

Project Title:	Prevalence, Quantity and Antibiotic Resistance Profiles of <i>Salmonella enterica</i> Late in the Feeding Period and at Slaughter in Response to Antibiotic use Early in the Cattle Feeding Period - Part 2
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Background

The threat of antimicrobial resistant bacteria and the implications for human health represent an area of research that has been receiving a great deal of attention in both the media and scientific community. In the recent Centers for Disease Control and Prevention (CDC) report, “Antibiotic Resistance Threats in the United States, 2013”, multidrug resistant *Salmonella enterica* is listed as a microorganism of serious threat. *Salmonella* outbreaks are most commonly associated with poultry and eggs; however, beef has also been implicated as a source of infection. The use of antibiotics in food animals may contribute to selection and expansion of antimicrobial resistant bacteria through the food chain. A major concern is that many antibiotics used in food animals are also important in human medicine. Strict regulations or bans on the use of antimicrobials in agriculture could have devastating effects on animal health and create food safety issues. Identifying optimal ways to minimize any risks to human health associated with antibiotic use while maintaining animal health and welfare are important goals.

The objective of this study was to determine the effects of tulathromycin and ceftiofur treatment on the prevalence, quantity, and antimicrobial resistance of *Salmonella* in feedlot cattle immediately following treatment, through the feeding period, and at slaughter.

Methodology

Individual fecal samples were collected at an experimental feedlot in Canyon, Texas. The randomized and controlled field trial was comprised of 134 steers in three different treatment groups to assess the impact of ceftiofur and tulathromycin use as metaphylaxis early in the feeding period. Twelve pens (11(12) steers/pen) were assembled with steers blocked by starting weights. Cattle fecal samples from Days 0, 7, 28, 56, and 99 then pre-slaughter) were enriched and plated to selective media to identify *Salmonella* positive samples. Spiral plating onto brilliant green agar with novobiocin was used to obtain crude estimates of *Salmonella* quantities. Antibiotic susceptibility was performed for 14 different antimicrobials by the microbroth dilution method using the Sensititre® automated inoculation delivery and fluorometric plate reading system. Genotypic antimicrobial susceptibility profiles were determined by whole genome sequencing of *Salmonella* isolates. Sequencing data were analyzed for the presence of antimicrobial resistance genes using the online databases Resfinder, ARG-ANNOT and CARD. *Salmonella* sequence types, virulence genes and plasmids were determined using whole genome sequencing data and short read sequence typing for bacterial pathogens (SRST2), while serotypes were classified at SeqSero. Hide swabs (1m2) and subiliac lymph nodes were sampled at slaughter with similar analysis conducted as described for fecal samples.

Findings

Use of antibiotics early in the feeding period has a limited impact on the ecology of *Salmonella* in the feces of cattle at later periods. Observed effects were transient, and the dominant serotypes present in the beef cattle environs represent a highly antibiotic susceptible population of *Salmonella*. The major effect on *Salmonella* prevalence and quantity appears to be climatic and may be limited to this region.

Implications

The dynamics of the *Salmonella* population in cattle during the feeding period and at slaughter has important food safety implications. Our study suggests that by the time antibiotic treated cattle are sent to slaughter that fecal bacterial populations have returned to baseline conditions. The prevalence and quantity of *Salmonella* in hide swabs is nearly identical across all treatment groups at slaughter suggesting a reversion to the local environment. There also is no significant impact of antibiotic use early in the feeding period on the quantity of *Salmonella* in lymph nodes at slaughter.

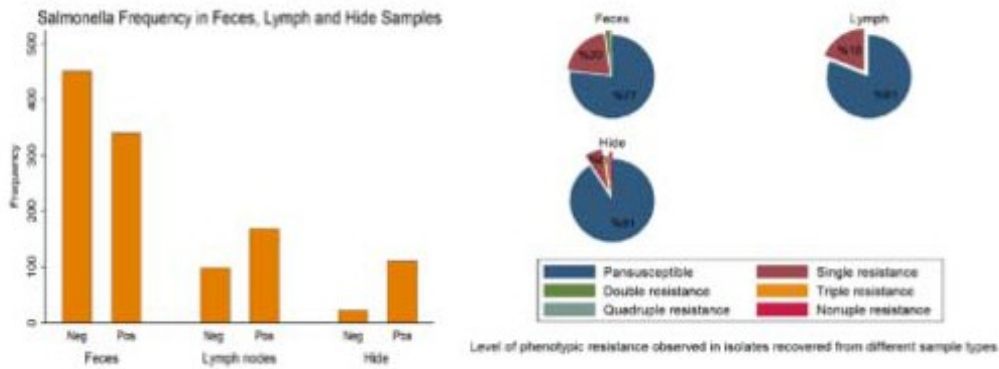


Figure 1. *Salmonella* status (overall, and by resistance profile) in feces, lymph nodes, and hides.

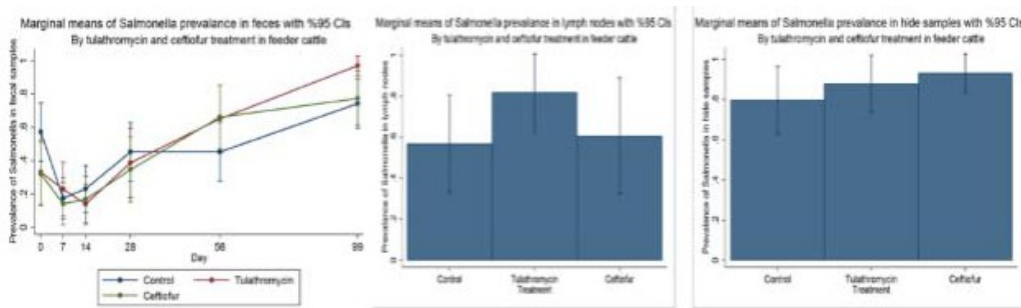


Figure 2. *Salmonella* prevalence in feces, lymph nodes and hides.