Prevalence of faecal shedding of verocytotoxigenic *Escherichia coli* serogroups O26, O103, O111 and O145 on Scottish cattle farms.

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Summary

This study examines the shedding of *Escherichia coli* serogroups O26, O103, O111 and O145 in Scottish adult beef cattle. The farm level prevalence of serogroup O26 and O103 shedding was comparable to rates associated with *E. coli* O157. Only among serogroup O26 was there a significant number of isolates carrying virulence factors consistent with strains that cause human disease.

Introduction

Verocytotoxigenic *Escherichia coli* (VTEC) O157 is a well recognised human pathogen. There is increasing recognition of the association of other VTEC serogroups with diarrhoea, haemorrhagic colitis and haemolytic uraemic syndrome in humans[3]. Cattle are known to carry many of these VTEC serogroups but the prevalence of carriage in UK cattle is unknown.

Objectives

This paper presents interim results of a study to estimate the prevalence of shedding for VTEC serogroups O26, O103, O111 and O145 in beef cattle closest to sale or slaughter on Scottish cattle farms during the period 2002–2003.

Materials and Methods

Beef cattle closest to sale or slaughter (target group) from a probability sample of 257 farms, stratified by season and six animal health divisions, were screened for *E. coli* serogroups O26, O103, O111 and O145 by examining faecal pats. The number of faecal pats to be sampled on each farm was determined by the number of cattle in the target group. A predetermined sampling plan ensured an 80% probability of sampling at least one positive faecal pat if shedding was occurring in the sample group.

Faecal pats were tested using immunomagnetic separation (IMS) and slide agglutination to give provisional identification. Isolates positive by slide agglutination were further tested by tube agglutination to increase screening specificity, and the serotype of all provisional isolates is to be confirmed by the Laboratory of Enteric

Pathogens (LEP), Colindale. Isolates have been characterised by molecular typing to determine the presence of genes encoding verocytotoxins and intimin.

Results

So far, 4,607 faecal pat samples from 257 farms have been tested. Provisional results following slide agglutination indicate that the farm level prevalence of shedding is 27.6% for serogroup O26, 34.2% for serogroup O103 and 15.2% for serogroup O145. No *E. coli* O111 have been detected to date. The mean within farm prevalence of shedding was 4.6% (range 0.0–100%) for serogroup O26, 5.0% (range 0.0–100%) for serogroup O103, and 1.5% (range 0.0–44.4%) for serogroup O145.

The occurrence of verocytotoxins and intimin in provisional isolates is shown in Table 1. Over half the provisional serogroup O26 isolates (57.4%) and serogroup O145 isolates (61.5%) carried intimin genes. In contrast, only 26% of serogroup O103 isolates possessed intimin genes. Among serogroup O26 isolates, 41.1% carried VT1 genes and of these 6.4% carried VT2 genes. Carriage of both VT1 and VT2 genes was rare in serogroups O103 (2.2%) and O145 (3.1%).

Table 1. *Provisional isolates carrying intimin and verocytotoxin genes (percent).*

Serogroup	Intimin	Verocytotxin			
		VT –ve	VT1	VT2	VT1+VT2
O26	+	26.2	25.7	0.0	5.4
(n = 202)	–	32.7	8.9	0.0	1.0
O103	+	26.0	0.0	0.0	0.0
(n = 181)	–	71.8	0.6	0.0	1.7
O145	+	58.5	1.5	1.5	0.0
(n = 65)	–	38.5	0.0	0.0	0.0

Discussion

E. coli O26 and O103 were the most frequently isolated serogroups and the number of herds in which these serogroups were shed by cattle closest to sale or slaughter is comparable to levels seen with *E. coli* O157[1]. The absence of *E. coli* O111 shedding is striking given that it has frequently been reported to occur in cattle faeces[2].

In strains of *E. coli* O26 associated with diarrhoea and HUS in humans, it is usual to find genes encoding VT1 and intimin[4]. The pattern of virulence factors carried by bovine strains detected in this study is therefore consistent with strains pathogenic to

humans. Carriage of genes encoding intimin was not uncommon in serogroups O103 and O145, but unlike serogroup O26, the carriage of VT genes was rare.

References

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Acknowledgements

This study was funded by Food Standards Agency Scotland, and the International Partnership Research Award in Veterinary Epidemiology (IPRAVE), *Epidemiology and Evolution of Enterobacteriaceae Infections in Humans and Domestic Animals*, funded by the Wellcome Trust. The Scottish Agricultural College receives financial support from Scottish Executive Environment and Rural Affairs Department (SEERAD).