

Whole genome molecular epidemiology of E.coli O157 isolates from humans, food and the environment

Maes o ddiddordeb ymchwil: [Foodborne pathogens](#)

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Background

Verocytotoxin-producing *Escherichia coli* O157 (VTEC) is a gastrointestinal zoonotic pathogen of public health importance in the UK and worldwide. Although the disease is relatively rare, Scotland has one of the highest reported incidences in Europe (4.8 cases per 100,000 in 2011). VETC is a major cause of haemorrhagic colitis and haemolytic uraemic syndrome in humans. The current understanding of *E.coli* O157 evolution and epidemiology is limited. Therefore this project was commissioned to examine geographical distribution, host specificity, distribution in food chain, strain phylogeny and disease severity.

Typing of VTEC has traditionally been carried out by phage typing and pulsed field gel electrophoresis. The developments in next generation sequencing (NGS) have now made it possible to readily sequence isolates at a reasonable cost. The availability of whole genome information enables a number of methods to be applied that can be used to characterise the particular isolate and to determine the genetic relatedness of isolates. These include single nucleotide polymorphism (SNP) analysis, pathotyping and multi-locus variable number tandem repeats (MLVA).

Research Approach

This project is a pilot which has used genome sequence on a selection of isolates primarily from the Grampian Region of Scotland. In total, 148 isolates were whole genome sequenced using an Illumina HiSeq sequencer. Shigatoxin typing was performed by in silico (computer-based) Polymerase Chain Reaction (PCR) and phylogenetic analysis (analysis of the evolution of genetic structure over time) was based on core genome single nucleotide polymorphisms. This pilot has shown the potential of whole genome sequencing to advance our knowledge base on the types of *E.coli* O157 strains circulating in the environment in Scotland and how these relate to the strains which are transmitted through the food chain and those which lead to illness in humans.

Results

The results from this pilot study can only be viewed as preliminary due to the time-frame and sample size of the project. However there were interesting findings that resulted from this small project. The main findings were that VTEC isolates from clinical, cattle and sheep appear to be distributed throughout the phylogeny of *E. coli* O157. This suggests that VTEC is circulating between both cattle and sheep, both of which are potential reservoirs of infection in humans. Another project outcome showed that PT21/28 carries the shigatoxin 2a which is reported to

cause the very severe disease cases.

The association between shigatoxin genes and phage types indicates that these isolates have a different evolutionary history compared with other toxin types. The pilot study has also shown that the sequenced Scottish VTEC isolates cluster across a global phylogeny indicating that VTEC diversity is spread worldwide. The results from this research will be used to plan future research opportunities to help increase our understanding about this organism using WGS. These should help to inform intervention strategies.

Research report

England, Northern Ireland and Wales

PDF

[Gweld Research report: Whole genome molecular epidemiology of E.coli O157 isolates from humans, food and the environment as PDF\(Open in a new window\)](#) (581.47 KB)