

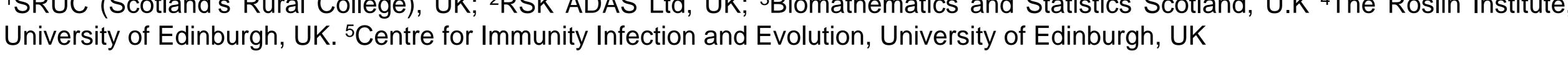
The prevalence of verocytotoxigenic E. coli O157 Food Standards Agency (VTEC O157) in British cattle populations*

SRUC

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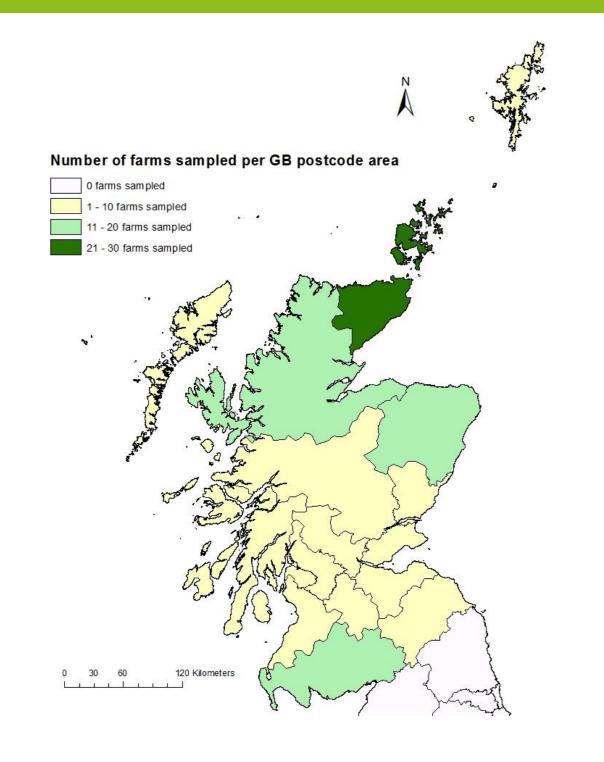
Gunn, G.J. et al. 2007 Vet. Journal 174 (3) 554-564 Pearce et al. 2009 BMC Microbiology http://www.biomedcentral.com/1471-2180/9/276

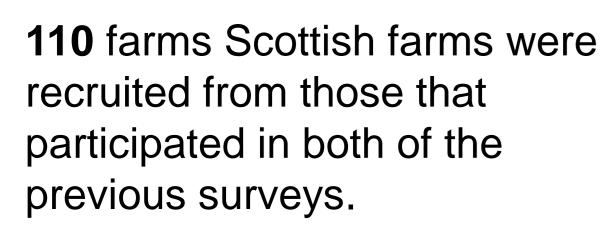


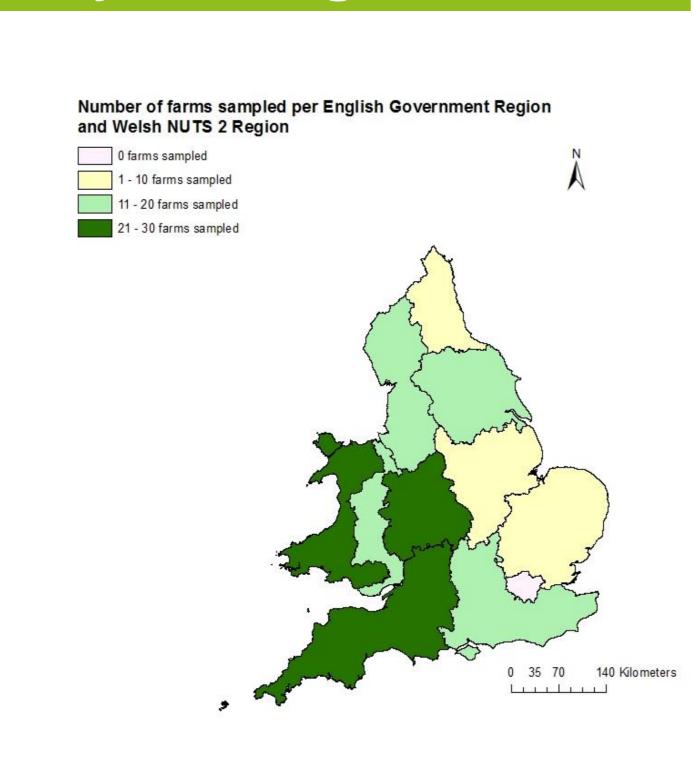
Cattle are a recognised reservoir for human clinical VTEC O157 infection. In previous Scottish surveys approximately one in five herds were affected.

The British *E. coli* O157 in Cattle Study (BECS)* aimed to establish the current baseline prevalence in cattle destined for slaughter in Scotland and in England & Wales in 2014/2015

Materials and Methods Two cross sectional surveys during 2014/2015







160 farms from England & Wales were recruited via a randomised survey that replicated the 1998/2000 Scottish survey

All farms were recruited, visited, sampled and completed a questionnaire between September 2014 & November 2015

- The E. coli O157 status of 1g of each faecal pat was determined using an enrichment – IMS – culture method.
- Isolate serogroup was confirmed by PCR. One *E. coli* O157 isolate per positive pat was tested for Vero toxins 1 and 2.
- Pat *E. coli* O157 counts were also enumerated, by limiting dilution on CT-SMAC agar plates.

Herd and pat level prevalence were calculated using generalised linear mixed models.

Acknowledgements and further information

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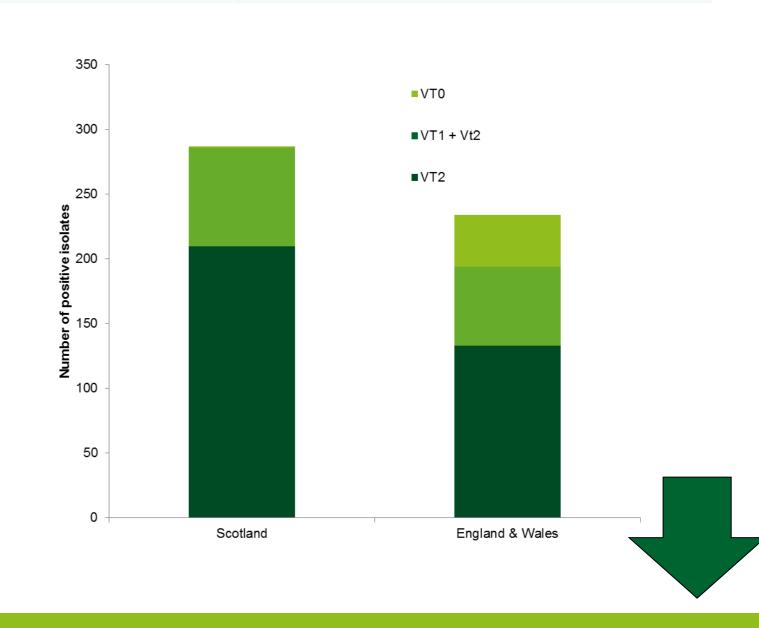
*British E.coli O157 in cattle study (BECS): to determine the prevalence of Escherichia coli O157 in herds with cattle destined for the food chain. Henry et al. Epidemiology and Infection (accepted 02/08/2017)

Results



Prevalence estimates for E. coli O157 did not differ significantly between the two BECS surveys.

The majority of isolates were verocytotoxin positive.



Outcome and next steps

- E. coli O157 continues to be common in British beef cattle herds.
- Contact with cattle and their environments therefore continues to be a potential source of infection for humans.
- Isolates were phage-typed and a subset was whole genome sequenced.
- analyses Future will include: current strain composition; comparisons with contemporaneous human clinical cases plus comparison with previous Scottish surveys.

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