Prevalence of Enterohemorrhagic *Escherichia coli* O26, O45, O103, O111, O121, O145, and O157 on Hides and Pre-intervention Carcass Surfaces of Feedlot Cattle at Harvest

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Abstract

Cattle hides are a main source of enterohemorrhagic *Escherichia coli* (EHEC) contamination of beef carcasses. The objectives of this study were to (1) determine the prevalence of “top 6” non-O157 plus O157:H7 EHEC (EHEC-7) on feedlot cattle hides and their matched pre-intervention carcasses; (2) assess the agreement among detection methods for these matrices; and (3) conduct a molecular risk assessment of EHEC-7 isolates. Samples from 576 feedlot cattle were obtained at a commercial harvest facility and tested for EHEC-7 by a culture-based method and the polymerase chain reaction/mass spectrometry–based NeoSEEK™ STEC Detection and Identification test (NS). Prevalence data were analyzed with generalized linear mixed models. The cumulative prevalence of EHEC-7 in hide samples as detected by NS was 80.7%, with a distribution of 49.9%, O145; 37.1%, O45; 12.5%, O103; 11.0%, O157; 2.2%, O111; 2.0%, O121; and 0.2%, O26. In contrast, the cumulative prevalence of EHEC-7 in hide samples by culture was 1.2%, with a distribution of 0.6%, O157; 0.4%, O26; 0.2%, O145; and 0%, O45, O103, O111, and O121. The cumulative prevalence of EHEC-7 on matched pre-intervention carcasses as detected by NS was 6.0%, with a distribution of 2.8%, O157; 1.6%, O145; 1.2%, O103; 1.1%, O45; 0.2%, O26; and 0.0%, O111 and O121. Although the culture-based method detected fewer positive hide samples than NS, it detected EHEC in five hide samples that tested negative for the respective organism by NS. McNemar’s chi-square tests indicated significant (*p*<0.05) disagreement between methods. All EHEC-7 isolates recovered from hides were seropathotype A or B, with compatible virulence gene content. This study indicates that “top 6” and O157:H7 EHEC are present on hides, and to a lesser extent, pre-intervention carcasses of feedlot cattle at harvest. However, continued improvement in non-O157 detection methods is needed for accurate estimation of prevalence, given the discordant results across protocols.


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