

# CLOSTRIDIUM DIFFICILE, A ZONOTIC AGENT

## CHARACTERIZATION AND RELATEDNESS OF *C. DIFFICILE* STRAINS ISOLATED FROM ANIMALS, FOOD AND HUMANS IN BELGIUM

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### INTRODUCTION

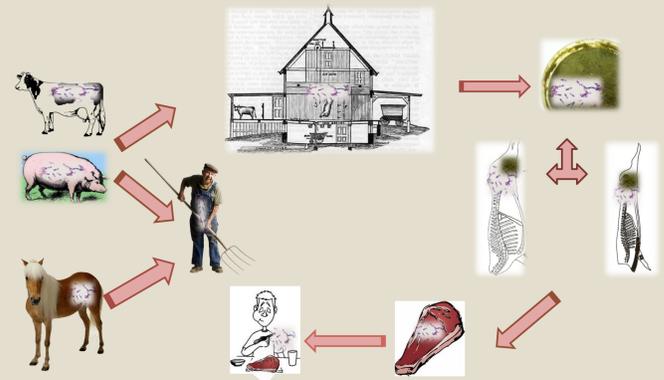
*Clostridium difficile* is an anaerobic spore-forming bacterium recognised as a major cause of nosocomial colitis and antibiotic associated diarrhea in humans, with faecal-oral route as the primary mode of transmission. In animals, *C. difficile* acts as both a gut colonizer and a cause of diarrhea. 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

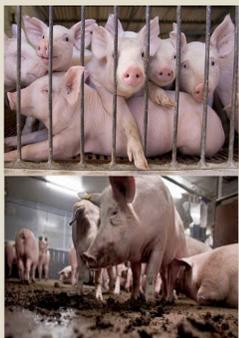
- ✓ Faecal samples of newborn pigs and calves were collected from breeding farms.
- ✓ Intestinal contents and carcasses samples were collected from cattle and pigs at slaughter.
- ✓ Raw meat was obtained from the retail trade.
- ✓ Horse faecal samples were collected from hospitalized animals.
- ✓ Human *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

##### Farm



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

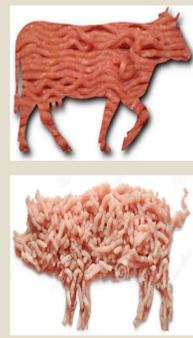
Prevalence 6.9- 9.9%  
N= 203  
Main PCR-ribotypes  
078 (great variety of types)

#### *Clostridium difficile* in carcasses and meat



Prevalence 7.9%  
N= 101  
Great variety of types

Prevalence 7%  
N= 100  
Main PCR-ribotypes  
081/014



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

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

##### Slaughterhouse

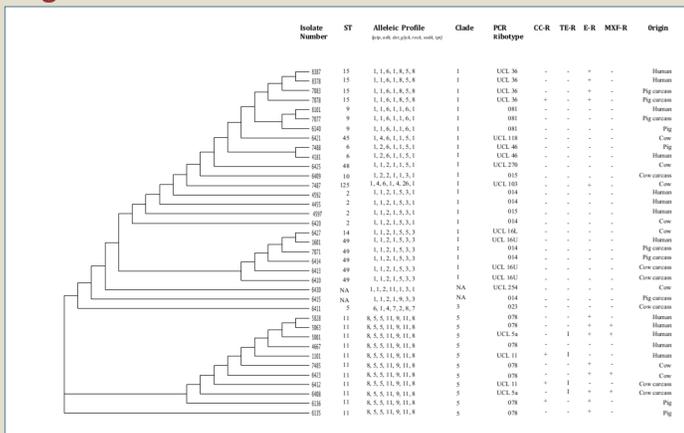


Figure 1. Neighbour-joining phylogenetic tree showing the relationships between animal (carcasses or faecal samples) and human *C. difficile* strains. ST: sequence type; MXF-R: moxifloxacin resistance; E-R: erythromycin resistance; CC-R: moxifloxacin resistance; I: intermediate antimicrobial resistance.

