Healthy heards, hidden risk: genomic antimicrobial resistance profile of commensal *E. coli* in cattle in the Great Britain

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Introduction
Beef cattle farming has a crucial role in the British agricultural economy, with a production value of £4.1 billion (1). The use of genomic as a tool for antimicrobial resistance (AMR) surveillance ensures the monitoring trends of antimicrobial resistance genes (ARG) in livestock, enabling a high-resolution characterization of how it disseminates across distinct evolutionary foodborne bacteria lineages (2). Currently, national genomic ARG monitoring baselines in target bacteria isolated from healthy cattle is missing (3).

Methods
Evolving of the Pathogen Surveillance in Agriculture, Food and Environment (PATH-SAFE) programme (4), we cultured 350 commensal *Escherichia coli* isolates from caecal contents of healthy beef cattle at slaughter across Great Britain for eight months (2023–2024), using non-selective and extended-spectrum cephalosporin (ESC) selective media. A subset of 200 commensal *E. coli* plus all ESC-resistant isolates (*97*) recovered from the 350 cultivated non-selective and ESC selective media, respectively, were whole-genome sequenced by illumina. Resistance profiles were assessed with AMRFinderPlus (5) and *E. coli* lineages were identified by sequence types (ST) assigned using MLST (6). A maximum likelihood tree was constructed from the core-genome alignment of 297 sequences parsnp and visualized with iTol. Single nucleotide polymorphisms (snp) calling was estimated by snippy, and the distance od snps calculated by snp-dist. Plasmid replicon types were identified using Plasmidfinder tool.

Preliminary results
Among all isolates, ARGs against 12 antibacterial classes with 63 distinct resistance profiles were established. Besides beta-lactams, present in 97 isolates, ARG against quinolones (*67*), tetracycline (*36*) and aminoglycosides (*31*) were most frequently found. From the 97 ESC-resistant isolates, at least one ESC gene was found in all ESC-resistant *E. coli,* showing the high concordance between phenotypic test and genotypic founds. Extended-spectrum beta lactamases (ESBL) represented 69% (67/97), all harboured a *bla*CTX-M genes, whereas 27% (26/97) were phenotypically AmpC, where point mutation C_42T was main resistance mechanism detected (20/97). Genotypically multidrug resistance was detected in 45% of ESC-resistant and in 3% of indicator *E. coli* (7/200). ST58 and ST10 accounted for 16% (*49*) and 5% (*16*) of isolates, respectively. The closest pairwise distance was 12 SNPs (*1*). IncFIA and IncFIB were the most frequently harboured plasmid replicon types.

Discussion
Genomic surveillance provides early detection of emerging ARG variants and AMR lineages, supporting effective monitoring and control strategies (7). In our dataset, ARGs were identified across multiple *E. coli* lineages, strongly indicating horizontal gene transfer mediated by mobile genetic elements (MGEs). A cluster of 35 isolates in two sister-clades, belonging to ST58 but separated by more than 12 SNPs, were identified. This level of diversity suggests that the lineage has been established and evolving within the population for a considerable period. ST58 carrying ARGs has been reported in environmental sources, food-producing animals, and humans (8). As a next step, we aim to characterise in depth the MGEs involved in the ARGs detected, supported by ongoing long-read sequencing, to better understanding targets of monitoring.

Conclusion
Genomic analysis offers powerful insights into AMR dynamics across target bacterial species, providing strong application for targeted AMR monitoring.

Keywords: Whole-genome sequencing, Genomic surveillance, Genomic insight, Livestock, extended-spectrum cephalosporin.

References:

1. DEFRA (2025). https://www.gov.uk/government/statistics/livestock-populations-in-the-unitedkingdom/livestock-populations-in-the-united-kingdom-at-1-december (Accessed 15 March 2026)
2. Tiwari et al. (2025). Life (15): 1848. https://doi.org/10.3390/life15121848
3. VMD (2024). https://vmd.blog.gov.uk/2023/11/24/vmds-path-safe-project-an-update-on-amr-surveillance (Accessed 30 March 2026)
4. Food Standards Agency (2025). FSA Research and evidence. https://doi.org/10.46756/001c.138396.
5. Feldgarden et al. (2019). Antimicrob Agents Chemother 63(11): e00483-19. https://doi.org/10.1128/AAC.00483-19. (Accessed 30 March 2025)
6. Jolley et al. (2010). BMC Bioinformatics 11: 595. https://doi.org/10.1186/1471-2105-11-595. (Accessed 19 November 2025)
7. Djordjevic et al (2024). Nat Rev Genet 25: 142–157 https://doi.org/10.1038/s41576-023-00649-y
8. Reid et al. (2022). Nat Commun. 13:683. https://doi.org/10.1038/s41467-022-28342-4