

# Association of Coagulase Negative *Staphylococcal* Species and Milk Somatic Cell Count of Cows from the Canadian National Cohort of Dairy Farms

J. Perry<sup>1</sup>, DVM; J. Middleton<sup>1</sup>, DVM, PhD; S. Dufour<sup>2</sup>, DVM; D. Scholl<sup>2</sup>, DVM, PhD; C. Calloway<sup>3</sup>, DVM, MS; S. Andersen<sup>3</sup>, DVM

<sup>1</sup>College of Veterinary Medicine, University of Missouri, Columbia, MO 65211

<sup>2</sup>Canadian Bovine Mastitis Research Network, University of Montreal, Montreal, QC H3C 3J7

<sup>3</sup>Department of Health Management, Atlantic Veterinary College, Charlottetown, PE C1A 4P3

## Introduction

*Staphylococci* are a diverse group of gram-positive cocci that can infect the cow's mammary gland. For the purposes of diagnosing intramammary infection (IMI), *staphylococci* are classified based on their ability to clot plasma (coagulase test) as either coagulase-positive or coagulase-negative. The most commonly isolated coagulase-positive *staphylococci*, *S. aureus*, is considered a major mastitis pathogen. In contrast, coagulase-negative *staphylococci* (CNS) have historically been classified as minor mastitis pathogens and are rarely, if ever, further differentiated when diagnosing an IMI. The assumption has been that, as a group, CNS cause minor elevations in milk somatic cell count (SCC). However, there has been recent interest in the role of CNS in mammary gland inflammation. The aim of this study was to evaluate the relationship between CNS species and mammary quarter SCC.

## Materials and Methods

Coagulase-negative *staphylococcal* isolates were obtained from the Canadian Bovine Mastitis Research Network (CBMRN) culture collection (n = 1495). Isolates were harvested from mammary quarters of cows with subclinical intramammary infections before and after the dry period or during lactation. Data associated with each sample was obtained from the CBMRN database. The isolates presented here were speciated by *rpoB* gene sequencing. To date, 938 isolates from 696 mammary quarters have been evaluated. The quarter infections were from samples collected prior to dry-off (289), post-calving (159), and mid-lactation (249). Geometric mean SCC were calculated when quarters had the same CNS isolated at more than one time point in mid-lactation and late-lactation samples (n=159), and these geometric mean SCC's were used in calculating median SCC's. For samples taken post-calving, SCC's from samples taken the first week after calving were considered separately. Somatic cell count was compared between CNS species within stage of lactation using a one-way analysis of variance (ANOVA) with post-hoc pair-wise comparisons ( $P < 0.05$ ).

## Results

Twenty species of CNS were identified and significant differences in SCC were noted between species in both first week post-calving and pre-dry groups, but not in the mid-lactation group. *Staphylococcus chromogenes*, *S. simulans*, *S. xylosus*, *S. haemolyticus*, *S. cohnii*, and *S. epidermidis* were the most commonly isolated species, accounting for more than 90% of total isolates. Of the commonly isolated species, *S. epidermidis* and *S. simulans* were significantly more inflammatory (median of SCC's 682,000 and 288,000 cells/mL, respectively) in late-lactation quarters sampled, while *S. haemolyticus*, *S. epidermidis* and *S. simulans* were significantly more inflammatory in samples taken in the first week of lactation (median SCC's of 4,020,000, 4,907,000, and 2,797,000 cells/mL, respectively). The remaining commonly isolated species were associated with SCC's less than 200,000 in all sampling groups with the exception of the early lactation group. *Staphylococcus hyicus* was an uncommon isolate in this study (n=7), but was associated with high median SCC's (347,000 and 1,575,000 in mid- and late-lactation groups, respectively).

## Significance

In common with several recent studies, *S. chromogenes*, *S. simulans*, and *S. xylosus* were among the most commonly isolated CNS species. Compared with previous studies, *S. hyicus* was uncommon in this study. This might be explained by regional or herd differences in prevalence of some CNS species or may reflect differences in speciation techniques or inclusion criteria. Though *S. hyicus* was uncommon, it was significantly more inflammatory than most of the commonly isolated species and, therefore, determining its prevalence among CNS isolates seems warranted. Overall, our data concur with the historical assertion that, on average, most CNS infections cause only mild to moderate increases in milk SCC. However, the data also demonstrate differences between species with regard to the degree of elevation in SCC that warrant further investigation.