**Clostridium difficile** beyond stools: dog nasal discharge as a possible new vector of bacterial transmission


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1. Introduction

**Clostridium difficile** (C. difficile), recently renamed as Clostridioides difficile (Lawson et al., 2016), is the most important cause of nosocomial infectious diarrhoea worldwide. Considered an enteric pathogen, the main risk factor for bacterial colonisation is a disruption of the normal gut microbiota, frequently due to the exposure to broad-spectrum antibiotics (Lübbert et al., 2018). The spread and severity of C. difficile infection (CDI) have been associated with specific strains, including PCR-ribotypes 078, 027, 014 and 020, among others. The prevalence rates of which have increased in both Europe and North America between 2012 and 2015 (Cheknis et al., 2018). Transmission of the bacterium occurs via the faecal-oral route, directly or indirectly (Lübbert et al., 2014), and the spores are considered the main form implicated in C. difficile transmission and infection. They have the ability to persist for months on environmental surfaces, while the vegetative cells of C. difficile die in hours in aerobic conditions and they are normally killed with acid gastric exposure (Jump et al., 2007). The infectious dose in humans is not clearly described and it appears to be low and to vary with the antibiotic class or dose previously used (Warriner et al., 2017; Best et al., 2012).

C. difficile is also an important enteric pathogen in farm animals and pets, causing acute diarrhoea and colitis (Baverud, 2002). This animal reservoir has been linked with the increased number of community-associated infections, as the same strains have been observed in both humans and animals simultaneously (Rodriguez et al., 2016). Recently, dogs and cats have attracted the attention of many researchers since pets are in continuous close contact with their owners and often share the same resting places at home (bedrooms, living rooms, kitchens). Previous studies have demonstrated that shoes, slippers and dog paws could spread C. difficile spores among the environment, humans and animals (Janezic et al., 2018; Lefebvre and Weese, 2009). Most recently, a systematic large-scale survey was conducted for the first time to determine the occurrence of C. difficile in dogs and cats and their owners, and a bacterium prevalence of 3% was observed in faecal samples from both pets and humans, with PCR-ribotype 014 as the

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**ABSTRACT**

Zoonotic transmission of *Clostridium difficile* has been largely hypothesised to occur after direct or indirect contact with contaminated animal faeces. Recent studies have reported the presence of the bacterium in the natural environment, including in soils and rivers. If C. difficile spores are scattered in the environment, they can easily enter the respiratory tract of dogs, and therefore, dog nasal discharge could be a direct route of transmission not previously investigated. This study reports for the first time the presence of *C. difficile* in the respiratory tracts of dogs. The bacterium was isolated from 6 (17.1%) out of 35 nasal samples, with a total of 4 positive dogs (19%). *C. difficile* was recovered from both proximal and distal nasal cavities. All isolates were toxigenic and belonged to PCR-ribotype 014, which is one of the most predominant types in animals and in community-acquired *C. difficile* infections in recent years. The findings of this study demonstrate that the nasal cavity of dogs is contaminated with toxigenic *C. difficile*, and therefore, its secretions could be considered as a new route by which bacteria are spread and transmitted.
When samples were not processed the same day, they were stored at -80°C, otherwise they were stored at -4°C. Dogs are likely to smell everything that is in their reach to analyse their surroundings. Therefore, if C. difficile spores are scattered in the environment, the noses of dogs should be the first place where the spores enter, and the nasal discharge, seemingly harmless, could be a more direct route of spore transmission than faeces. C. difficile transmission could occur after exposure to kisses and other licks, secretions and sneezes, specially in those dogs that are in close and continuous contact with their owners. The objective of this study is to demonstrate for the first time the presence of C. difficile in the respiratory tract of dogs and to perform a molecular characterisation of the isolates. This study will finally reveal a new route of C. difficile transmission.

2. Methods

2.1. Dog recruitment and sample collection

A prospective study was conducted over three months at the Small Companion Animals Clinic, Department of Companion Animals, Faculty of Veterinary Medicine of Liege, from April through June 2017. Respiratory tract swab samples and bronchoalveolar lavage fluid were collected from each dog enrolled in the study. Eligible dogs were animals in consultation or those staying in the hospital who had respiratory troubles. Eight additional samples were obtained from the Faculty of Veterinary Medicine, University of Helsinki. Blank controls of all types of samples were obtained to verify possible contaminations.

Data related to clinical history, diagnostic findings and treatment received were collected. In addition, all predisposing factors for developing C. difficile infection (CDI), such as the prescription of antimicrobials, were carefully recorded. The study was examined and approved by the Animal Faculty Ethics Committee of the University of Liège (1854).

Animals were anaesthetised for sample collection. Before the anaesthesia, dogs were fasted the same morning, with access only to fresh water. Clinical examination was performed to ensure the healthy status of the dog. A catheter was placed in the cephalic vein for simultaneous collection of blood via the blood test catheter, to ensure the healthy status of the animal. Then, the premedication was injected (butorphanol 0.3 mg/kg IV) with a subsequent wait time of 20 minutes (duration for the implementation of the premedication). After this period, the anaesthesia was induced with midazolam 0.2 mg/kg IV and IV propofol on demand. The dog was not intubated and breathed ambient air. The endoscope was inserted directly through the larynx into the trachea, taking care to minimise contamination of the final part when passing through the oral cavity. A sterile swab was introduced to brush the mucosa at the proximal nasal cavity. A second sterile swab was introduced to brush the mucosa at the distal third of the nasal cavity, after opening the nare using a sterile speculum. The top of the swabs were cut, stored in sterile cryotubes and sent to the laboratory. Overall, 35 samples were analysed from 21 different dogs.

2.2. C. difficile culture and identification

Samples were cultured according to a protocol for C. difficile detection based on the work of Delmée et al. (2005). A total of 300 μl of buffered peptone water was added to the cryotube containing the swab sampled or the bronchoalveolar lavage fluid. The sample was mixed by vortex for 1 minute and then incubated for 5 minutes at room temperature. Subsequently, 100 μl of the broth was spread on cycloserine cefoxitin fructose agar with taurocholate (CCFAF) (Deltée et al., 1987). Plates were incubated in an anaerobic workstation, Concept Plus (Led Techno, BE), for C. difficile direct detection. The remaining sample volume, around 200 μl minimum, was recovered and inoculated into 10 ml of cycloserine cefoxitin fructose taurocholate broth (CCTB) (Delmée et al., 1987), which was freshly prepared in the laboratory. The broth was incubated for 72 h at 37°C under anaerobic conditions. After incubation, a 10 μl aliquot of the enriched broth was spread onto CCFAT, and these plates were incubated anaerobically at 37°C for 2 days, for C. difficile detection after enrichment. Colonies of C. difficile were identified from culture plates by morphological criteria, subcultured onto blood agar (5% sheep blood; Bio-Rad, BE) and checked using a rapid C. difficile latex agglutination test kit (DR 1107A, Oxoid, FR). The toxin activity of the isolates was confirmed by a cytotoxicity assay using confluent monolayer MRC-5 cells as described previously (Rodríguez et al., 2013). Confirmation of C. difficile was performed by detection of a species-specific internal fragment of the tpi gene and detection of genes for toxin A, toxin B and binary toxin (cdtA) by classic PCR (Rodríguez et al., 2013).

2.3. PCR-ribotyping

PCR-ribotyping was performed as described previously (Bidel et al., 1999). The technique is based on capillary gel electrophoresis. International nomenclature was used for C. difficile strains that presented a PCR-ribotype profile matching the Cardiff PCR-ribotypes (Anaerobe Reference Unit (ARU), UK) from the strain collection available in our laboratory. Otherwise, strains were identified with an internal nomenclature beginning with UCL (database at Catholic University of Louvain, National Reference Laboratory for C. difficile in humans in Belgium). Strains were identified as rare profiles if they presented new PCR-ribotype profiles rarely or never before detected in our laboratory.

3. Results

Overall, 35 samples were analysed from 21 different dogs. C. difficile was isolated from 6 (17.1%) out of 35 samples, with a total of 4 animals positive for the bacterium (19%). The highest proportion of dogs (10 out of 21; 47.6%) was aged between 3 and 8 years old, whereas 7 dogs out of 21 were younger than 3 years old (33.3%). Surprisingly, all of the dogs that were positive for C. difficile belonged to the last group with the youngest ages, ranging between 1 and 3 years old (Tables 1 and 2). Dogs that were positive for C. difficile were detected among the animals suffering brachiocephalic airway obstructive syndrome (n = 3) and stress intolerance (n = 1).

None of the samples were positive by direct culture. Positive samples were only detected after three days of selective enrichment. One positive animal presented the bacterium in both nostrils (left and right). In another positive animal, C. difficile was isolated from both the proximal and distal nasal cavities. The bacterium was isolated from a third positive dog only from the right proximal nasal cavity, but C. difficile was not isolated from the left side or from the bronchoalveolar lavage fluid (Table 2).

Only one PCR-ribotype was identified among the 6 positive samples found. The isolates had a profile that corresponded with the ARU Cardiff collection PCR-ribotype 014. All of these isolates displayed cytotoxic activity in cultured cells and contained tcdA and tcdB genes. However, none of them presented cdtA and cdtB genes coding for the binary toxin CDT (Table 2).
4. Discussion

Carriage of *C. difficile* in domestic animals and its impact have been a major concern in the last decade. Several studies have underlined the presence of hypervirulent strains in farm animals and pets and their potential association with the increase in community-associated CDI (Rodriguez Diaz et al., 2018). The suggested routes of spore contamination include direct or indirect contact with animal faeces (Rodriguez et al., 2016). In addition to animal carriage, an important reservoir of toxigenic strains has recently been observed in the environment, with the presence of *C. difficile* spores in effluents, rivers, public parks and farmlands. These findings enhance the important role of dog paws and even shoes in *C. difficile* spread, but also suggest that there must be other vectors for the bacterium transmission (Zidaric et al., 2010). Most of the studies reported low levels of *C. difficile* spores in foods, animals or in the environment, as the bacterium was only detected after anaerobic enrichment. However, as the infectious dose and risk factors for CDI in the community are not fully understood, it has been suggested that continuous exposure to these contamination sources over days, weeks or even years can finally trigger the infection (Rupnik, 2010; Weese et al., 2009).

The noses of most domestic and farm animals are in constant contact with the ground. In the case of dogs, their extraordinary olfactory capability allows them to detect a vast number of chemical compounds, to detect a target odour among a myriad of odours in the environment and to communicate with other congeners (Jenkins et al., 2018). If dogs constantly smell the entire environment, including urine or faeces from other animals, their nasal cavities are exposed to *C. difficile* spores, and the bacterium could find a transient niche in this mucosa. Furthermore, dogs are continuously licking their noses. If the nasal discharge is contaminated, the spores can be disseminated in the environment or they can easily reach the intestinal tract of the dog by oral route. Once they are in the intestinal tract, these spores could trigger the infection or be transient. In any case, they will be excreted with the faeces, contributing to the dissemination in the environment and repeating the cycle of transmission.

This study demonstrates for the first time the presence of toxigenic *C. difficile* strains in the proximal and distal nasal cavities of dogs. *C. difficile* was isolated from the noses of dogs with a percentage of 19% by classical culture and after enrichment. The prevalence reported in adult dog paws and their households does not exceed 34% (Janezic et al., 2018). Therefore, the preliminary findings of this study indicate that animal nasal cavities merit further attention regarding the spread of *C. difficile* and the microbiota composition. It is important to highlight that dogs are very social pack animals. Therefore dog-to-dog transmission (direct via social interactions) is a likely route of spore transmission. Furthermore, dogs can expose their respiratory tracts directly from smelling faeces or even by investigating the terminal end of their own digestive tracts, which is a common behavior in these animals.

A previous study showed that the canine nasal cavity is inhabited by a highly species-rich bacterial community that is different between healthy dogs and those with disease, and the *Clostridiales* order was identified in

<table>
<thead>
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<table>
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<tr>
<th>Origin</th>
<th>Animal ID</th>
<th>Breed</th>
<th>Genre</th>
<th>Weight (Kg)</th>
<th>Hospitalization/Consultation</th>
<th>Date of naissance</th>
<th>Consultation/illness</th>
<th>Medical treatment</th>
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<td>Female</td>
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<td>15</td>
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<td>24.03.2015</td>
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<td>11</td>
<td>Consultation</td>
<td>13.05.2016</td>
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<td>Sedacil 20 mg; ½ tablet BID&lt;sup&gt;b&lt;/sup&gt;</td>
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<td>11 approx.</td>
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<td>AH</td>
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<td>NAD</td>
<td>Consultation</td>
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<td>Consultation</td>
<td>16.10.2008</td>
<td>Idiopathic pulmonary fibrosis</td>
<td>NAD</td>
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</table>

Animal ID: Animal identification; Malinois: Belgian Shepherd Malinois; Westie: West Highland white terrier; BAOS: Brachycephalic airway obstructive syndrome. NTR: not treatment registered; NDA: not available data; BID: bis in die (two times per day); SID: sem’ el in di’e (once a day).

<sup>a</sup> Antibiotic treatment, anti-acid treatment or others.

<sup>b</sup> Treatment at the moment of sampling.

<sup>c</sup> Treatment between 2 months and 2 weeks before sampling.
investigating the presence of *C. difficile* in recreational sandboxes for children and dogs, 8 of the 20 identified isolates belonged to PCR-ribotype O14 (Orden et al., 2018). In other environmental studies, PCR-ribotype O14 was also identified as predominant (16.2% of all isolates) (Zidaric et al., 2010). Furthermore, the highest sporulation rates were observed in these strains after 24 hours (Zidaric and Rupnik, 2016). The adaptability of this type of bacterium to different environments and whether there is an advantage to colonising the canine nasal cavity needs further investigation.

### 5. Conclusions

Generally, people wash and even disinfect their hands quickly after contact with faeces. However, it is uncommon to see this behaviour in the owners after touching the nose or the nasal discharge of their pets. In this study, we have demonstrated that the nasal cavity of dogs can be contaminated with *C. difficile* spores, and therefore its secretions could be considered as a new vector for transmission not previously described. The situation in other animal species as well as the impact not only for transmission but also for the host merits future investigations.

#### Declarations

**Author contribution statement**

C Rodriguez: Conceived and designed the experiments; Performed the experiments; Analyzed and interpreted the data; Contributed reagents, materials, analysis tools or data; Wrote the paper.

B Tamiaiu: Conceived and designed the experiments; Analyzed and
interpreted the data; Contributed reagents, materials, analysis tools or data.

I. Bouchafa: Performed the experiments; Contributed reagents, materials, analysis tools or data.

S Romijn, J Van Broeck: Contributed to sampling collection, reagents, materials, analysis tools or data.

M Delmée: Performed the experiments; Contributed reagents, materials, analysis tools or data.

C Clercx: Performed the experiments; Analyzed and interpreted the data; Contributed reagents, materials, analysis tools or data.

G Daube: Conceived and designed the experiments; Analyzed and interpreted the data; Contributed reagents, materials, analysis tools or data; Wrote the paper.

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Competing interest statement

The authors declare no conflict of interest.

Additional information

No additional information is available for this paper.

References


