

Human pathogenic potential of Shiga-toxin producing *E.coli* (STEC) isolated from wild Scottish deer

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1. INTRODUCTION

- Shiga toxin producing *E. coli* (STEC) are important foodborne zoonotic pathogens.
- Cattle are thought to be the main source of human STEC infections; however, a 2015 outbreak of STEC O157 in Scotland was linked to consumption of venison from wild deer.
- The presence of the Shiga toxin subtype Stx2a and the *eae* virulence gene are associated with more severe forms of human disease.

Study aims:

- Estimate the prevalence of STEC O157 in Scottish wild deer
- Determine risk factors for presence of *stx2a* within deer faeces
- Characterise O157 and non-O157 STEC isolated from Scottish wild deer by whole genome sequencing (WGS)

2. METHODS

- From July 2017 - June 2018 1087 faecal samples collected from wild deer culled for food were analysed for STEC O157 by immunomagnetic separation
- Samples were analysed by PCR for presence of *stx* genes to determine presence of non-O157 STEC
- Modelling was carried out to determine risk factors for presence of *stx2a* in samples
- Three O157 STEC strains and 72 non-O157 STEC strains were isolated and analysed by WGS
- Non-O157 STEC deer strains were compared to Scottish human clinical strains using WGS

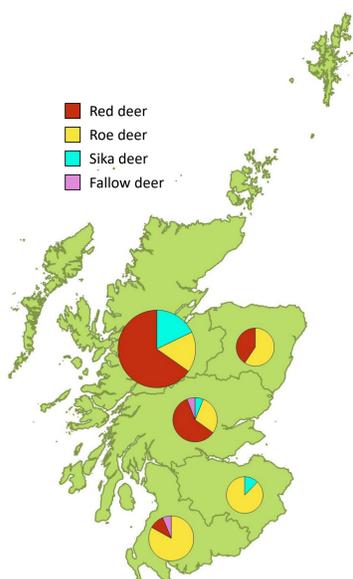


Figure 1. sampling locations and deer species sampled (n=1087)

Funding: Food Standards Scotland and The Scottish Government (CRF: MRI/104/17)

3. RESULTS

- STEC O157 was present in 3/1087 samples, giving an overall prevalence of 0.34% (95% CI = 0.02–6.30)
- The three STEC O157 isolates were present in high numbers ($>10^4$ CFU/g faeces) and contained both *stx2a* and *eae* genes (Table 1). Two isolates were of a phage type (PT21/28) commonly associated with more severe human infections.

Table 1: Characteristics of STEC O157 strains isolated from wild Scottish deer

Isolate	Deer species	Serotype	Virulence genes	Bacterial counts (cfu/g faeces)	Phage type
1	Red	O157:H7	<i>stx2a, stx2c, eae</i>	$>10^4$	21/28
2	Sika	O157:H7	<i>stx2a, eae</i>	$>10^4$	8
3	Red	O157:H7	<i>stx2a, eae</i>	$>10^4$	21/28

- 69.5% of samples were *stx+* (of which 12% were *stx2a+*), indicating presence of non-O157 STEC
- Risk factors for carriage of *stx2a* included samples from roe deer (OR = 7.8), increased sheep density (OR = 1.3), sampling from the South of Scotland (OR = 5.5), increased semi-natural grassland (OR = 1.02) and increased number of rain days in the month of sampling (OR = 1.08).
- A total of 72 non-O157 STEC deer isolates were characterised by WGS. Most isolates were *stx2b+* (Fig. 2) and all were *eae-*.
- Of deer isolates 11/20 had the same serotype and shiga toxin profile as Scottish human clinical isolates however the three most common human clinical serotypes (O26:H11, O103:H2 and O145:H28) were not present in deer.

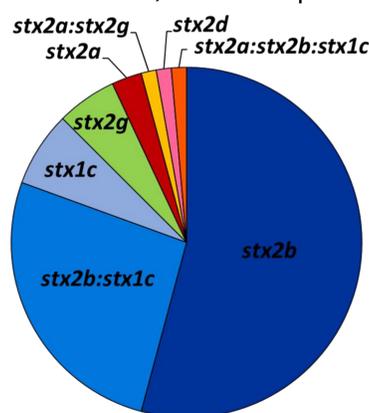


Figure 2. Shiga toxin gene profiles of deer non-O157 STEC isolates determined by whole genome sequencing (n=72)

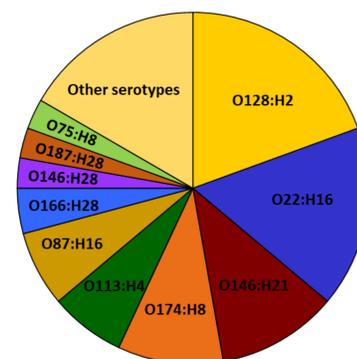


Figure 3. Serotypes of deer non-O157 STEC isolates determined by whole genome sequencing (n=72)

4. DISCUSSION POINTS

- All the STEC O157 strains isolated carried the virulence genes *stx2a* and *eae* which are associated with more severe clinical outcomes, suggesting that although STEC O157 prevalence is low in wild Scottish deer, they can carry STEC O157 strains with high human pathogenic potential.
- The majority of non-O157 STEC strains had Shiga toxin subtypes of low pathogenicity and none were positive for *eae*, suggesting they are less likely to cause severe human disease.
- Based on whole genome sequence data comparison of deer and human non-O157 STEC strains, deer are not a major source of Scottish human clinical cases of non-O157 STEC infection.
- Model outputs suggest possible environmental and livestock associations with presence of the highly pathogenic *stx2a* gene in deer faecal samples.



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