

# Bacteriocins of Bovine Non-*aureus* Staphylococci

Domonique Carson, Herman Barkema, Sohail Naushad, Diego Nobrega, Larissa Condas, Jeroen De Buck

Department of Production Animal Health, Faculty of Veterinary Medicine, University of Calgary. 3330 Hospital Dr NW Calgary AB T2N 4N1.  
Email: domonique.carson@ucalgary.ca

Non-*aureus* staphylococci (NAS) are the most commonly isolated bacteria from the bovine udder. Several studies have found that NAS have a protective effect against infection of the udder by major mastitis pathogens such as *Staphylococcus aureus*, while other studies have reported no protection. The inhibition is likely due to bacteriocins, which are peptides that inhibit the growth of similar bacterial species. As regulations surrounding antibiotic usage get stricter, bacteriocins represent potential alternatives to antibiotics. The first objective of this study is to determine the inhibitory capability of 441 NAS isolates from 26 different species against a bovine *S. aureus* and a methicillin-resistant *S. aureus* (MRSA). The second objective is to determine the genetic organization of the bacteriocin genes from 441 whole genome sequences of NAS. We hypothesize that some species will display inhibitory capabilities against major pathogens and that bacteriocin related genes are distributed throughout many different species of NAS.

**Materials and Methods:** NAS and an *S. aureus* isolate were obtained from the Mastitis Pathogen Collection of the Canadian Bovine Mastitis and Milk Quality Research Network. Species-specific inhibition was tested for using a modified cross-streaking method from De Vliegher et al. (2004). Next, the presence of bacteriocin-associated genes were determined in the newly obtained whole genome sequences of 441 NAS isolates.

**Results:** 41 isolates from 10 different species (*S. capitis*, *S. chromogenes*, *S. epidermidis*, *S. haemolyticus*, *S. pasteurii*, *S. saprophyticus*, *S. sciuri*, *S. simulans*, *S. warneri*, and *S. xylosum*) showed inhibition against *S. aureus*. Of the 41 inhibiting isolates, 24 isolates from *S. capitis*, *S. chromogenes*, *S. epidermidis*, *S. pasteurii*, *S. simulans*, and *S. xylosum* inhibited MRSA. 103 bacteriocin gene clusters from 93 NAS whole genomes from 16 species were found.

**Implications:** Identifying bacteriocins may lead to novel antimicrobials to be used for the prevention and treatment of Gram-positive pathogens, which will improve udder health and decrease the economic impact of mastitis.