

Characterization of Shiga Toxin Escherichia coli Recovered from a Beef Processing Facility within Southern Ontario and Comparative Performance of Molecular Diagnostic Platforms

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Abstract : There has been an increased incidence of non-O157 Shiga Toxin Escherichia coli (STEC) with six serotypes (Top 6) being implicated in causing haemolytic uremic syndrome (HUS). Beef has been suggested to be a significant vehicle for non-O157 STEC although conclusive evidence has yet to be obtained. The following aimed to determine the prevalence of the Top 6 non-O157 STEC in beef processing using three different diagnostic platforms then characterize the recovered isolates. Hide, carcass and environmental swab samples (n = 60) were collected from a beef processing facility over a 12 month period. Enriched samples were screened using Biocontrol GDS, BAX or PALLgene molecular diagnostic tests. Presumptive non-O157 STEC positive samples were confirmed using conventional PCR and serology. STEC was detected by GDS (55% positive), BAX (85% positive), and PALLgene (93%). However, during confirmation testing only 8 of the 60 samples (13%) were found to harbour STEC. Interestingly, the presence of virulence factors in the recovered isolates was unstable and readily lost during subsequent sub-culturing. There is a low prevalence of Top 6 non-O157 STEC associated with beef although other serotypes are encountered. Yet, the instability of the virulence factors in recovered strains would question their clinical relevance.

Keywords : beef, food microbiology, shiga toxin, STEC

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