

BIOENGINEERING & BIOMEDICAL ENGINEERING RESEARCH SEMINAR

INTER-BACTERIAL COMPETITION IN THE LIVESTOCK MICROBIOME



Dr. Jennifer Ronholm
Canada Research Chair in Agricultural Microbiology
Associate Professor, Faculty of Agricultural and
Environmental Sciences
Associate Member, Faculty of Medicine
and Health Sciences

Dr. Ronholm obtained her BSc in Microbiology from the University of Waterloo in 2007 and her Doctoral degree in microbiology and immunology from the University of Ottawa in 2013. She completed post-doctoral training at McGill University and at Health Canada. She was hired as an Assistant Professor in the Faculty of Agricultural and Environmental Sciences in 2017. Her interests are primarily in understanding the role of the microbiome in determining susceptibility of individuals (both humans and agricultural animals) to infections.

The human health effects of antibiotic resistance are a growing international crisis. In 2019 an estimated 4.95 million human deaths were associated with antibiotic resistance, and it is estimated that by 2050 there will be 10 million deaths a year due to antibiotic resistance infections. However, 70-80% of all antimicrobials that are produced internationally are used in agriculture to increase growth, provide prophylaxis, and treat bacterial infections in livestock. Continued use of antibiotics in agriculture is unsustainable, unacceptable, and unethical given that it is a driving factor behind increasingly drug resistant human infections. The Ronholm laboratory aims to address this problem by characterizing the microbiota of livestock, identifying antagonistic interactions that occur naturally between bacterial pathogens and members of the endogenous microbiota, obtain isolates, and then engineering designer, disease resistant microbiotas to replace the functional need for antibiotics on farms. The three primary strategies are used in my lab to understand inter-bacterial interactions between pathogenic and endogenous bacteria are: 1) culture-independent investigations of how the microbiota responds to infection, 2) reductionist co-culture assays, and 3) in vitro and in vivo challenge studies. We have engaged in two longitudinal studies to identify the differences between the microbiota present in healthy dairy cows and mastitic cows, as well as in healthy chickens and chickens infected with *Salmonella enterica*.

Culture-independent techniques are used generate hypotheses about which endogenous bacteria might demonstrate antagonism against pathogens. My most advanced research theme examines how the composition of the microbiome in the mammary quarters of dairy cattle influence the development of mastitis caused by *Staphylococcus aureus*, *Escherichia coli*, and *Klebsiella pneumoniae*. To provide insight into these interactions, we collected milk samples with correlated health status data from 698 dairy cows over the course of 1.5 years to compare the composition of the microbiome of healthy quarters to the microbiome of infected quarters before, during, and after infections. We determined that the presence *Aerococcus urinaeequi* and *Staphylococcus xylosum* in raw milk was negatively correlated to *S. aureus* mastitis infection. After this finding we were able to isolate *A. urinaeequi* and *S. xylosum* from healthy cattle and have found that several isolates are able to inhibit the growth of *S. aureus* in co-culture. We are currently working to learn more about the complex relationships between *S. aureus*, *A. urinaeequi*, and *S. xylosum* and the role that each play in udder health in dairy cows. This has included developing a high-throughput assay to screen bacteria isolated from healthy cattle for antagonistic activity against *S. aureus*. We have also determined that presence of *Aerococcus* sp., UCG-005, and *Lachnospiraceae* in the quarters of dairy cattle negatively correlate with *K. pneumoniae* infection; and that the presence of non-*Aureus* staphylococci, *A. urinaeequi*, and *Serratia marcescens* negatively correlate with *E. coli* infections.

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Department of **Biomedical Engineering**
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