

Prevalence and Antimicrobial Resistance of *Salmonella enterica* Isolated from Beef Cows and Feedlot Steers from Post-weaning to Slaughter

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Abstract

Salmonella spp are considered one of the most important foodborne pathogens that affect humans. *Salmonella* present in feces and on the hides of beef cattle during harvest has been linked to beef carcass contamination. The objectives of this study were to 1) estimate the prevalence of *Salmonella* in beef cows and steer calves at post-weaning, finishing, and slaughter, and 2) to determine the antimicrobial resistance patterns of the isolates, and 3) to determine the presence of class 1 integrons in the isolates, and assess the association between AMR and the presence of class 1 integrons. Fecal samples were collected from cows at four sampling periods and from steers at five sampling periods. Mid-line sponge samples were obtained from the hides of steers before slaughter. Laboratory culture of fecal and sponge samples for *Salmonella* were performed. National Antimicrobial Resistance Monitoring System (NARMS) panels were used to test for antimicrobial resistance (AMR) of *Salmonella* isolates. Polymerase chain reaction (PCR) was performed to test for the Integrase 1 gene in *Salmonella* isolates, and positive isolates were analyzed for the presence of a conserved sequence. In cows, the prevalence of *Salmonella* faecal shedding varied from 8% (3/38) to 92% (35/38) over the four sampling periods, and a higher prevalence was observed in the warmer months (May and September) compared to cooler months (November and February). In steers, prevalence varied from 28% (13/47) to 100% (24/24) over the five sampling periods, with a higher prevalence observed at post-weaning (63%; 60/96) compared to finishing (28%; 13/47) and slaughter

(47%; 22/47). Over half of the isolates 116/200 (58%) were resistant to at least one antimicrobial drug, and 111/200 (56%) displayed multiple drug resistance (resistance to 2 or more antimicrobials). Most frequent resistance was observed to chloramphenicol (57%), followed by tetracycline (56%), sulfizoxazole (56%), streptomycin (56%), ampicillin (55%), and amoxicillin/clavulanic acid (47%). The integrase 1 gene was isolated from 98/200 (49%) isolates, with 88 (90%) of the isolates harboring a conserved sequence, the *aadA* resistance gene which encodes for streptomycin/spectinomycin resistance. A significant association was observed between the presence of Integrase 1 gene and antimicrobial resistance to amoxicillin/clavulanic acid, chloramphenicol, ampicillin, streptomycin, sulfizoxazole, and tetracycline, and the observed resistance was attributed to presence of Integrase 1 gene. Study findings revealed that most steers shed *Salmonella* at the post-weaning stage, suggesting widespread exposure either before or after weaning while on pasture. These findings highlight the need for pre-harvest monitoring for *Salmonella* fecal shedding in feedlot cattle at the stage of post-weaning. The detection of antimicrobial resistant *Salmonella* further highlights the dilemma and potential public health significance associated with the use of antibiotics such as streptomycin in veterinary prophylaxis and therapy involving beef cattle.

Key words: *Salmonella*, cattle, beef, feedlot, prevalence, antimicrobial resistance