

Staphylococcus aureus transmission and control in a robotic milking dairy herd

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Introduction

Robotic or automated milking systems (AMS) are being introduced as an alternative to conventional milking systems. Investment in an AMS may be advantageous for some dairy farmers, particularly in terms of reducing labor costs and shifting labor from the repetitive, physical task of milking to other areas of farm management. Research on the effect of AMS on udder health has focused on somatic cell count measures. Theoretically, the consistency of milking hygiene practices is improved with AMSs, where quarters are milked individually, pre-milking stimulation, and pre- and post-milking teat disinfection are applied uniformly, and individual quarter milking teat cups are sanitized between cows. These AMS factors should contribute to the control of the transmission of contagious mastitis pathogens; however, to our knowledge, no study has been conducted to quantify the dynamics of mastitis pathogen transmission in AMS under field conditions. The objectives of this study were to describe the transmission dynamics of *Staphylococcus aureus* intramammary infections (IMI) in dairy herd with an AMS and to estimate the diversity of *S. aureus* strains in that herd by multilocus sequence typing (MLST) of selected isolates.

Materials and Methods

This study was conducted with approval of the University of Vermont Institutional Animal Care and Use Committee. A commercial dairy herd that was milking approximately 247 Holstein cows with four Lely Astronaut A3 AMS units was monitored from May to October, 2011. During the study period, individual quarter milk samples were collected from all lactating cows monthly; from all cows at calving, dry-off, or culling; and from all cases of clinical mastitis prior to and weekly for four weeks following any treatments. Bacteriologic status of milk samples was determined using established methods, and all gram-positive, catalase-positive, hemolytic cocci were further evaluated with the tube coagulase method. Presumptive *S. aureus* isolates were confirmed

by PCR amplification of the thermonuclease gene and screened for *mecA* and *blaZ* antibiotic resistance genes. Intramammary infection status, including prevalence of chronic infections and the incidence of new infections each month, was determined from serial culture results using established criteria. The transmission parameter (β) was estimated from a generalized linear model on the basis of the observed number of new IMI events each month. Strain typing of selected isolates via MLST was conducted as described by Enright *et al* (2000) with alleles and strain types assigned using the MLST database (www.mlst.net).

Results

A single strain type (ST 151) of *S. aureus* was associated with all cases of clinical and subclinical mastitis in this herd. Prevalence of *S. aureus* ranged from 5.6% of cows in June to 2.1% of cows in September. Incidence of new IMI ranged from 0.0064 (May) to 0.0032 (October) new IMI per quarter-month at risk and appeared to be a function of prevalence, which was consistent with contagious transmission. The estimated transmission parameter (β) of *S. aureus* in this herd during the study was 0.0093 (95% confidence interval, 0.0056 to 0.0153).

Significance

The use of AMS is anticipated to increase in North America. Data on mastitis transmission and control in AMS are critical for the production of high-quality milk and milk products. The single *S. aureus* strain type identified in this herd has been previously described as a bovine-host adapted strain. Transmission parameters for this *S. aureus* strain in this AMS herd are similar to those seen in conventional milking herds that successfully apply post-milking teat disinfection and are consistent with limited contagious transmission. This case study provides preliminary data to support subsequent studies of longer duration that may include additional herds and other factors related to mastitis epidemiology and control on farms implementing AMS.