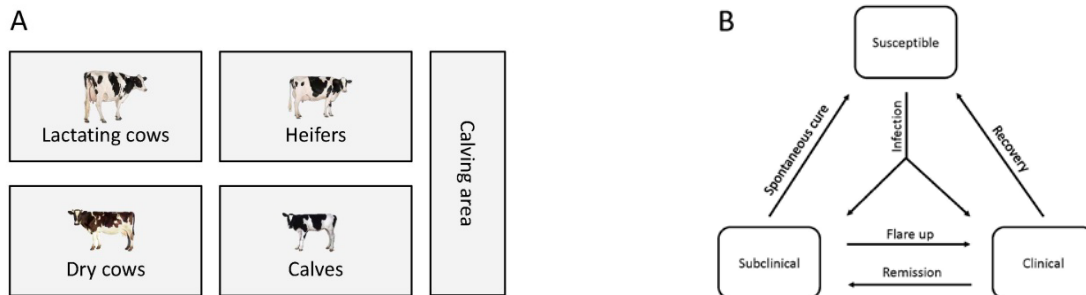


Figure 1. A: The farm sections in the simulation model. B: Transmission framework.

Methods

We used an existing mechanistic, stochastic simulation model framework to create an IMI simulation model (Kirkeby et al. 2016). This mechanistic model simulates a dairy herd in great detail; i.e. with individual lactation curves for all cows, continuous movement of cows between farm sections and continuous culling decisions made by the farmer. We expanded the model to simulate the individual quarters of cows. This procedure made it possible for cows to have up to four different infections at a time, one per quarter. We implemented two different transmission modes, namely environmental transmission based on a continuous reservoir of pathogens in the

farm, and contagious IMI originating from other infected animals in the herd. Currently, the environmental pathogen included is *Escherichia coli*, and the contagious pathogens are *Staphylococcus aureus*, *Streptococcus agalactiae* and *Streptococcus uberis*. The contagious transmission is simulating transmission, e.g. via milk liners, and depends on the number of quarters with contagious pathogens in the herd. We chose to focus on these four pathogens because they are common in Danish dairy farms.

We modelled the increase in somatic cell count (SCC) due to subclinical infection. The reduction in milk yield for individual cows is then based on their SCC (Hortet et al. 1999). Thus we are able to estimate the economic consequences of each IMI pathogen in the herd, simulate different control scenarios and estimate their epidemiological and economic effects.

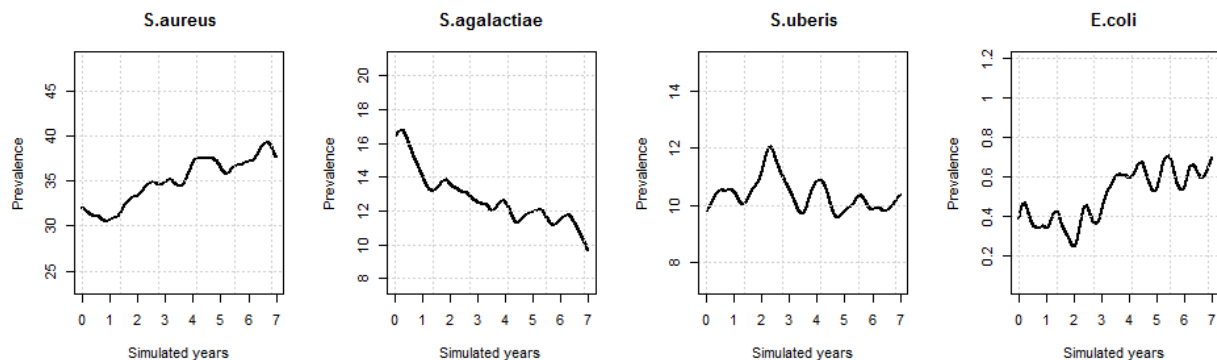


Figure 2. Example of a simulation of one herd over 7 years. The graph shows the quarter prevalence (subclinical plus clinical) of four different pathogens simulated in the same herd, with an IMI problem caused mainly by *S. aureus* and occasional occurrence of other pathogens.

Perspectives

The model will be used to simulate the situation on different farms, where we especially will focus on herd- and cow-specific treatments, reflected by the extent of the IMI problem within the herd, the main causative agent, the characteristics of the infected cow and the udder health management protocol of the farm.

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