Clostridioides difficile in GB pigs and risks to the food chain

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1. Introduction

Clostridioides difficile infection in humans is usually associated with hospital settings. A world-wide increase in community acquired *C. difficile* infection indicates a source of *C. difficile* exposure outside of hospital settings. The bacterium's emergence in animals, farms, and food classifies as a One Health pathogen. Global prevalence in pigs has been well documented in other countries such as Australia, USA, Canada and European countries where guidance and interventions can limit contamination and transmission. However, no prevalence information is available for pig and pork production in the GB. This poster presents preliminary findings.

2. Aims

This project aims to establish a baseline prevalence of *C. difficile* in GB pig farms and abattoirs, to better understand *C. difficile* transmission in different biomes, and the risk of *C. difficile* in the food chain.

3. Objectives

3.1 Sampling of farms and abattoirs for *C. difficile*. Recruitment of 22 farms and 9 abattoirs to the study for sample collection and *C. difficile* isolation.

3.2 Analysis of *C. difficile* isolates To characterise *C. difficile* isolates by toxigenicity, antimicrobial profiling and ribotyping.

3.3 Whole Genome Sequencing. To compare human, pig and environmental isolates and determine directionality of transmission.

4. Methodology

4.1 On-farm sampling

Floor faeces from indoor farrowing crates with piglets ≤ 1 week old were collected. Straw bedding from outdoor farrowing arcs with piglets ≤ 1 week old were sampled. Soil and puddle water were collected from around pig sheds and surrounding area. *C. difficile* was isolated by enrichment and selective culture and identified by MALDI-TOF mass spectrometry (MS) (**Fig. 1**).

4.2 Abattoir sampling

Faeces and carcass swabs of slaughtered pigs from different farms were sampled. Where possible scald tank water was sampled. *C. difficile* was isolated by enrichment culture and identified my MALDI-TOF MS (**Fig. 1**)

4.3 Analysis of *C. difficile*

Isolates was characterised by multiplex polymerase chain reaction (PCR) for toxin profiling, and are currently being ribotyped. Selected ribotypes will be sequenced by whole genome sequencing (**Fig. 1**)

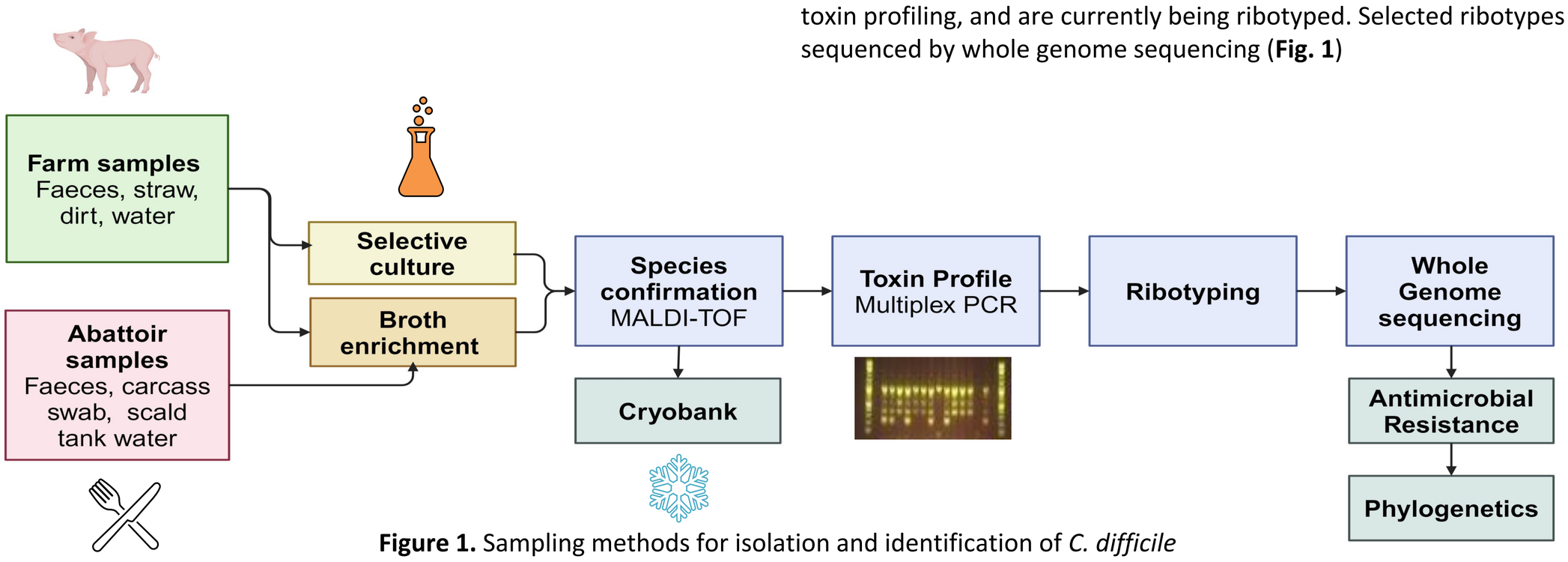

Figure 1. Sampling methods for isolation and identification of *C. difficile*

5. Results

Preliminary results are presented. *C. difficile* was isolated from all farm sample types collected so far (**Table 2**), and 38 of 40 isolates were toxigenic. *C. difficile* was also isolated from all abattoir sample types collected so far (**Table 3**), and 9 of 9 isolates were toxigenic.

Table 2. Farm samples positive for *C. difficile*

Sample	Number	Percentage
Faecal	20/40	50%
Straw	10/10	100%
Soil	6/6	100%
Water	2/13	15%

Table 3. Abattoir samples positive for *C. difficile*

Sample	Number	Percentage
Faecal	6/246	2.4%
Carcass swabs	2/248	0.8%
Scald tank water	3/17	18%

6. Discussion

- Preliminary prevalence of *C. difficile* in breeding farms with piglets ≤ 1 week old is similar to other reports (0 – 100 %) worldwide [1].
- *C. difficile* was also found in 62% of environmental samples. This is within the range of other reports worldwide (0 - 87.5%) [2]
- Preliminary prevalence of *C. difficile* in abattoirs (0 - 18%) is similar to other reports (0 - 28%) worldwide [3].
- Methodology, sample sites, and age of piglet may contribute to differences in detection.

7. Future work

- Recruit more farms for sampling and process all abattoir samples
- Antimicrobial profiling of isolates
- Whole genome sequencing
- Genomic comparisons between pig and human isolates

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References

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