Research

Shedding of OXA-181 carbapenemase-producing Escherichia coli from companion animals after hospitalisation in Switzerland: an outbreak in 2018

Aurélien Nigg¹, Michael Brilhante¹,², Valentina Dazio³, Mathieu Clément³,⁴, Alexandra Collaud¹, Stefanie Gobeli Brawand¹, Barbara Willi¹, Andrea Endimiani⁵, Simone Schuller³, Vincent Perreten¹

¹. Institute of Veterinary Bacteriology, Bern, University of Bern
². Graduate School of Cellular and Biomedical Sciences, Bern, University of Bern
³. Department of Clinical Veterinary Medicine, Bern, University of Bern
⁴. Clinic for Small Animal Internal Medicine, University of Zurich, Zurich, Switzerland
⁵. Institute for Infectious Diseases, University of Bern, Bern, Switzerland

Correspondence: Vincent Perreten(vincent.perreten@vetsuisse.unibe.ch)

Citation style for this article:

Article submitted on 22 Jan 2019 / accepted on 19 May 2019 / published on 26 Sep 2019

Background: Carbapenem-resistant Enterobacteriaceae pose a serious threat to public health worldwide, and the role of companion animals as a reservoir is still unclear. Aims: This 4-month prospective observational study evaluated carriage of carbapenem-resistant Enterobacteriaceae at admission and after hospitalisation in a large referral hospital for companion animals in Switzerland. Methods: Rectal swabs of dogs and cats expected to be hospitalised for at least 48 h were taken from May to August 2018 and analysed for the presence of carbapenem-resistant Enterobacteriaceae using selective agar plates. Resistant isolates were further characterised analysing whole genome sequences for resistance gene and plasmid identification, and ad hoc core genome multilocus sequence typing. Results: This study revealed nosocomial acquisition of Escherichia coli harbouring the carbapenemase gene bla_{OXA-181}, the pAmpC cephalosporinase gene bla_{CMY-42} as well as quinolone resistance associated with qnrS1 and mutations in the topoisomerases II (GyrA) and IV (ParC). The bla_{OXA-181} and qnrS1 genes were identified on a 51 kb IncX3 plasmid and bla_{CMY-42} on a 47 kb IncI1 plasmid. All isolates belonged to sequence type ST410 and were genetically highly related. This E. coli clone was detected in 17 of 100 dogs and four of 34 cats after hospitalisation (21.6%), only one of the tested animals having tested positive at admission (0.75%). Two positive animals were still carriers 4 months after hospital discharge, but were negative after 6 months. Conclusions: Companion animals may acquire carbapenemase-producing E. coli during hospitalisation, posing the risk of further dissemination to the animal and human population and to the environment.

Introduction

Companion animals nowadays not only share the owner’s home environment but also benefit from intensive veterinary care in case of serious illness. Veterinary referral hospital environments are similar to human hospitals in that animal patients face similar risks of developing nosocomial infections.

Bacterial infections in dogs and cats are frequently treated with critically important antimicrobials such as fluoroquinolones or cephalosporins. In very rare cases, even the last resort antibiotics of human medicine such as carbapenems may be used in companion animals in Switzerland to treat infections refractory to any other standard antimicrobial used in veterinary medicine (Ordinance on Veterinary Medicinal Products, SR 812.212.27, Art. 6).

Such treatments pose the risk of selecting resistance to these classes of antibiotics in Enterobacteriaceae through the acquisition of plasmid-mediated cephalosporinase genes (e.g. bla_{CTX-M}, bla_{CMY}) and fluoroquinolones resistance genes (e.g. qnr, aac-(6)-Ib-cr), but also through chromosomal mutations in the promoter region of the AmpC β-lactamase and in the quinolone resistance-determining region (QRDR) of the topoisomerases II (GyrA) and IV (ParC) [1,2]. Resistances to carbapenems have also emerged in Escherichia coli and Klebsiella pneumoniae [3]. Three main groups of carbapenemases are referenced according to the Ambler classification: class A (e.g. KPC), class B (IMP, VIM, NDM) and class D (e.g. OXA) [4]. Among the OXA carbapenemases, OXA-48-like ones have been described as phantom carbapenemases since they...
may be difficult to detect using phenotypic susceptibility testing [5].

Until now, animals were considered to play a minor role in the dissemination of OXA-48-like carbapenemases [6], but reports of sporadic infections in dogs caused by carbapenemase-producing (CP) Enterobacteriaceae in Europe [7,8], in the United States (US) [9] and in Northern Africa [10] suggest that companion animals may represent an unsuspected reservoir of carbapenem-resistant bacteria. Recently, hospitalised companion animals in Italy were found to acquire carbapenem-resistant bacteria such as Acinetobacter spp. [11]. Nonetheless, very little is known about carriage and dynamics of CPE in dogs and cats before and after hospitalisation.

Results as detected at admission and discharge to a companion animal clinic, as well as once or twice within 175 days after hospitalisation.

Shapes in green: test negative for CP E. coli carriage; shapes in red: test positive for CP E. coli carriage. Blue dotted line: timeline of screened animals; grey dashed line: animals which were not resampled.
Here, we characterised by whole genome sequencing (WGS) CP E. coli isolated from cats and dogs at admission and after hospitalisation to a large veterinary referral hospital in Switzerland, identifying their antimicrobial resistance genes (ARG) and mobile genetic elements (MGE) as well as the phylogenetic relationship among the isolates.

**Methods**

**Study design and sampling**

This study was part of a larger prospective study which included three large veterinary referral clinics and two smaller veterinary practices in Switzerland. The present prospective observational study was performed at a university referral hospital with a 24/7 emergency service. The hospital provides advanced medical care for 6,000 dogs and cats annually. Dogs and cats were included irrespective of their underlying problems and previous treatments if they were expected to be hospitalised for at least 48 h and the owner gave informed consent. All animals presented here were recruited via the emergency service of the hospital. During the enrolment period of 4 months (1 May–31 August 2018), ca 2,000 animals were treated at the hospital and 134 of them fulfilled the study criteria and were screened.

Rectal swabs were collected in awake animals at admission to the hospital and at discharge, using polyurethane foam culture swabs with Ames transport medium (BBL CultureSwabs). If available, animals positive at discharge were retested once or twice within 36 to 166 days after their discharge of the clinic.

**Isolation and identification of the strains**

Swabs were placed into 5 mL of Luria-Bertani (LB) broth for overnight enrichment at 37°C. A loopful of the culture was streaked onto CHROMID OXA-48

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Dogs (n=17)</th>
<th>Cats (n=4)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age median in years (IQR)</td>
<td>7.0 (4.0–9.0)</td>
<td>4.5 (2.3–10.5)</td>
</tr>
<tr>
<td>Weight median in kg (IQR)</td>
<td>16.6 (7.8–34)</td>
<td>4.2 (3.0–5.7)</td>
</tr>
<tr>
<td><strong>Sex</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Female (entire/neutered)</td>
<td>9 (5/4)</td>
<td>2 (0/2)</td>
</tr>
<tr>
<td>Male (entire/neutered)</td>
<td>8 (6/2)</td>
<td>2 (1/1)</td>
</tr>
<tr>
<td><strong>Gastrointestinal disease</strong></td>
<td>7</td>
<td>1</td>
</tr>
<tr>
<td><strong>Neurological disease</strong></td>
<td>5</td>
<td>0</td>
</tr>
<tr>
<td><strong>Urinary tract disease</strong></td>
<td>2</td>
<td>2</td>
</tr>
<tr>
<td><strong>Other</strong></td>
<td>3</td>
<td>1</td>
</tr>
<tr>
<td><strong>Hospitalisation days; median (IQR)</strong></td>
<td>4 (3–5)</td>
<td>5 (1.8–8.3)</td>
</tr>
<tr>
<td><strong>ICU days; median (IQR)</strong></td>
<td>3 (1–5)</td>
<td>2.3 (1.5–8.6)</td>
</tr>
<tr>
<td><strong>Antimicrobial pre-treatment</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Yes</td>
<td>4</td>
<td>1</td>
</tr>
<tr>
<td>No</td>
<td>11</td>
<td>3</td>
</tr>
<tr>
<td>Unknown</td>
<td>2</td>
<td>0</td>
</tr>
<tr>
<td><strong>Antimicrobial treatment during hospitalisation</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Yes</td>
<td>14</td>
<td>3</td>
</tr>
<tr>
<td>No</td>
<td>3</td>
<td>1</td>
</tr>
<tr>
<td><strong>Antimicrobials used during hospitalisation</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ampicillin/sulbactam</td>
<td>9</td>
<td>3</td>
</tr>
<tr>
<td>Cefazolin</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Clindamycin</td>
<td>2</td>
<td>0</td>
</tr>
<tr>
<td>Doxycycline</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>Enrofloxacin</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>Metronidazole</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>Sulfamethoxazole/trimethoprim</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>Amoxicillin/clavulanic acid</td>
<td>1</td>
<td>0</td>
</tr>
</tbody>
</table>

ICU: intensive care unit; IQR: interquartile range.

*Antimicrobials used for pre-treatments (i.e. prior to presentation/referral) were amoxicillin/clavulanic acid (n = 2), amoxicillin (n = 1), enrofloxacin (n = 1) and metronidazole (n = 1).

*Includes mono- and combination therapy.*

---

Table 1

Demographic, hospitalisation and antimicrobial treatment details of dogs and cats positive for OXA181-producing *Escherichia coli* ST410, Switzerland, May–August 2018 (n = 21)
Colonies were sub-cultivated onto trypton soy agar plates containing 5% sheep blood (TSA-S) (Becton and Dickinson Company, Franklin Lakes, US) and identified to the species level by matrix-assisted laser desorption/ionisation time-of-flight mass spectrometry (MALDI-TOF MS) (Bruker Daltonics GmbH, Bremen, Germany).

Biochemical and molecular tests
Carbapenemase production was detected using the Blue-Carba test [12]. Before WGS, carbapenemase-producing isolates were tested for the presence of bla genes by PCR [5].

Antimicrobial susceptibility testing
Minimal inhibitory concentrations (MIC) of 16 antimicrobials (ampicillin, cefepime, cefotaxime, ceftazidime, chloramphenicol, ciprofloxacin, colistin, ertapenem, gentamicin, imipenem, meropenem, nalidixic acid, sulfamethoxazole, tetracycline, tigecycline and trimethoprim) were determined by broth microdilution using Sensititre EUVSEC and EUVSEC2 plates (Thermo Fisher Scientific, Waltham, US) and following the guidelines from the European Committee on Antimicrobial Susceptibility Testing (EUCAST) [13]. MIC results were interpreted using the EUCAST criteria, except for nalidixic acid, sulfamethoxazole and tetracycline, for which criteria from the Clinical and Laboratory Standards Institute (CLSI) were used [14].

The tree was generated and drawn using SeqSphere+ (v. 4.01, Rindom GmbH, Münster, Germany) for the comparison of 3,778 genes from the core genome (cgMLST) of the genomic sequences.

Blue: isolates from animals; green: isolates from humans; orange: isolates from the environment.

E. coli isolates used for the comparison were carrying the following resistance genes to β-lactams, cephalosporins and carbapenems:

- **CP018965:** blaKPC-2, blaOXA-1, blaCTX-M-15
- **CP023899:** blaCTX-M-15, blaTEM-1B
- **CP024801:** blaCMY-2, blaNDM-5, blaTEM-1B, blaCTX-M-15, blaOXA-1
- **CP027205:** blaCMY-2, blaTEM-1B, blaCTX-M-65, blaNDM-5
- **CP026473:** blaCMY-2, blaNDM-5, blaTEM-1B, blaCTX-M-15, blaOXA-1, blaOXA-181
- **CP029630:** blaTEM-1A, blaOXA-9, blaCTX-M-15, blaNDM-1
- **CP031653:** blaNDM-5, blaCMY-42, blaTEM-190
Whole genome sequencing and in silico analysis

Total DNA from OXA-48-like-positive strains was isolated using the DNeasy Blood and Tissue Kit (Qiagen, Venlo, the Netherlands), and purified using the AMPure XP paramagnetic bead-based chemistry (Beckmann Coulter, Brea, US). All CP E. coli were sequenced (2 × 150 bp paired-end) using the Illumina HiSeq technology (Illumina Inc, San Diego, US) at the Eurofins Institut (Konstanz, Germany). The genomic DNA of strain AR24.2b was additionally sequenced with MiNiON on a R9.4 Spot On flow cell using the library preparation kit SQK-LSK108 (Oxford Nanopore Technologies (ONT), Oxford, United Kingdom (UK)). Genome assembly of all strains was performed using SPAdes (v3.12.0) and the obtained contigs were used for in silico analysis. The genome assembly of strain AR24.2b was performed by Unicycler (v0.4.4), using both long (ONT) and short reads (Illumina), as well as by CANU (v1.7) that only uses the ONT long reads. The obtained scaffolds were polished by read-mapping with paired-end Illumina reads using Pilon (v1.22) and with Geneious software v10.1.3 (Biomatters Ltd, Auckland, New Zealand). Annotation was performed with PROKKA v1.12. The paired-end reads of all CP E. coli strains were mapped to the final annotated plasmid sequences of AR24.2b. Online tools available at the Center for Genomic Epidemiology (Technical University of Denmark DTU, Lyngby, Denmark) were used to detect known ARG (ResFinder 3.0) to determine incompatibility (Inc) groups of the plasmids, (PlasmidFinder 1.3) and for multilocus sequence typing (MLST 2.0).
Transposable elements present in the plasmids were identified using ISfinder (https://isfinder.biotoul.fr/). Blast ring image generator (BRIG) was used to generate circular map comparisons of plasmids (based on BLASTn) [15]. Comparison with closely related plasmids from the National Center for Biotechnology Information (NCBI) was achieved using the NCBI tool BLASTn (https://blast.ncbi.nlm.nih.gov/Blast.cgi, accessed November 2018).

Phylogenetic analyses
An ad hoc core genome multilocus sequence typing (cgMLST) scheme was created using SeqSphere+ (v. 4.01, Rindom GmbH, Münster, Germany). The E. coli of sequence type (ST) 410 from a dog in the UK (GenBank accession number CP031653) was defined as the reference genome from which 4,177 coding regions of genes were extracted by the cgMLST Target Finder v1.4. The contigs obtained from SPAdes of all 24 CP E. coli in this study, together with the reference genome and with six other genomes of E. coli ST410 isolated from humans or from the environment and published in GenBank (GenBank accession numbers CP029630, CP027205, CP026473, CP024801, CP023899 and CP018965), were loaded and searched for the 4,177 gene targets using built-in BLAST. Overall, 3,778 genes were shared among all isolates, which we defined as the core genome. The visualisation of the phylogenetic distance was achieved using the allelic profile of all strains to generate a neighbour-joining tree using SeqSphere+ with the parameters ‘pairwise ignoring missing values; % columns difference’ for the distance calculation.

Ethical statement
The study protocol was approved by the national ethics committee (BE 16/18) and signed informed consent was obtained from the owners before enrolment of the animals in the study.

Results
Occurrence of carbapenemase-producing Escherichia coli
Rectal swabs were taken from 100 dogs and 34 cats at admission to a large veterinary referral clinic in Switzerland between 1 May and 31 August 2018. Carriage of CP E. coli was detected in only one dog and none of the cats at admission (0.75%; 95% confidence interval (CI): 0–2.2).

In contrast, 17 of 76 dogs and four of 21 cats that were resampled at discharge were found to harbour CP E. coli (21.6%; 95% C: 13.4–29.8) indicating nosocomial acquisition of the bacteria. The 37 remaining animals were not available for resampling (n = 22) or deceased (n = 15).
The coloured outer rings indicate regions of homology of the pAN-OXA-181 (GenBank accession number MK416154) and pAN-CMY-42 (GenBank acc. no. MK416155) plasmid of strain AR24.2b with other plasmids, based on BLASTn.

Left panel: pAN-OXA-181. The rings from the inner to the outer represent plasmids pAMA1167-OXA-181 (GenBank acc. no. CP024806; 99.99% identity, 1 single nucleotide polymorphism (SNP)), pOXA181_14828 (GenBank acc. no. KP400525; 100% identity), pKS22-OXA-181 (GenBank acc. no. KT005457; 99.98%, 3 SNP), pEC31346-OXA-181 (GenBank acc. no. KX894452; 99.99% identity, 1 SNP), pSTIB (GenBank acc. no. MG570092; 99.99% identity, 1 SNP) and pEC21-OXA-181 (GenBank acc. no. MG893567; 99.99% identity, 1 SNP).

Left panel: pAN-CMY-42. The rings from the inner to the outer represent plasmids pCMY42_M217 (GenBank acc. no. AP019190; 99% identity, 65% coverage), pCMY42_AR_0137 (GenBank acc. no. CP021882; 100% identity, 68% coverage), pCARB35_03 (GenBank acc. no. CP013166; 100% identity, 79% coverage), pCMY42_WCHEC13–8 (GenBank acc. no. KP789015; 100% identity, 71% coverage), pV233-b (GenBank acc. no. LC056425; 99% identity, 46% coverage) and pIBAC_IncI1_CMY-42 (GenBank acc. no. KY463221; 100% identity, 78% coverage).

The scale circle shows the coordinates in kbp of each plasmid. Genes are portrayed as coloured blocks in the inner ring of each circular map. Genes are coloured according to their classification. Red: antimicrobial resistance genes; dark purple: surface disinfectants resistance genes; orange: transposases; fuchsia: genes implicated in replication; green: transfer-associated genes; brown: partition genes; grey: other genes. The \( \Delta umud \) and \( \Delta arsR \) genes are coloured in darker grey, flanking the composite transposon of pAN-OXA-181. The \( blc \) gene of pAN-CMY-42 is indicated in the map to better represent the composition of the native 4 kb element.
The dog positive for CP *E. coli* at admission was not under antimicrobial treatment at arrival and had no previous history of hospitalisation at this clinic, but whether it was previously hospitalised in another clinic is not known. Nor was it the first animal tested positive during the study period. This dog was still positive at discharge (Figure 1).

The demographics, hospitalisation details and antimicrobial treatments of the CP *E. coli*-carrying animals are summarised in Table 1. Animals were presented to the emergency service of the hospital with a wide range of complaints. All cats and 13 of the 17 dogs spent time in the intensive care unit of the hospital. The majority of dogs (14/17) and cats (3/4) were treated with antimicrobials during their hospitalisation; however, none of them received carbapenems.

Follow-up samples were obtained within 36 to 101 days after discharge from 12 of 21 CP *E. coli*-positive animals. The other nine animals could not be retested because they had died (n = 3), or because the owners withdrew their participation in the study (n = 6). Two cats still carried CP after the first follow-up. None of them received carbapenems.

Characterisation of the plasmids containing resistance genes

The *bla* and *qnrS1* genes were co-localised on a 51 kb incX3 plasmid (pAN-OXA-181) in strain AR24.2b (Figure 3). Plasmid mapping showed that all other 23 isolates also harboured this same plasmid. Plasmid pAN-OXA-181 was 99.9% similar to other IncX3 plasmids from human *E. coli* strains in China (pOXA181_14828 and pEC21-OXA-181 [18,19], Denmark (pPAMA167-OXA-181) [20], and Lebanon (pSTIB) [21], as well as from a porcine *E. coli* strain in Germany (pEc31346-OXA-181) [22]. Plasmid pAN-OXA-181 differed by 3 SNPs from pKS22-OXA-181 which was detected in a *Klebsiella variicola* isolated from fresh vegetables imported into Switzerland [23] (Figure 3).

Both *bla* and *qnrS1* were found within a composite transposon in pAN-OXA-181, which was integrated between *umuD* and *asrR*, similarly to pOXA-181 [18]. The composite transposon was flanked by two copies of the insertion sequence IS26 which were oriented in the same direction. Two 50 bp inverted repeats IRL and IRR, each preceded by a 2 bp AC direct repeat, were found at both ends of the IS26-flanked composite transposon, which is indicative of a transposition event [19]. Plasmid pAN-OXA-181 also contained the replication gene *repB* and a 23 kb transfer region containing the *virB1–2–4–5–6–8–9–10–11*, *traG* and *trmB* genes (Figure 3).

Strain AR24.2b also contained a 47 kb Incl plasmid (pAN-CMY-42) which harboured the pAmpC gene *bla* (Figure 3). The *bla* gene is commonly found in plasmids within a 4 kb element composed by *ISeCP1*, an outer membrane lipoprotein gene *blc* and a quaternary ammonium compound (QAC) resistance gene *sugE* (*ISeCP1 – *bla* – *blc* – *sugE*) [24]. In pAN-CMY-42 however, Δ*ISeCP1* of this element was split by the insertion of a copy of IS1, and subsequent homologous recombination with another copy of IS1 led to its modified structure, as previously described [24]. This recombination is supported by the inversion of the insertion repeats (GATAA and TTATC) (Figure 3).
Plasmid pAN-CMY-42 also contains the replication gene repA and transfer genes traA, traE, tral, traI, traY and trbA.

Plasmid pAN-CMY-42 differed from other CMY-42-containing IncI1 plasmids by its size and structure. The most closely related IncI1 CMY-42 plasmids deposited so far in GenBank were larger than pAN-CMY-42 by 1–50 kb, including plasmids isolated from canine E. coli in the UK (pCARB35_03) [16], human patients in Myanmar (pCMY42_M217) [25], China (pCMY42_WCHEC13–8) [24] and Italy (pIBAC_IncI1_CMY-42) [26], as well as from E. coli isolated from the environment (pV233-b) [27], and from an unknown source (pCMY42_AR_0137 (Figure 3).

Plasmid mapping of the other 23 E. coli showed that 21 isolates also contained this same plasmid (pAN-CMY-42), whereas the two isolates AR89.2 and AR144.2 lacked the 4 kb element (ISEcp1 – blaCMY-42 – blc – sugE) on their IncI1 plasmid.

Plasmids pAN-OXA-181, pAN-CMY-42 and the chromosome of E. coli strain AR24.2b have been deposited in GenBank under accession numbers MK416154, MK416155 and CP035944, respectively.

**Discussion**

Surveillance of enteral carriage of antimicrobial-resistant bacteria in dogs and cats before and after hospitalisation in a companion animal hospital in Switzerland revealed the potential role of small animal clinics as an underestimated hotspot for acquisition of CP E. coli. In the particular situation presented here, almost one quarter of the hospitalised animals acquired a specific carbapenem-, cephalosporin- and fluoroquinolone-resistant clone of ST410 within a time span of 1-9 days of hospitalisation. The only dog found to be carrier of this clone at admission was chronologically not the first to be found positive during the study period, indicating that it was not the primary source of this strain. It may, however, have contributed to further enhance dissemination of the clone into the hospital. Long-term carriage beyond 108 days was only documented in one cat among the 10 dogs and two cats that were followed up. Nevertheless, all 21 animals that returned home with CP E. coli posed a potential risk of disseminating hospital-acquired CP E. coli into the environment and possibly to other animals and humans (Figure 4).

Although the risk of CP Enterobacteriaceae transmission may be related to their relative abundance in faeces, our study was not set up to quantify the effective number of CP Enterobacteriaceae in faeces because it used enrichment and selective plates.

This figure shows the results of the screening of 134 animals at admission to the veterinary hospital and of 97 animals at discharge. It illustrates the potential risk for the environment, humans and other companion animals with regard to the carriage of CP E. coli by animals that have returned to their homes after having acquired CP E. coli during hospitalisation.
It is important to extend screening and detection methods in veterinary settings and diagnostic laboratories to detect such bacteria of medical and public health importance [4]. Detection of carbapenemases of the OXA-48 family may be challenging because of their low hydrolysing activity which specifies low MIC to carbapenems [4,5]. Application of low MIC screening values would allow identifying the OXA-181-producing E. coli isolates in our study since they exhibited MICs higher than the resistance breakpoint of >0.5 μg/mL for ertapenem and higher than the meropenem screening cut-off value of >0.125 μg/mL recommended by EUCAST [13].

Phylogenetic analyses of the CP E. coli using 3,778 genes of the core genome (cgMLST) confirmed high genetic relationship shared among all the E. coli isolates of ST410 from this study. This sequence type has recently been reported as a new emerging international high-risk clone, non-susceptible to critically important antibiotics such as fluoroquinolones, third-generation cephalosporins and carbapenems and with the potential of cross-sectorial transmission between wildlife, humans, pets and the environment [28,29]. Escherichia coli ST410 from this study at the diagnostic unit of our institute. Of note, this referral hospital faced several cases of infections caused by a nosocomial clone of third-generation- cephalosporin-resistant K. pneumoniae ST11 producing the pAmpC DHA in 2010–2013 [31].

As an infection control measure, thorough disinfection of the hospital environment was performed after this outbreak in 2018 using disinfectant without QAC since ST410 also contained a QAC resistance gene (sugE) on the cephalosporinase plasmid pAN-CMY-42. Furthermore, stringent hospital hygiene and environmental cleaning protocols were introduced and a staff screening campaign was initiated. Staff training was also intensified to improve hand and environmental hygiene. The results and the impact of these measures are still being analysed and will be part of a follow-up study. Although no conclusion can be drawn at this stage of the study on the impact of possible colonisation of the staff or the pet owners, the results indicate that companion animals probably disseminated CP Enterobacteriaceae via faeces in the environment after hospitalisation and may represent a potential risk for transmission of CP Enterobacteriaceae to other animals and humans in the community and a serious One Health concern.

This outbreak stresses the need for national routine monitoring of carbapenemase-producing bacteria in companion animals using a representative sampling strategy analogous to the national surveillance of antibiotic resistance in food-producing animals at slaughterhouses in Switzerland and the European Union [32]. Based on the results of our study, we strongly recommend monitoring hospitalised companion animals for CP Enterobacteriaceae carriage at discharge using a sampling strategy representative of the number of hospitalised animals in the enrolled clinics. Such a surveillance programme should identify high-risk companion animal clinics and improve infection prevention and control as well as hygiene standards.

**Conclusion**

This study provided evidences that dogs and cats can acquire CP Enterobacteriaceae within a short time of hospitalisation. Even if the colonisation of the animals did not last longer than 40 days in the majority of the animals, shedding of CP Enterobacteriaceae after
hospitalisation represents a public health and environmental concern. Early detection and nationwide surveillance of carbapenemase-producing isolates, as well as effective infection prevention and control measures, need to be implemented in veterinary settings to limit the spread of high-risk clones in animals, humans and the environment.

Acknowledgements
This study was financed by the Swiss Federal Food Safety and Veterinary Office (FSVO) Grant no. 18.10 “Prevention and Identification of critical points for transmission of multidrug-resistant bacteria in small animal clinics - towards evidence-based guidelines for infection prevention and control” to SS, BW, SGB, AE and VP, and by the Swiss National Science Foundation (SNSF) grant no. 177378 within the National Research Programme NRP72 “Antimicrobial Resistance” to AE and VP. We are grateful to all participating owners who kindly made the sampling of their animals possible.

Conflict of interest
None declared.

Authors’ contributions
SS, BW, SGB, AE and VP contributed to the design of the study. VD sampled the animals. AN and AC isolated and identified the strains. SS and VD collected and analyzed the clinical data. AN and MB performed experiments and genomic analysis. MB and MC performed MinIon sequencing. AN, MB and VP interpreted bacteriological and molecular data, and AN and VP wrote the manuscript. All authors reviewed the manuscript.

References


License, supplementary material and copyright
This is an open-access article distributed under the terms of the Creative Commons Attribution (CC BY 4.0) Licence. You may share and adapt the material, but must give appropriate credit to the source, provide a link to the licence and indicate if changes were made.

Any supplementary material referenced in the article can be found in the online version.

This article is copyright of the authors or their affiliated institutions, 2019.