Shiga toxin-producing *Escherichia coli:* strains & sequencing to inform strategies for this Scottish scourge

SRUC-B6-1

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1. Why do we need to do this research?

Some Shiga toxin-producing *Escherichia coli* (STEC) are priority zoonotic pathogens that place a significant burden on health services.

Scotland reports more human cases per head of population than the rest of the United Kingdom and ranks third worldwide.

Research has demonstrated relationships between STEC found in Scottish cattle, wild deer, retail beef mince, and those isolated from Scottish human clinical cases.

British *E. coli* O157 in Cattle Study (BECS*)

Prevalence of STEC O157 in Wild Scottish Deer

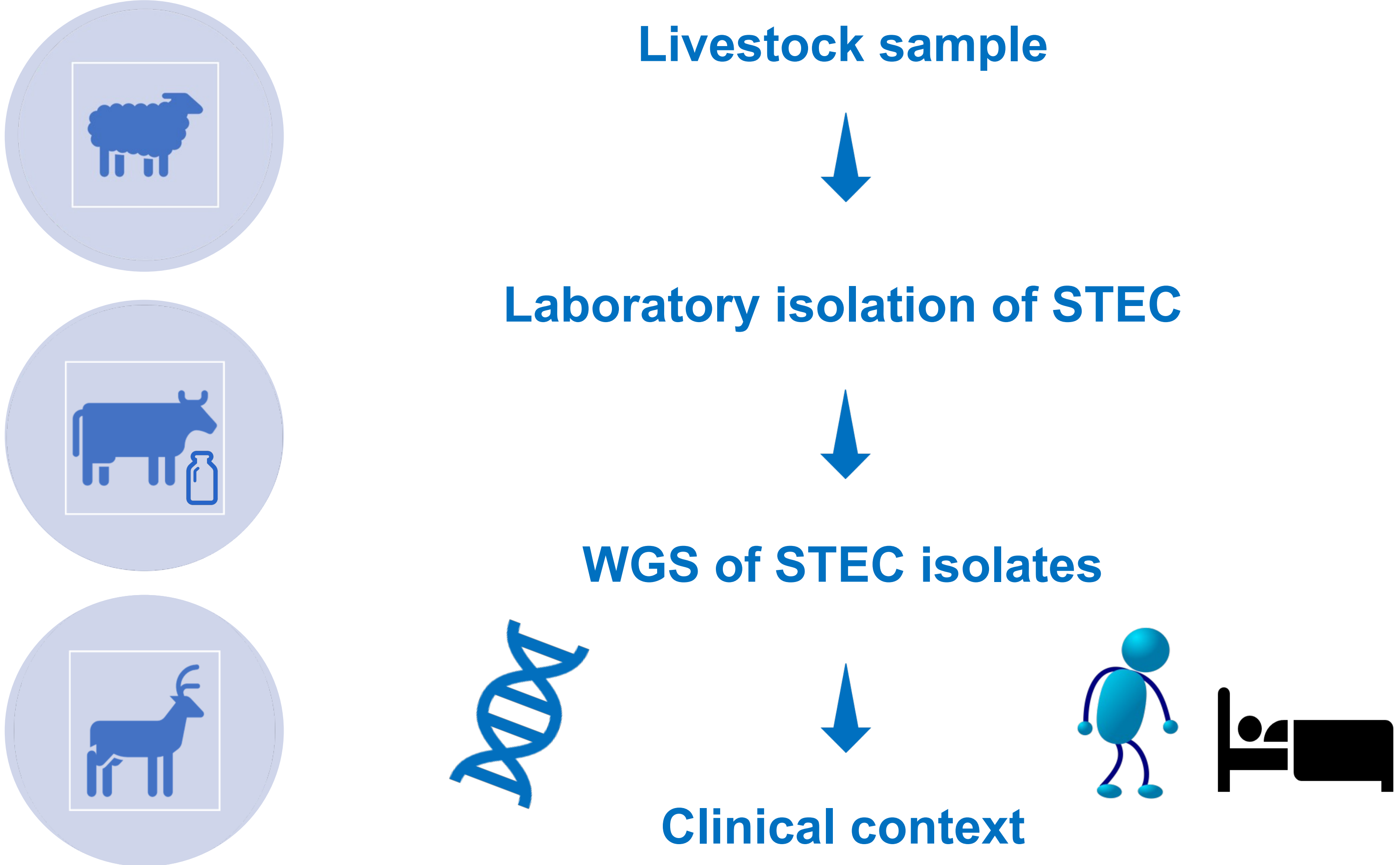
Survey of Beef Mince at retail level in Scotland

- Gaps remain in our understanding of transmission pathways
- Some STEC strains are difficult to detect, meaning we don't fully understand their role or relevance for human cases and STEC outbreaks.

If we can address these challenges, we can target intervention strategies more effectively to reduce the burden of human STEC infection in Scotland, reduce health service costs, and save lives.

2. Project Aims

Whole genome sequencing (WGS) can give detailed information about individual bacterial isolates. We have used/are using WGS to explore what types of STEC exist in different Scottish livestock and whether they are similar to STEC from human clinical cases.



Livestock sample

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Laboratory isolation of STEC

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WGS of STEC isolates

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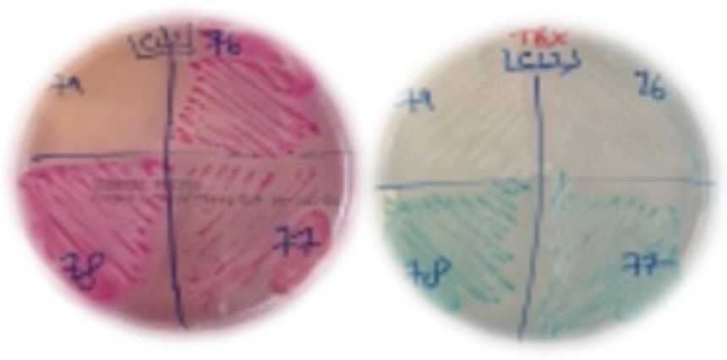
Clinical context

We are using sequence data, traditional culture methods and alternative sequencing approaches to try to improve detection and characterization of STEC.

Can bioinformatic analysis of sequence data identify STEC associated with fresh produce?



How well do different media select for STEC in a sample?

How well can a different sequencing method identify STEC in a sample?

3. Project outcomes to date

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Harnessing diverse prophages of STEC O157:H7 phage-type 8 for rapid identification of fresh produce-associated STEC strains

JYN Nale, SC Tongue, NH Holden

Centre for Epidemiology and Planetary Health (CEPH), New North Agri Cost Centre, Food Security Challenge Centre

Research output: Contribution to conference › Paper

We **can** use bioinformatic analysis of sequence data to identify STEC strains associated with fresh produce.

Potential inter-species transmission

High levels of STEC O157 in farmed Deer — Some deer STEC are **similar** to those causing human clinical disease.

Low levels of STEC O157 in Scottish sheep. — Some sheep O157 STEC found are **closely related** to eight of the human O157 STEC isolates, with one **exact match**.

Flock-specific strain circulation of non-O157 STEC — **Differ** from human non-O157 STEC cases.

STEC found; still generating sequence data.

Dairy cattle - supports policies for hygiene at slaughter and adequate pasteurisation of milk and dairy products.

Ecosystem case studies

4. Project Impact

- Communicated to **policy client** (Food Standards Scotland)
- Contribute to **Incident Management Team**
- Contribute to **SERL STEC genome database**, feeding into FSS Strategy 2021-2026
- New **collaborative relationship** with Animal and Plant Health Agency STEC team
- Input to **Advisory Committee on Dangerous Pathogens**, 2024
- **Presentation to diverse audiences**: scientific, policy, livestock sector, veterinary, environmental health practitioners – raising awareness
- Contribution to **Scottish Health Protection Network**
- **VTEC 2026 Conference**

5. Future Perspective

Sequencing data and knowledge gained will be applied to aid the development of STEC diagnostics and intervention strategies

Authors and Acknowledgements

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