



RESEARCH BRIEF

BEEF SAFETY

BEEF

RESEARCH

Investigating Effects of Tulathromycin Metaphylaxis on the Fecal Resistome and Microbiome of Commercial Feedlot Cattle Early in the Feeding Period

Enrique Doster^{1,2}, Pablo Rovira^{1,3}, Noelle R. Noyes^{1,4}, Brandy A. Burgess⁵, Xiang Yang^{1,3}, Margaret D. Weinroth^{1,3}, Steven M. Lakin^{1,2}, Christopher J. Dean^{1,2}, Lyndsey Linke⁶, Roberta Magnuson⁶, Kenneth I. Jones⁷, Christina Boucher⁸, Jamie Ruiz⁸, Keith E. Belk^{1,3} and Paul S. Morley^{1,2,6}

¹Microbial Ecology Group, Colorado State University, Fort Collins, CO, United States

²Department of Microbiology, Immunology and Pathology, Colorado State University, Fort Collins, CO, United States

³Department of Animal Sciences, Colorado State University, Fort Collins, CO, United States

⁴Department of Veterinary Population Medicine, University of Minnesota, St. Paul, MI, United States

⁵Department of Population Health, University of Georgia, Athens, GA, United States

⁶Department of Clinical Sciences, Colorado State University, Fort Collins, CO, United States

⁷Department of Biochemistry and Molecular Genetics, University of Colorado Denver School of Medicine, Aurora, CO, United States

⁸Department of Computer and Information Science and Engineering, University of Florida, Gainesville, FL, United States

Abstract

The objective was to examine effects of treating commercial beef feedlot cattle with therapeutic doses of tulathromycin, a macrolide antimicrobial drug, on changes in the fecal resistome and microbiome using shotgun metagenomic sequencing. Two pens of cattle were used, with all cattle in one pen receiving metaphylaxis treatment (800mg subcutaneous tulathromycin) at arrival to the feedlot, and all cattle in the other pen remaining unexposed to parenteral antibiotics throughout the study period. Fecal samples were collected from 15 selected cattle in each group just prior to treatment (Day 1), and again 11 days later (Day 11). Shotgun sequencing was performed on isolated metagenomic DNA, and reads were aligned to a resistance and a taxonomic database to identify alignments to antimicrobial resistance (AMR) gene accessions and microbiome content. Overall, we identified AMR genes accessions encompassing 9 classes of AMR drugs and encoding 24 unique AMR mechanisms. Statistical analysis was used to identify differences in the resistome and microbiome between the untreated and treated groups at both timepoints, as well as over time. Based on composition and ordination analyses, the resistome and microbiome were not significantly different between the two groups on Day 1 or on Day 11. However, both the resistome and microbiome changed significantly between these two sampling dates. These results indicate that the transition into the feedlot—and associated changes in diet, geography, conspecific exposure, and environment—may exert a greater influence over the fecal resistome and microbiome of feedlot cattle than common metaphylactic antimicrobial drug treatment.

doi: [10.3389/fmicb.2018.01715](https://doi.org/10.3389/fmicb.2018.01715)

*This peer-reviewed journal article was based in part on the following checkoff-funded Project Summary: [Use of Shotgun Metagenomic NGS Combined with a Previously-developed Bioinformatics Pipeline vs. Traditional Culture/Screening Diagnostics to Evaluate Ecology of AMR and Diagnose *Salmonella spp.* in Cattle Feces Before and After Ceftiofur Metaphylaxis](#)

Internal links within this document are funded and maintained by the Beef Checkoff. All other outgoing links are to websites maintained by third parties.