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Presentation Abstracts

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21 - Metagenomic investigations of antimicrobial resistance in beef, pork, and broiler production systems

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Session: Antimicrobial Resistance – 4, Room 1, 12/5/2017 9:00 AM

Antimicrobial drug use in production of food animals is recognized as a global public health concern based on concerns that resistant bacteria could be present in food products, and this could in turn have negative impacts on public health. Antimicrobial drugs are used in animal agriculture for treatment and prevention of disease and to improve feed efficiency; however, different antibiotics are more commonly utilized in different species. In order to address public health concerns related to antibiotic resistance, information is needed to understand the impact of antibiotic usage in food animals. The objective of this study was to use targeted shotgun metagenomic sequencing to characterize and contrast the fecal resistome of market cattle, pig, and chicken feces. Sixty composite fecal samples were collected from each production system (20 samples from five pens of cattle, 20 samples from five chicken houses, and 20 samples from five hog barns). Metagenomic DNA was extracted from the fecal samples and a customized bait-pulldown system (Agilent, SureSelect XT) was used to build libraries targeting AMR gene sequences. These libraries were sequenced using the Illumina HiSeq platform. Raw sequences were analyzed using the AMR++ bioinformatics pipeline and MEGARes database of AMR gene sequences. Hits to resistance gene accessions were characterized hierarchically by class, mechanism, and group and were compared among the different production systems. Additionally, the resistomes from each production system were described in relation to The World Health Organization's list of Critically Important Antimicrobials for Human Medicine. Beef cattle shed resistance genes primarily associated with tetracycline resistance, followed by the MLS class. This was similar to the swine operation that had the most hits to tetracycline resistance bacteria, though in terms of relative abundance, swine operations had a high percentage of aminoglycoside resistance. Broiler production had the most even ratio of MLS to tetracycline resistance genes when compared to the other systems. These data show antibiotic resistance genes vary by livestock production system.

22 - Incorporating traditional bacterial culture methods and metagenomic sequencing to evaluate antimicrobial use and resistance in beef feedlot production

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Session: Antimicrobial Resistance – 4, Room 1, 12/5/2017 9:15 AM

The increasing prevalence of antimicrobial resistance (AMR) is a global public health concern, and is commonly hypothesized to be "driven" by antimicrobial use (AMU) in humans and food producing animals. Traditionally, studies of AMR use aerobic culture to study just a few bacterial species from a complex bacterial community (the microbiome), and results can differ depending on the species under study. However, advancements in high-throughput sequencing can be used to provide a holistic perspective into AMR ecology by sequencing DNA from the entire microbiome, including the "population" of resistance genes (the resistome). In this study we used metagenomic sequencing to analyze the microbiome and resistome in feces collected during a previously published 3-year longitudinal study of Canadian beef feedlot operations. The goal of the previous study was to investigate the effect of AMU practices on susceptibility patterns of non-type-specific *Escherichia coli* and *Mannheimia haemolytica*. Pens of cattle were randomly selected for inclusion into the study and pooled fecal samples were collected from the pen floor when cattle arrived to the feedlot and at a second date during the feeding period. All AMU, including parenteral treatments and in-feed exposures, was recorded and summarized using animal defined daily dose (ADD). Pen level AMU was calculated as the sum of ADDs for all cattle housed in a pen. A subset of 42 pens was randomly selected for inclusion in the present study, based on categorization of when the second set of fecal samples was obtained: < 100 days after arrival at the feedlot (n=21) and >100 days (n=21.) Our results characterize the microbiome and resistome ecology in beef feedlot operations; further, we were able to make a unique comparison of studies investigating the impact of AMU on AMR when using traditional aerobic culture methods in comparison to newer methods using shotgun metagenomic sequencing.