Project Title: Characterizing Variation in Antimicrobial Resistance between Environments within Natural and Conventional Beef Operations

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Objective: It is thought that less antimicrobial use will lead to less selective pressure for Antimicrobial Resistance (AMR) and result in a more secure food supply, however direct characterizations of this haven't been performed. This study aims to characterize the microbial communities and resistomes in natural and conventional beef feedlots using metagenomic, Next-Generation Sequencing (NGS) methods.

Experimental Design & Analysis:

Composite fecal (N=12) and catch basin water samples (N=13) were taken from four feedlots in Alberta, Canada. One feedlot runs both conventional and natural operations. Engineered wetland (N=1) and human wastewater treatment plant (N=6) samples were taken from the surrounding area. Total DNA was extracted and sequenced on the Illumina HiSeq platform. Antimicrobial resistance profiles were obtained using manually curated data from public sources. Microbiomes were profiled using the software Kraken. Additional sample data will be available by the time of presentation.

Key Results:

Microbial profiles and resistomes varied significantly between the type of matrix (environment) sequenced. Fecal composite and human wastewater treatment (influent) samples showed the highest within-group variation. Environmental samples, including catch basin and wetlands, showed the lowest within-group variation. For the natural and conventional operation, the conventional fecal composite samples had a higher relative proportion of AMR mechanisms and lower relative microbial diversity than did the natural samples. The catch basin resistome and microbiome also varied between natural and conventional but less so than the fecal samples.

How can this information be applied in the industry?

While the use of antimicrobials in industry does change the microbial resistome and microbiome, it is important to note that these changes are happening as a small part of a larger, background resistance and microbial environment. The presence or finding of antimicrobial genes in a given environment does not necessarily indicate a threat to food safety, and further work is necessary to characterize the risk associated with various resistome profiles. Industry experts can utilize our findings to help educate on antimicrobial resistance and to make more informed decisions on the use of antimicrobials and assessment of risk in the food production chain.

Figure 1: The abundance of antimicrobial resistance genes was highest in the fecal composite samples and showed characteristic profiles for Beef feedlot fecal samples. The abundance in the conventional operation was higher than the natural operation. Significantly more genes were found in the fecal samples than in the catch basin samples.