Characterization of *Salmonella spp*. from Post-weaning to Slaughter

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Abstract

The occurrence of *Salmonella* in cattle has been well documented but little is known of tracking its prevalence and antimicrobial resistance (AMR) from post-weaning to slaughter. This study follows a longitudinal approach, allowing for the best analysis of *Salmonella* prevalence and AMR in cattle. It was carried out to monitor variation in *Salmonella* prevalence and antimicrobial resistance (AMR) patterns in beef cattle from range (calves post weaning in North Dakota (ND)) to feedlot cattle up to slaughter (Nebraska). Two separate groups were analyzed, cattle which remained at the Dickinson Research Extension Center (DREC) throughout the course of the study and calves which initially were housed at the DREC, then transferred to a University of Nebraska Feedlot, where they remained until slaughter. Fecal samples were taken four times over a sampling period of eleven months, September 2008 – July 2009; a mid-line sponge sample was taken of the steers before slaughter. Laboratory culture of fecal and sponge samples for *Salmonella* followed a standard published procedure. Presumptive *Salmonella* positive isolates were further analyzed using API20E strips. National Antimicrobial Resistance Monitoring System (NARMS) panels were used for antimicrobial resistance (AMR) testing of *Salmonella* isolates. Additionally, PCR was performed to determine the prevalence of Integrase 1 gene in the *Salmonella* isolates and presumptive integrase positive isolates were further analyzed for the presence of a conserved sequence. Overall, the prevalence of *Salmonella* ranged from 7.9% to 92.1% in adult cattle throughout the study. The prevalence of *Salmonella* in calves at post weaning ranged from 27.7% to 54.4%, with one month, December 2008, displaying 100% prevalence. At the final sampling of calves which included a midline sponge sample along with a fecal grab, prevalence of *Salmonella* was 45.8% and 46.8%, respectively. *Salmonella* isolates displayed the most AMR towards chloramphenicol (57.3%), streptomycin (54.7%) and tetracycline (54.7%) in both groups. Overall, the integrase 1 gene was isolated from 100 (50.0%) isolates, with 88 (44.0%) isolates harboring a conserved sequence. In conclusion, this study provided data on AMR patterns of *Salmonella* shed by beef cattle at the different stages of production. Also, an association between AMR towards the various antimicrobials tested and presence of integron 1, on the *Salmonella* isolates recovered was investigated providing some information on the mechanisms of resistance to these antimicrobials. Most importantly, this research contributes information to the scientific literature on *Salmonella* prevalence and ARM risk assessment in the beef cattle food chain that can allow for development of appropriate control measures.

Foodborne illnesses in the United States (US) are caused by a wide variety of microorganisms and are estimated to cause 76 million illnesses, 325,000 hospitalizations, and 5,000 deaths annually (Mead et al., 1999).

Of all food borne pathogens that affect humans, *Salmonella* is widely considered to be one of the most important. A foodNet report estimated *Salmonella* related infections in the US to be 1.4 million illnesses, 15,000 hospitalizations and 400 deaths annually (Voetsch et al., 2004).

Among the many *Salmonella* serotypes, the most common associated with infection in humans are S. typhimurium and S. enteritidis. *Salmonella* can live in the intestinal tracts of humans, other animals, and

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birds. Foods of animal origin may be contaminated with *Salmonella*; therefore, eating raw or undercooked eggs, poultry, or meat can cause infection. Foods prepared with raw eggs can be an unrecognizable origin of contamination. Meat from poultry and ground beef are sources of contamination that should be well cooked before consumption.

The ability of Salmonella to become resistant to antimicrobials has hampered efforts in treating illnesses caused by this pathogen and has made the production and tracking of food products, especially those from cattle, more important. Antimicrobial resistance is the ability of microorganisms to evade the effects of antimicrobials through newly developed biological mechanisms (CDC, 2008). The ability of microorganisms to evade or to become

resistant to antimicrobials can be acquired through integrons, which are genes that consist of a central variable region that often harbors antibiotic-resistance gene cassettes (Amita et al., 2004).

Procedure

Using cow-calf pairs located at the Dickinson Research Extension Center, the purpose of this pathogen survey project is to track the prevalence of pathogenic *E. coli* and *Salmonella* serotypes through the production continuum beginning on fall native range and ending at final harvest (steer calves). *Objectives*: (1) Determine seasonal prevalence change for pathogenic *E. coli* that carry shiga toxin genes and *Salmonella* spp., (2) Determine the level of antimicrobial resistance (AMR) and multidrug resistance in Salmonella strains isolated from beef cattle at different stages of production, and (3) Determine the association between the presence of Integron-1and AMR to 15 different antimicrobials (amikacin, amoxicillin/ clavulanic acid, ampicillin, ceftiofur, chloramphenicol, ciprofloxacin, gentamicin, kanamycin, nalidixic acid, streptomycin, sulfizoxazole, and trimethprim-sulfamethoxazole) in isolated *Salmonella* strains.

Fecal grab samples and rectoanal swab samples are being collected beginning before weaning on fall pasture and continuing through weaning, mid-winter (Feb), at spring pasture turnout on improved crested wheat, and on pasture mid-summer. The calves will be sampled on fall pasture, at weaning, at the end of unharvested corn grazing, midway through the finishing period (Feb), and just prior to final harvest. Laboratory isolation and definitive PCR serotype determinations were conducted under the direction of Dr. Margaret Khaitsa, Veterinary Epidemiologist, NDSU Veterinary and Microbiological Sciences Department.

Expected outcomes include: (1) Establishment of seasonal shedding patterns for shiga toxin producing *E. coli* serotypes and *Salmonella* spp., (2) Establishment of antimicrobial resistance patterns of Salmonella isolated from beef cattle throughout the production continuum, (3) Establish the connection between Integron-1 presence and resistance patterns to the antimicrobials tested.

Literature Cited

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