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Characterization of Fecal Shiga Toxin-Producing *Escherichia coli* from Post-Weaning Cattle

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Objectives

Shiga toxin-producing *E. coli* (STEC), which are often found in the intestinal tract of cattle and in their fecal matter, are among the most common foodborne pathogens of concern in beef production. Contamination from the fecal matter, both directly and indirectly, during harvest may compromise the safety of the beef products, which can have devastating impact on consumers and producers alike. While the microbial load present in cattle fecal matter may change as the cow matures, previous research has generally focused on analysis of the pathogen load late in the life cycle of cattle. There is merit in the analysis of this load earlier in the life cycle of cattle, as this may serve to subsequently control the pathogen load during later stages of production. As such, this study aims to assess the prevalence and characteristics of STEC in beef cattle production at the early post-weaning stage.

Materials and Methods

Rectal fecal samples from post-weaning cattle (n = 68) were collected. Ten grams of each sample was mixed and manually homogenized with 90mL tryptic soy broth (TSB) with added phosphates. The homogenized samples were spread-plated on CHROMagar STEC plates and incubated at 35°C for 24h before enumeration. To determine STEC prevalence, the homogenized samples were incubated at 42°C for 6 h, and streaked onto a second set of CHROMagar STEC plates, which were incubated at 35°C for 24h. Colonies with a purple coloration were STEC-positive. Two random STEC-presumptive colonies from each sample were tested via subsequent PCR amplification and gel electrophoresis to confirm the presence of *stx1*, *stx2*, and/or *eae* genes.

Acid-resistant strains of presumptive STEC colonies from the enriched samples were collected and inoculated into TSB for recovery. One hundred microliters of the inoculated sample were then transferred into TSB without dextrose and incubated at 35°C for 24h, and finally challenged in acidified TSB without dextrose (pH = 3.50) for 1h and 6h. One hundred microliters of each survival sample were plated onto tryptic soy agar (TSA), and incubated at 35°C for 48h.

Results

The fecal samples had an average 4.79 ± 1.24 log CFU/g (ranging 2.30 to 6.83) of STEC colonies. All samples were STEC-positive, as all samples had at least one of the three genes tested for (*stx1*, *stx2*, *eae*). All sixty-eight samples were confirmed positive for gene *stx1*, 12% (8 of 68) samples were confirmed positive for *stx2*, 62% (42 of 68) of samples were confirmed positive for *eae*, and 12% (8 of 68) were positive for all three genes. Of 67 samples tested for acid resistance, 34% (23 of 67) survived after 6 h in acidified growth media (pH = 3.50).

Conclusion

This study provided preliminary data on the pathogen load of early post-weaning cattle. The prevalence of acid resistance shown may be a possible cause of concern, as these surviving bacteria can survive high acidic conditions. This may expedite the spread of acid-resistant pathogens within the food supply chain as acidic antimicrobial chemicals become ineffective in reducing pathogen populations. These results may be used as a baseline for future research regarding STEC prevalence or acid resistance aimed at reducing pathogen load in beef cattle production. Given the prevalence of acid resistance, further development is recommended for non-acid post-harvest antimicrobial interventions to reduce the presence of acid resistant STEC.