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Molecular epidemiology: a tool for source attribution investigation of *Escherichia coli* O157:H7 infections in New Zealand

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Since the first case of *Escherichia coli* O157:H7 was detected in New Zealand (NZ) in 1993, the number of Shiga toxin-producing *E. coli* (STEC) notifications per year has increased steadily. Cattle are considered as a source of infection for both environmental and foodborne outbreaks of STEC in humans. As part of a source attribution investigation, *E. coli* O157:H7 isolates were obtained from the national Enteric Reference Laboratory and compared to bovine *E. coli* O157:H7 isolates from faecal samples collected from very young calves and adult cattle at four slaughter plants. A total of 28 bovine and 209 human isolates, originating from the North and South Islands of NZ, were screened for the presence of virulence genes characteristic of STEC, and genotyped using pulsed-field gel electrophoresis (PFGE), stx-encoding bacteriophage insertion (SBI) and single nucleotide polymorphisms (SNP) typing. The genotypic analysis of bovine isolates revealed three distinct PFGE profiles, each represented by a specific SBI type (1, 3, and 5). A distinct between-Island prevalence distribution of SBI types was observed among bovine and human isolates (P=0.001). SBI type 5 (SNP IVa) accounted for 21% of the studied human isolates. Internationally, this genotype has been reported only rarely in association with STEC infections in humans and is therefore of particular interest. Findings of this molecular study provide evidence for historical introduction of O157 strains into NZ and localised transmission between cattle and humans. A prospective case-control study is underway currently to investigate source attribution risks and possible exposure pathways for human cases of STEC in NZ.