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Prevalence, distribution and seasonality of Shiga toxin-producing *Escherichia coli* (STEC) O157 and non-O157 in feces of commercial feedlot cattle in USA.

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Although there has been extensive research on STEC O157 in cattle, information on the frequency, distribution and seasonality of STEC non-O157 in the cattle reservoir and their production environment is limited. The objective of this study was to determine variability in feedlot- and pen-level prevalence as well as seasonal effects of seven STEC serogroups (O26, O45, O103, O111, O121, O145, and O157) and their associated virulence genes (*stx1* and/or *stx2*, and *eae*) in feces from commercial feedlot cattle in the United States. To evaluate prevalence and seasonality, 24 pen-floor fecal samples were collected from each of 24 pens of ready-to-harvest cattle, in both summer 2013 and winter 2014, at a commercial feedlot. To assess differences in distribution, eight commercial feedlots in Nebraska and Texas were sampled in summer 2014. Up to 16 pen-floor fecal samples were collected from each of 4 to 6 pens per feedlot, per visit, for a total of three visits. Fecal samples were subjected to culture- and molecular-based detection methods. Generalized linear mixed models were used to estimate prevalence accounting for the hierarchical structure of the study. Model-adjusted sample-level prevalence estimates of STEC O26, O103, O145, and O157 during summer 2013 were 1.0, 1.6, 0.8, and 41.4%, respectively. Serogroups O26, O45, O103, and O121 were isolated from cattle feces in winter but no virulence genes of interest were detected. In summer 2014, all study feedlots and 23.0% of pens tested positive for STEC non-O157, whereas sample-level prevalence estimates ranged from 0.0% for STEC O121 to 18.7% for STEC O157. Although statistically significant ($P < 0.05$) seasonal differences in the prevalence of STEC O103 and O157 were found, STEC non-O157 were rarely detected in cattle feces tested in summer, and STEC isolates were not identified in winter months. No differences were found in prevalence estimates between states, however most of the variability occurred within pens. Prevalence estimates at different hierarchical, geographical and seasonal levels provide a much needed microbiological foundation for risk assessment models of STEC and other foodborne pathogens along the beef chain.