

Development of an alternative therapeutic method for the control of Bovine mastitis in dairy cows.

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Mastitis is one of the most frequently occurring diseases affecting dairy cattle. Cattle with mastitis suffer from painful inflammation of the udder, which results in low milk production, culling, discarded milk and sometimes death, factors that have a great economic impact on the dairy industry. Current treatments of bovine mastitis include antibiotics, which increase the burden of antimicrobial resistance in livestock and as a result also in humans and the environment. In this project, we aim to develop alternative therapies for bovine mastitis by understanding the causative and beneficial organisms in the commensal microbiota of the mammary gland. We propose the use of state-of-the-art genomics and metagenomics approaches to identify influential members of the udder microbiota with central roles in maintaining udder health and modulating susceptibility to mastitis. Metagenomics is the use of genomic technologies and bioinformatics to help study the entire microbial community. Milk samples will be collected from commercial farms in Alberta at different time points of lactation for each quarter. An innovative approach will be used for targeted isolation and characterization of these beneficial "foundation species" from the native microbial community of the udder. The goal of this research is to develop a combination of these foundation species that will be used for the development of a synthetic mini-microbial community, the antimicrobial activities of which will be tested against major mastitis pathogens under laboratory conditions.