Investigation of the relationship between bedding materials, bedding characteristics, and intramammary infection in late lactation dairy cows: Interim findings

S.M. Rowe, BVSc, MVM, DABVP; S.M. Godden, DVM, DVSc; E.E. Royster, DVM, MS; J.A. Timmerman, BS; B.A. Crooker, MS, PhD; M. Boyle, DVM

¹ Department of Veterinary Population Medicine, University of Minnesota, St. Paul, MN 55108

² Department of Animal Science, University of Minnesota, St. Paul, MN 55108

³Zoetis, Hager City, WI 54014

Introduction

Many cows acquire subclinical intramammary infections (IMI) during lactation, necessitating antimicrobial treatment at dry-off (dry cow therapy). If the dairy industry moves toward the adoption of selective dry cow therapy, one essential strategy to reduce mastitis-associated antimicrobial use at dry off will be to reduce the incidence of new IMI during lactation. One important source of mastitis-causing pathogens is bedding. However studies are needed to investigate the association between bedding management, bedding bacteria count (BBC), and IMI risk in late lactation cows.

The objectives of this prospective cross-sectional study are to: 1) describe associations between BBC and IMI prevalence for individual pathogens and specific pathogen groups in late lactation cows, 2) identify bedding-related risk factors for high BBC, and 3) identify critical levels of bacteria in bedding that might be used as cut-points to guide practitioners when interpreting BBC reports. This study is ongoing, with winter 2018 results currently being assembled.

Materials and Methods

Dairy herds (N=80) were recruited from 10 dairy states with assistance from Zoetis Quality Milk Specialists. Where possible, herds were purposively selected to balance bedding material type within each major dairy region (North East, Midwest, North West and South West). Bedding types were manure solids (MS), other organic (OB), new sand (NS) or recycled sand (RS). A convenience sample of new and used bedding and aseptic quarter milk samples from 20 late gestation (>185 days pregnant) cows were collected from each farm between July and August 2017 (summer) and between December and March 2018 (winter). A management questionnaire was used to collect information about the bedding management practices on each farm.

Total bacteria count (TBC) and density (cfu/mL) of coliform bacteria, non-coliform bacteria, *Klebsiella* spp, *Bacillus* spp, *Streptococcus* spp, *Staphylococcus* spp, and *Prototheca* spp was determined for each bedding sample. Dry matter (%), organic matter (%), and pH were also determined for each bedding sample. Quarter milk samples were cultured on Columbia CNA and MacConkey agar and isolates were identified using standard laboratory procedures, including the use of MALDI-TOF. Associations between bedding management and log-transformed BBC will be determined using mixed linear models. Associations between BBC and IMI risk will be determined using multivariable logistic regression models.

Results

Interim descriptive results from the summer sampling period are reported. The median number of milking cows was 1820 (235 to 9650) and the average daily milk production was 84 (51 to 106) lb (38 [23 to 48] kg). For new bedding, the mean (log10 cfu/ml) total bacteria counts for MS (n=22), OB (n=15), NS (n=18), and RS (n=21) were 5.59, 3.55, 4.28, and 5.53, respectively. For new bedding, the mean coliform count for MS, OB, NS, and RS was 1.71, 1.48, 0.40, and 0.82, respectively. In used bedding, the average total bacteria count among the bedding type categories were similar to each other (MS: 6.84; OB: 6.43; NS: 6.80; RS: 6.71).

Bacteriological analysis of 5,317 quarters indicated 22.9% had an IMI. Quarter prevalence of IMI for MS (n=1,669), OB (n=1,049), NS (n=1,117), and RS (n=1482) cows was 19.9, 26.7, 27.1, and 22.9%, respectively. A total of 1,326 pathogens were isolated from 1,217 infected quarters. Gram positive bacteria accounted for 96.9% of isolates from infected quarters, while gram negative isolates only accounted for 2.2% of isolates. Non-aureus *Staphylococcus* species (NAS) was the predominant pathogen group (53.2% of isolates). No *Prototheca* spp were isolated from milk or bedding samples.

Significance

In this study, we were able to successfully enroll and sample US dairy farms using a broad cross-section of commonly used bedding types. Final results from this study are expected to provide important insights into how bedding management is associated with IMI risk at dry-off.