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Clostridium difficile is present in retail meat in Belgium RODRIGUEZ C.*1, TAMINIAU B.1, VAN BROECK J.2, AVESANI V.2,

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INTRODUCTION

Clostridium difficile is a major cause of nosocomial acquired diarrhoea and colitis after use of antibiotics. With the recent isolation of this bacterium in healthy carrier food animals and retail meats, the possibility for foodborne transmission is a current concern.

OBJECTIVE

The objective of this study was to evaluate the presence of Clostridium difficile spores in freshly minced meat obtained from local butchers and supermarkets and to characterize the isolates.

MATERIALS AND METHODS

A total of 240 samples of minced meat (133 of beef and 107 of pork) were analyzed.

✓ Culture was carried out using an enrichment step. Ten grams of feces were inoculated into 90 ml of CCFBT and incubated anaerobically for 72h at 37 °C. Subsequently, 10μ l of the enrichment broth of each type of sample was spread onto CCFAT and incubated at 37 °C for two days.

- ✓ An identification of the isolated colonies was done by PCR detection of tpi, tcdA, tcdB and cdtA genes.
- ✓ Toxic activity was also confirmed by a fecal cytotoxininmmunoessay.
- ✓ Further characterization was performed by PCR ribotyping



RESULTS

Samples	PCR- ribotype	nº strains	Cytotoxicity assay	tcdA	tcdB	cdtA
Beef meat	BR014	2	POS	POS	POS	NEG
	BR078	1	POS	POS	POS	POS
Pork meat	BR014	2	POS	POS	POS	NEG
	BR078	1	POS	POS	POS	POS
	UCL57	1	POS	POS	POS	NEG
	UCL378	1	NEG	NEG	NEG	NEG

Table 1. PCR-ribotypes and toxin gene profiles of Clostridium difficile isolates

CONCLUSIONS

This study demonstrates the presence of Clostridium difficile in minced retail meat in Belgium. The PCR-ribotypes 014 and 078 are the predominant isolates from humans in hospitals in Belgium.

This suggests a relationship to be carefully analysed between food and human infection.

Clostridium difficile was isolated from 3,3% (8/240) of the total samples:

5 (4,7%) from minced pork meat and 3 (2,3%) from the minced beef meat. Four different PCR ribotypes were identified with predominance of PCR ribotype 078 and 014. The other isolates were not associated with any international nomenclature (UCL57 and UCL378). A total of 7 isolates were tcdA+tcdB+ and two of them were also cdtA+. One isolate (UCL378) was negative for all types of toxin genes. (Refer to table.1)



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