

# Transcriptomic Analysis Of *In Vivo*-Expressed Genes In *Staphylococcus Aureus* During Bovine Mastitis

M. Allard\*<sup>1</sup>, C. Ster<sup>2</sup>, L. St-James<sup>2</sup>, P. Lacasse<sup>2</sup>, M. S. Diarra<sup>3</sup>, C. L. Jacob<sup>1</sup> and F. Malouin<sup>1</sup>

<sup>1</sup>Université de Sherbrooke, Sherbrooke, QC, <sup>2</sup>AAFC-Dairy and Swine R&D Centre, Sherbrooke, QC and <sup>3</sup>AAFC-Pacific Agri-Food Research Centre, Agassiz, BC  
Email: [Marianne.Allard@USherbrooke.ca](mailto:Marianne.Allard@USherbrooke.ca)

The human and animal pathogen *Staphylococcus aureus* is involved in intramammary infections in cows, creating health problems and milk quality concerns and thus causing major economic losses for the dairy industry. Our hypothesis is that *S. aureus* expresses specific genes that are essential for intramammary infections and that may represent new and unexploited targets for therapeutic intervention against this pathogen. Previously in *S. aureus*, we showed that iron-regulated and many other virulence genes were strongly expressed *in vivo* using an infection model in the mouse. This demonstrated that the mammalian host environment can modulate gene expression in *S. aureus*. Based on these results, our current objective is to identify genes specifically expressed in *S. aureus* directly isolated from the milk of cows presenting mastitis after an experimental infection.

Individual quarters of the mammary gland of healthy lactating cows were infected with 50 cfu of one of four different *S. aureus* strains. Three of these strains were originally isolated from cows with chronic mastitis, *i.e.*, isolated from cows shedding a genetically identical *S. aureus* strain 60 days apart, between dry off and calving. Milk was collected at several time points over a period of two weeks during the experimental infections. The studied *S. aureus* strains showed some differences in their ability to cause an infection with a sustained level of bacteria in milk. To study the transcriptional profiles, we developed a method to quickly isolate bacteria from freshly collected milk and to extract total bacterial RNA before performing reverse-transcription to obtain cDNAs. The cDNAs will be used for microarray hybridization or for amplification by quantitative PCR.

**Implications for the dairy industry:** The genes strongly expressed during all the phases of infection and that are common to several strains of *S. aureus*, including those causing chronic mastitis, will be the ones considered as ideal targets for the development of new control strategies against this pathogen.