

Distribution of Coagulase-Negative Staphylococci from Milk and Extramammary Sites on Saskatchewan Dairies

Colleen E. Walpole¹, Herman W. Barkema², Jeroen De Buck², Janet E. Hill¹, and Christopher D. Luby¹

¹Department of Large Animal Clinical Sciences, Western College of Veterinary Medicine, University of Saskatchewan, 52 Campus Drive, Saskatoon, SK, S7N 5B4

²Department of Production Animal Health, Faculty of Veterinary Medicine, University of Calgary, 3330 Hospital Drive NW, Calgary, AB, T2N 4N1

Email: colleen.fitzpatrick@usask.ca

Coagulase-negative staphylococci (CNS) are a very prevalent group of bacteria isolated from mammary glands and have been widely studied over the past 10 years. Although there is a significant amount of research on CNS, their ecology and reported effects on udder health have not been completely characterized. The objective of this study was to determine the distribution of CNS species from milk and extramammary sites, and to characterize the effects of these species on milk production and udder health.

Ten farms from Saskatchewan were selected for the study. Each herd was sampled 3 times at 3-week intervals. Quarter milk samples were collected aseptically at each sampling for milk culture. At the third sampling period, body site samples were taken from enrolled cows, and environmental samples were taken from the parlour and housing areas. Samples were cultured for identification of staphylococci. Isolated CNS were speciated by partial *cpn60* gene sequencing.

A total of 923 cows were enrolled in the study. Of these, 158 cows had a CNS intramammary infection, with 198 milk and 154 body site samples processed. An additional 25 environmental samples had CNS isolated. The most common species recovered from milk and body site samples were *S. chromogenes* (54%) and *S. equorum* (47%), respectively. Equal proportions of *S. xylosus* were recovered from both milk and body site samples (19 and 21%, respectively). Ten cows shared similar species between milk and extramammary isolates, 9 of which were *S. xylosus*. The most common species isolated from environmental samples was *S. equorum* (52%). Analysis of health and production data to compare the effects of each species is ongoing.

Implications: Some CNS species are more detrimental to udder health than others, and it is important to recognize the source of infection. By targeting which species may have a more negative impact on udder health, we can begin to implement control strategies to try and eliminate these infections.