Fandards Standards Scotland

For safe food and healthy eating

PATH-SAFE FSS Scottish Pilot – ws1b

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FSS Scottish Pilot



The FSS Scottish Pilot for PATH-SAFE is a ~£570K project over 3 years (due to finish March 2024) which aims to use WGS to understand the source attribution, infection threat and AMR of *E. coli* isolated from a range of different sources in Scotland.

Why E. coli?

- Non-pathogenic (commensal) and pathogen strains (e.g., STX)
- Frequently used as an indicator species, e.g., water quality
- Can be found in several animal hosts, throughout the environment and a variety of food commodities
- Excellent model organism for understanding transmission from farm to fork.
- FSS was able to build upon existing sampling initiatives already in place, such as *E. coli* testing in water, shellfish and abattoir sampling















Samples currently analysed, curated and submitted to Enterobase Dogs (201) Deer (175) Poultry (139) Bovine (156) Sheep (160) Swine (142)

Humans (108 Urinary Track Infection – 623 Blood stream)

EnteroBase

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Detailed pipeline for genomic analyses*

*Based on A. Chalka 2022 with modifications

1. Multi Locus Sequence Type (MLST) and <u>Serotype</u> characterisation

Multi Locus Sequence Type (MLST) diversity across 1691 *E. coli* isolates analysed through *PATH-SAFE Scottish pilot project.*

> 565 MLST detected Human (132) Bovine (88) Ovine (107) Swine (75) Poultry (56) Canine (58) Deer (89)

25 out of 565 STs concentrate ~55% of the sampled isolates

Not only the diversity but also its distribution across distinct species show significant differences between them and only one common ST.

Above all, the most frequent <u>SEROTYPES</u> correspond to the most common detected MLST

<u>SEROTYPES</u> from ST10 (the only common subtype) show a significant diversity between and within *E. coli* from different host.

Only the serotypes -/H40, O107/H21, O13/H11, O16/H48 and O89/H9 were detected simultaneously in different host, whilst all other serotypes are unique by host.

Could <u>ST10</u> be a critical priority *E. coli* under a ONE HEALTH scenario?

ST10 complex strains are host-generalist *E. coli* that are frequently found as intestinal commensal inhabitants of mammals and avian species, and are devoid of the virulence-associated genes known to be required for pathogenesis.

Colistin (polymyxin E) is one of the few cationic antimicrobial peptides commercialized in both human and veterinary medicine. It has been extensively used since the 1960s in food animals, and particularly in swine with different purposes: therapeutically, prophylactically, and even for growth promotion (<u>Rhouma et al., 2016</u>).

The growing number of colistin-resistant isolates carrying *mcr*-type genes was associated with the successful expansion of international ST10

Short report Open Access Published: 09 January 2022

Recurring outbreaks by the same *Escherichia coli* ST10 clone in a broiler unit during 18 months

Anders Miki Bojesen 🖾, Umran Ahmed, Hanne Skaarup & Carmen Espinosa-Gongora

 Veterinary Research
 53, Article number: 2 (2022)
 Cite this article

 2004
 Accesses
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 Citations
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ORIGINAL RESEARCH article Front. Microbiol., 05 November 2018 Sec. Antimicrobials, Resistance and Chemotherapy Volume 9 - 2018 | https://doi.org/10.3389/tmicb.2018.02659

Swine Enteric Colibacillosis in Spain: Pathogenic Potential of *mcr-1* ST10 and ST131 *E. coli* Isolates

ENVIRONMENTAL MICROBIOLOGY

Applied Microbiology

Research Article

High diversity of pathogenic *Escherichia coli* clones carrying *mcr-1* among gulls underlines the need for strategies at the environment–livestock–human interface

Marisa Ribeiro-Almeida, Joana Mourão, Ângela Novais, Sofia Pereira, Joana Freitas-Silva, Sofia Ribeiro, Paulo Martins da Costa, Luísa Peixe, Patrícia Antunes 🔀

First published: 21 June 2022 | https://doi.org/10.1111/1462-2920.16111 | Citations: 1

E. coli ST10 diversity and distribution

Phylogeny of specific bacterial subtypes enables to dissect the distribution patterns of hosts containing the bacteria and their possible geographic or temporal trends

2. Phylogeny and evolutionary relationships

E. coli from distinct hosts show predominant phylotypes

Phylogeny of a subset of 1200 *E. coli* genomes analysed though *PATH-SAFE Scottish pilot project.*

3. antimicrobial resistant genes (AMR)

AMR

Visualization of the number AMR genes detected along with the *E. coli*

phylogeny: example of the Deer dataset

* The bars represent the number of AMR genes detected in each sample and the blue numbers below the MLST classification.

Difference in the abundance of AMR genes detected between wild and livestock host

* *E. coli* shows an important difference in the number of AMR genes detected between wild and livestock. The maximum number and average of AMR genes per sample in deer is 12 and 5 whilst in Livestock is 17 and 7 respectively.

A total of 130 AMR genes were identified in *E. coli* across different animal host.

Count number of AMR genes identified

Efflux, Beta-lactam and Fosfomycin are the most prevalent AMR gene classes

E. coli from deer show a median of five (5) AMR genes per isolate, but regions like Argyll and **Bute, Dumfries and Galloway, and Highland** show outliers with 8 to 12 AMR genes

Distribution of E. coli AMR genes by Geographic origin identified in Deer

4. Virulence genes

108 virulence genes were detected across all the *E. coli* isolates analyzed (1691). STX genes were detected in ~ 5% (83) *E. coli* from deer.

Summary

Whole Genome Sequence data has allow us to characterise the genomic diversity of *E.coli* from different sources and at different levels. This permitted us to identify:

- A large MLST diversity with a total of 565 subtypes of bacteria across the different host, including ST 131, 73, 69 and 10 which are the most frequently detected.
- A phylogeny with five major phylogroups A, B1, B2, D and E, in which B1 are more commonly represented with *E.coli* from livestock and B2 with *E. coli* from clinical human and dogs isolates.
- A total of 130 AMR genes and a significant difference in the number of AMR genes detected between wild animal, livestock and human sources which could have an impact in the food chain transference and the clinical management of the infections.
- STX genes on ~5% of the analysed isolates which were obtained from deer host.

Ongoing and future work:

E. coli present in Scotland display a wide genomic diversity across the different animal hosts. Understanding patterns, prevalence and differences within and between these bacterial groups hosted by different animals will lead us to a better understanding of its transmission and epidemiology, applying a "ONE-HEALTH" approach.

Ongoing and future work:

- Machine learning analyses to predict the host attribution of *E.coli* isolates using SNPs, AMR genes, protein variants and intergenic variants.
- Compare to *E.coli* throughout the food chain (water, food, shellfish, wastewater).
- Second and final analysis report will be carried out by December 2023 and March 2024

Potential implications of the use of *Phylogeny* + *Host attribution* + *Pathogenicity threat* data for informed decision making

THANK YOU. Gracias!

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