

Faecal shedding of *Escherichia coli* O157 on Scottish cattle farms: 1998–2003

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Summary

Two surveys, four years apart, were conducted to determine the prevalence of shedding and virulence factors of *E. coli* O157 in Scottish cattle closest to sale or slaughter. The prevalence of farm level shedding decreased from 22.6% to 19.1%, between the two surveys. Carriage of genes encoding VT1 doubled but carriage of genes encoding VT2 and intimin remained the same. The dominant phage type shed by cattle was 21/28 in both surveys. Farms with cattle shedding *E. coli* O157 during the first survey were more likely to have shedding cattle during the second survey.

Introduction

Escherichia coli O157 is an important human pathogen, causing clinical symptoms ranging from diarrhoea to haemorrhagic colitis, and haemolytic uraemic syndrome—which may be fatal¹. Scotland has one of the highest prevalence rates of *E. coli* O157 related disease in the world⁴, and cattle are regarded as a major reservoir of this organism².

Objectives

This study investigates the prevalence of shedding and virulence factors of *E. coli* O157 in Scottish cattle closest to sale or slaughter. It examines temporal changes in the prevalence of shedding and virulence factors of *E. coli* O157 by comparing results from the current survey with those from the survey conducted four years previously.

Materials and Methods

A survey of *E. coli* O157 shedding by store and finishing cattle (target group) using a stratified random sample of 952 Scottish beef farms was conducted in 1998–2000. In this survey, sufficient faecal pats were sampled from each target group to give an 80% probability of detecting at least one positive pat if shedding occurred within the group. One gram of faeces from each pat sample was tested for *E. coli* O157 by

immunomagnetic separation and latex slide agglutination. Isolates were phage typed and tested for genes encoding verocytotoxins and intimin.

A second survey began in 2002: 450 of the 952 farms examined in the first survey are to be sampled again with a 90% probability of detecting at least one positive faecal pat if shedding is occurring within the target group. For comparative purposes, results from the second survey were entered into a simulation model to determine what results would have been obtained with the sampling plan used in the first survey.

Results

A total of 361 farms sampled in the first survey have also been sampled in the second survey. So far, the proportion of farms in the second survey on which shedding has been detected is 19.1%—a decrease from 22.6% of the same farms in the first survey (paired exact test: $P=0.093$). At farm level, the mean proportion of pats in which *E. coli* O157 has been detected in the second survey is 4.1% (range 0–100%).

Farms with shedding present in the first survey have been more likely to have shedding present in the second survey (RR=1.36; 95%cl 0.86, 2.14). However, this difference is not statistically significant (Fisher exact test: $P=0.21$).

Ten phage types were detected in both the first and second survey. Among isolates from the second survey, the most common phage types were 21/28 (54%), 32 (19.9%), 2 (11.8%) and 8 (9.5%). Type 21/28 (58.7%) was the most common among isolates from the first survey, followed by 2 (14.7%), 32 (11.8%) and 4 (6.0%).

In the first survey, carriage of genes encoding VT1 was uncommon (5.1% isolates), carriage of genes for VT2 was almost universal (99.8% isolates), and all isolates carried genes encoding intimin. In the second survey, carriage of genes encoding VT1 increased to 10.8% but the proportion of isolates carrying genes encoding VT2 (98.1%) and intimin (100%) were similar.

Discussion

Results so far in the second survey suggest that there has been a moderate (15%) relative decrease in the prevalence of *E. coli* O157 shedding among cattle closest to sale or slaughter on Scottish cattle farms over the last four years. Almost all *E. coli* O157 isolates continue to carry genes encoding VT2 and intimin which is consistent with strains that cause human disease¹. The carriage of genes encoding VT1 has doubled over the last four years.

Phage type 21/28 continues to be the dominant phage type shed by cattle, accounting for over half the isolates detected. Type 21/28 is the phage type most commonly associated with human *E. coli* O157 infection in Scotland⁴. Shedding of phage type 32 has become more common while type 2 less so. Although 8 other phage types were isolated, shedding of these types by Scottish cattle is rare.

Farms with cattle shedding *E. coli* O157 in the first survey were more likely to have shedding cattle at the time of the second survey but statistical confidence in this association is currently low. Statistical power will increase as the second survey progresses. Recent work shows that the detection of *E. coli* in pats is sensitive to the number of 1g samples tested from each pat and that testing just 1 x 1g sample may result in substantial loss of sensitivity³. It is possible, therefore, that the presence of shedding may be a much better predictor of subsequent *E. coli* shedding status than our results currently suggest.

References

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