ACM/1232

ADVISORY COMMITTEE ON THE MICROBIOLOGICAL SAFETY OF FOOD

DISCUSSION PAPER

Shiga toxin producing *Escherichia coli* associated with food in England; surveillance, trends in outbreaks, recent developments and use of WGS.

1. Background

Shiga toxin-producing *Escherichia coli* (STEC) are a group of bacteria associated with human disease and are defined by the presence of one or both phage encoded Shiga toxin genes; *stx*1 and *stx*2. Compared to other bacterial pathogens, it is a relatively rare infection but is of public health concern due its potential to cause severe disease (3).

Healthy cattle are the main reservoir of STEC although they are also carried by sheep and other animals. The infectious dose for human infection has been estimated to be <100 bacteria. Transmission to humans occurs through either consumption of contaminated food or water, or exposure to a contaminated environment involving direct or indirect contact with animals or their faeces. The low infectious dose of STEC means that once in the population person-to-person spread is common (3).

STEC cause both sporadic and epidemic infections. While small outbreaks due to person-to-person spread are reported in closed settings, particularly childcare facilities, large outbreaks are often associated with foodborne transmission, and contact with ruminants, such as in open farms (3).

The O157 STEC serogroup is most commonly associated with human disease in the UK. The majority of STEC O157 do not ferment sorbitol and frontline diagnostic laboratories in England use standard methods, to exploit this characteristic to preferentially detect STEC O157 from other faecal E. coli (3).

Despite interventions to control and reduce transmission, incidence in England has remained fairly constant with annual variation introduced by outbreak activity (1).

2. Surveillance developments

The National Enhanced STEC Surveillance System (NESSy) was introduced in England in 2009. This system collects standardised microbiological, demographic, clinical and exposure

data that are then collated with reference microbiology results. These data are used to improve outbreak detection and elucidate the epidemiology of STEC in England.

As a complement to traditional phenotypic typing methods, multi locus variable number tandem repeat analysis (MLVA) and whole genome sequencing (WGS) have been used for routine surveillance and cluster detection since 2012 and 2015 respectively (5,7). Whole genome sequencing has also provided insight into the emergence and persistence of STEC in ruminants and humans (7).

Because there are no simple, generally applicable culture based tests for the detection of STEC other than serogroup O157 (non-O157 STEC) in faecal specimens, the true number of infections caused by these strains is unknown. However, an increasing number of laboratories are using PCR based diagnostic methods designed to detect all STEC resulting in an increasing library of fully characterised non-O157 isolates (3, 4).

3. Epidemiology and risk factors

Incidence is highest in children aged 1-4 years (7·63/100 000 person-years) and incidence is higher amongst females than males [rate ratio (RR) 1·24, $P < 0·001$]. The majority of cases reported to national surveillance are white British and incidence is higher amongst this group than non-white ethnic groups. Progression to haemolytic uraemic syndrome (HUS) is more frequent in females and children (3).

The epidemiology based on phage type has altered considerably since 1983. Phage type (PT) 2 decreased to account for just 3% of cases by 2012, whereas PT8 and PT21/28 strains concurrently emerged, constituting almost two thirds of cases by 2012 (1).

Although the virulence and pathogenicity factors of STEC of serogroups other than O157 are less well understood, these strains are associated with higher hospitalisation and HUS rates than O157 STEC strains. The most common non-O157 serogroup in England is O26 (3, 4).

In STEC O157 cases, phage type (PT) 21/28, predominantly indigenously acquired, was also associated with more severe disease than other PTs, as were strains encoding stx2 genes (3).

There are marked geographical differences in incidence with the highest rates in the North and South West of England (3). These areas map closely to ruminant animal populations.

Incidence of STEC is over four times higher in people residing in rural areas than urban areas and exposure to livestock and/or their faeces was reported twice as often in cases living in rural areas than urban areas. Recreational water contact and consumption of water form a private water supply is also reported more frequently by cases living in rural areas (3).

Significant risk factors for the development of HUS are being aged 1-4 years, female gender, being infected with phage type (PT) 21/28 or PT 2, receiving β-lactam antibiotics and presenting with vomiting or bloody diarrhoea. The predicted percentage chance of developing HUS varied from under 1% to 50% if all risk factors were present (11).

Most isolates of STEC O157 and STEC O26 are fully susceptible to antimicrobial agents. Of those that exhibit resistance, the most common resistance profile was ampicillin, streptomycin, trimethoprim/sulphonamide and tetracycline occurring in 25 (5.8%) isolates. Resistance to other antimicrobials, including resistance to chloramphenicol (2.1%), resistance to azithromycin (0.2%) and reduced susceptibility to ciprofloxacin (2.6%), was less frequent. Isolates that were resistant to ampicillin, streptomycin, sulphonamide, tetracycline and azithromycin and had reduced susceptibility to ciprofloxacin were associated with cases who reported recent travel abroad (9).

4. Outbreaks

Between 1983 and 2012, a total of 335 outbreaks were reported. These outbreaks constituted 3,107 (17.4%) cases (median 5 cases, range 2–257 cases) and ranged in frequency from 0 to 25 outbreaks annually (1).

The principle mode of transmission has changed since 1983: foodborne transmission, particularly associated with meat and dairy products has declined as have outbreaks attributed to person to person spread, particularly in institutional settings such as prisons, care homes and hospitals. Outbreaks attributed to direct or indirect animal contact, particularly those linked to petting farms have increased in frequency (1).

Notable foodborne outbreaks in the last five years are the largest STEC O157 outbreak recorded in England and Wales associated with exposure to raw vegetables (12), two outbreaks associated with the consumption of watercress (11), the first outbreak associated with raw drinking milk in over a decade (2) and a large national outbreak of STEC O157 PT 34 associated with mixed salad leaves distributed through the wholesale catering market.

6. Presence in food samples

STEC O157 is infrequently detected from routine food samples or those taken as part of coordinated food studies. Recent outbreak investigations have detected STEC O157 in watercress (10) and unpasteurised cows' milk (PCR +ve, culture-ve) (2). Isolates that match human cases are occasionally referred to PHE Reference laboratories by private companies and these are followed up in collaboration with the Food Standards Agency.

Prepared by Richard Elson on the 10th October 2016

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