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

Introduction. Mastitis, or intramammary infection (IMI), is one of the most significant diseases in dairy herds worldwide. It is caused by environmental and contagious bacteria. Simulation models have proven useful for evaluating the effect of different control strategies. 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.

Methods

We used an existing mechanistic, stochastic simulation model framework to create an IMI simulation model. 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.

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