**INTRODUCTION**

Clostridium difficile is an anaerobic spore-forming bacterium recognised as a major cause of nosocomial colitis and antibiotic associated diarrhea in humans, with faecal-oral route as the primary mode of transmission. In animals, C. difficile acts as both a gut colonizer and a cause of diarrhea. Over the past years, several studies have focused on the possible role of animals and food as contamination sources for human C. difficile infections in the community.

**OBJECTIVE**

The aim of this study was to isolate and compare the C. difficile strains circulating in animals, food and humans. This work summarizes the available data on C. difficile in animals and foods in Belgium and discusses the potential for foodborne transmission of this pathogen.

**MATERIALS AND METHODS**

- Faecal samples of newborn pigs and calves were collected from breeding farms.
- Intestinal contents and carcasses samples were collected from cattle and pigs at slaughter.
- Raw meat was obtained from the retail trade.
- Horse faecal samples were collected from hospitalized animals.
- Human C. difficile isolates were obtained from patients of healthcare settings
- All the isolates were characterized with respect to their antibiotic resistance
- MLVA, MLST and Whole genome sequencing analysis were used in order to investigate genetic relationships between C. difficile strains.

**RESULTS**

**Clostridium difficile in young farm animals and slaughter animals**

- **Prevalence 78.3%**
  - N = 23
  - Main PCR-ribotypes 078/002

- **Prevalence 0-1%**
  - N = 294
  - Main PCR-ribotypes 078/UCL46

**Prevalence 22.2%**

- N = 18
- Main PCR-ribotypes 078/015

**Prevalence 6.9-9.9%**

- N = 203
- Main PCR-ribotypes 078 (great variety of types)

**Prevalence 7%**

- N = 100
- Main PCR-ribotypes 081/014

**Clostridium difficile in carcasses and meat**

- **Prevalence 7.9%**
  - N = 101
  - Great variety of types

- **Prevalence 2.3%**
  - N = 133
  - PCR-ribotypes 078/014

- **Prevalence 4.7%**
  - N = 107
  - PCR-ribotypes 078/014

**CONCLUSIONS**

The prevalence of C. difficile in food animals, companion animals and meat is significant in Belgium. The major PCR-ribotypes found are 078 and 014 that are also dominant in human C. difficile infections. Phylogenetic analysis reveals that an obvious overlap exists between strains from animal, food and human origins, and highlights a potential risk of interspecies and foodborne transmission.