



Infection (news) report

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National outbreak of verocytotoxin-producing *E. coli* O157 phage type 34

On 21 June 2016, the South West PHE Centre observed higher than expected notifications of *E. coli* O157 cases from front line laboratories. An outbreak control team (OCT) was convened on 22 June to investigate this increase and, on the 24 June, the first samples associated with this increase were confirmed as VTEC serogroup O157 phage type 34, positive for the *eae* (intimin) and verocytotoxin 2 genes but negative for the verocytotoxin 1 gene (hereafter referred to as 'the outbreak strain').

On 27 June a significant increase in the outbreak strain was observed nationally, and the incident was declared and managed as a national outbreak.

Analysis of whole genome sequencing data has identified that isolates fall within a 5-SNP (single nucleotide polymorphism) cluster. This strain is not related to strains currently circulating amongst the UK bovine reservoir. The outbreak strain is most closely related (> 70 SNPs) to sequences identified in people reporting recent travel to the Mediterranean region. This suggests that the strain is likely to be imported.

A total of 158 cases have been identified as of 14 July, of which 105 meet the confirmed case definition and 53 the probable case definition*. Onset dates for primary cases range from 31 May 2016 to 5 July 2016. Cases have been identified in England (144), Wales (six) and Scotland (one). Reports of secondary transmission in households are infrequent. Cases are predominately female (119/158). Fifteen cases are under 18 years old and ages range from one to 98 years.

Sixty two cases are known to have sought tertiary care at some point during their illness (57 in England, four in Wales and one in Scotland). As of 14 July four patients remain in hospital. Features of haemolytic uraemic syndrome (HUS) have been reported in seven cases. Two cases have died, both of whom have *E. coli* infection listed as a causative factor.

The outbreak is characterised by multiple small clusters linked to catering and residential care premises with particular foci in the South West, South East and North West of England (see map).

Multiple analytical studies have provided evidence that consumption of mixed salad leaves, particularly from catering establishments such as cafes and restaurants, is associated with infection. Traceability information provided by local investigators and the Food Standards Agency is being used to identify the source of the outbreak. Sampling and microbiological examination of salad products is continuing although all results to date have been negative for VTEC O157.

As an additional precautionary measure, control measures have been implemented by a small number of wholesalers to cease adding some imported leaves to their mixed salad products pending further investigations. The outbreak has been reported internationally under the WHO International Health Regulations and the European Early Warning and Response System, as well as to the European Centre for Disease Prevention and Control (ECDC) epidemic intelligence system (EPIS). Similar increases have not been reported from other European member states indicating that the outbreak is restricted to the UK at present.

*Case definitions

Confirmed case: A case resident in UK or the Channel Islands with a reference laboratory confirmed infection of VTEC O157 with the 5 SNP cluster address 5.156.1329.2502.2965.3081.%.

Probable case: A case resident in the UK or the Channel Islands with an onset or specimen date from 31 May 2016 with a reference laboratory confirmed infection of VTEC O157 phage type 34 that is VT2 positive, VT1 negative and eae positive, and for which whole genome sequencing results are pending, OR a case who is epidemiologically linked to a confirmed case with serological evidence of *E. coli* O157.

Secondary case: A confirmed or probable case with onset two or more days after another confirmed or probable case that is a household contact, if the exposure likely occurred outside the place of residence.

Map of confirmed and probable cases by WGS 5-SNP cluster

