Detection of IncN-pST15 one-health plasmid harbouring \( \text{bla}_{\text{KPC-2}} \) in a hypermucoviscous \textit{Klebsiella pneumoniae} CG258 isolated from an infected dog, Brazil

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Abstract
The emergence and rapid spread of carbapenemase-producing Enterobacterales represents a serious public health concern. Critically, these global priority bacteria have begun to be reported in companion animals, implying a potential risk of cross-transmission between humans and pets. Using long-read (MinION) and short-read (Illumina) sequencing technologies, we have identified and characterized a hypermucoviscous KPC-2-producing \textit{Klebsiella pneumoniae} strain belonging to the high-risk international clone ST11/CG258, in a dog with urinary tract infection. Strikingly, the \( \text{bla}_{\text{KPC-2}} \) gene was carried by a 54-kb IncN plasmid assigned to ST15, which shared 99.8% and 96.8% pairwise identity with IncN-pST15 plasmids from human and environmental \textit{K. pneumoniae} strains, respectively; all come from an area with high endemicity of KPC-2. Our findings suggest that IncN-pST15 plasmids conferring carbapenem resistance can play as important a role as clonal transmission of \textit{K. pneumoniae}, representing another major challenge for One Health.

KEYWORDS
carbapenemase, global priority pathogens, one health, pets, plasmidome

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1 | INTRODUCTION

Epidemiological studies have revealed that carbapenemase-producing Enterobacterales have emerged in healthy and sick animals, and community settings (Kelly et al., 2017; Wang et al., 2020; Zhang et al., 2019), implying a potential risk of transmission of these pathogens between humans and companion animals (Grönthal et al., 2018; Sellera & Lincopan, 2019). Additionally, the transfer of carbapenem resistance genes can be facilitated by mobile genetic elements (e.g. plasmids and transposons), which is a concerning possibility (Baquero et al., 2019; Brandt et al., 2019).

KPC family has been the most widespread of all carbapenemases associated with Enterobacterales (van Duin & Doi, 2017). The occurrence of KPC-producing bacteria in human hospital settings has rendered nosocomial infections particularly difficult to treat or even untreatable (Wang et al., 2016). To date, the identification of KPC producers in companion animals has been sporadically reported from dogs in Brazil (KPC-2-producing Escherichia coli) and United States (KPC-4-producing Enterobacter xiangfangensis) (Daniels et al., 2018; Sellera et al., 2018).

In this study, under a ‘One Health’ view, we report the identification of a KPC-2-positive Klebsiella pneumoniae belonging to the international high-risk clone sequence type 11/clonal group 258 (ST11/CG258) in a dog suffering from urinary tract infection, highlighting the occurrence of KPC-2-producing bacteria in human hospital settings has rendered nosocomial infections particularly difficult to treat or even untreatable (Wang et al., 2016). To date, the identification of KPC producers in companion animals has been sporadically reported from dogs in Brazil (KPC-2-producing Escherichia coli) and United States (KPC-4-producing Enterobacter xiangfangensis) (Daniels et al., 2018; Sellera et al., 2018).

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2 | MATERIALS AND METHODS

In 2019, during a Brazilian surveillance study (OneBR project), conducted to characterize the burden of antimicrobial resistance associated with critical WHO priority pathogens, a carbapenem-resistant K. pneumoniae strain (PVT01) identified by BD Phoenix (BD Diagnostics, Sparks, MD, USA) was isolated from a urine culture of a 9-year-old female Spitz dog suffering from urinary tract infection.

Antimicrobial susceptibility testing was performed by the disc diffusion and/or Etest methods according to Clinical and Laboratory Standards Institute methods (CLSI, 2018, 2020). The antibiotics tested were amoxicillin/clavulanic acid, aztreonam, cefotaxime, ceftriaxone, cefepime, cefoxitin, ciprofloxacin, enrofloxacin, nalidixic acid, chloramphenicol, amikacin, gentamicin, tetracycline, sulfadiazine, sulfadiazine-trimethoprim and tetracycline. Colistin susceptibility testing was performed by broth microdilution method according to European Committee on Antimicrobial Susceptibility Testing (EUCAST, 2021) guidelines. ESBL production was screened by the double-disc synergy test (DDST) (Drieux et al., 2008), whereas phenotypic detection of KPC enzyme was performed by the combined disc test using imipenem disc supplemented with aminophenylboronic acid (Tsakris et al., 2011). In addition, PVT01 strain was screened for hypermucoviscosity by string test (Shon et al., 2013).

| TABLE 1 | Susceptibility profile and genomic features of KPC-2-producing Klebsiella pneumoniae strain isolated from an infected dog in Brazil |
|---------------------------------|---------------------------------|
| **Susceptibility profile** | 
| Amoxicillin/clavulanic acid | R |
| Aztreonam | R |
| Cefotaxime | R |
| Ceftriaxone | R |
| Cefazidime | R |
| Cefotiofur | R |
| Cefoxitin | R |
| Cefepime | R |
| Ertapenem | R |
| Imipenem (MIC mg/L) | R (>32) |
| Meropenem (MIC mg/L) | R (>32) |
| Amikacin (MIC mg/L) | R (64) |
| Gentamicin (MIC mg/L) | R (>256) |
| Sulfadiazine-trimethoprim | R |
| Nalidixic acid | R |
| Enrofloxacin | R |
| Ciprofloxacin | R |
| Chloramphenicol | R |
| Tetracycline | S |
| Colistin (MIC mg/L) | S (2) |
| **Molecular epidemiology** | 
| MLST (ST/CG) | 11/258 |
| K-locus | KL15 |
| wzi | 50 |
| Serotype | O4 |

**Susceptibility profiles** were determined using the CLSI guideline (CLSI, 2020). For ceftiofur, enrofloxacin and colistin, resistance profiles were determined using veterinary CLSI (CLSI, 2018) and EUCAST 2021 (https://www.eucast.org/) guidelines, respectively.

**Virulome**
- Yersiniabactin siderophore
- ybt, fyuA, irp

**Plasmidome**
- Inc-type [size, kb]
- IncFIB(K) [168], IncN [54], Col4401-like [76]

| GenBank accession number | JABSUB00000000.1 |

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| **Susceptibility profile** | 
| Amoxicillin/clavulanic acid | R |
| Aztreonam | R |
| Cefotaxime | R |
| Ceftriaxone | R |
| Cefazidime | R |
| Cefotiofur | R |
| Cefoxitin | R |
| Cefepime | R |
| Ertapenem | R |
| Imipenem (MIC mg/L) | R (>32) |
| Meropenem (MIC mg/L) | R (>32) |
| Amikacin (MIC mg/L) | R (64) |
| Gentamicin (MIC mg/L) | R (>256) |
| Sulfadiazine-trimethoprim | R |
| Nalidixic acid | R |
| Enrofloxacin | R |
| Ciprofloxacin | R |
| Chloramphenicol | R |
| Tetracycline | S |
| Colistin (MIC mg/L) | S (2) |

**Molecular epidemiology**
- MLST (ST/CG): 11/258
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**MLST, Multi-Locus Sequence Typing; ST, sequence type; CG, clonal group.**

**The IncFIB(K) plasmid, named pPVT01_P1, harboured blaKPCC-2, blaCTX-M-15, blaOXA-1, blasul1, aac(6’)-Ib-cr, aph(3’)-Ia, qnrS1, gyrA (S83I), parC (S800).**

**The IncFIB(K) plasmid, named pPVT01_P2, harboured blaOXA-1, blaGTX-M-15, aac(3)-IIa, aadA2, aph(3’)-Ia, mphA, sul and dfA12, whereas Col4401-like plasmid (pPVT01_P2) harboured blacma1, blalap2, qnrS1 and aac(6’)-lb-cr resistance genes.**
Total genomic DNA was extracted and sequenced using long-read (MinION, Oxford Nanopore) and short-read (NextSeq, Illumina) sequencing technologies. Hybrid de novo assembly was performed using Unicycler v0.4.8 (https://github.com/rrwick/Unicycler), whereas Mlplasmids (https://sarredondo.shinyapps.io/mlplasmids/) was used to predict plasmid and chromosome-derived sequences (Arredondo-Alonso et al., 2018). Genome sequences were annotated with NCBI PGAP v.3.2 (http://www.ncbi.nlm.nih.gov/annotation_prok/). ABRicate v0.9.8 (https://github.com/tseemann/abricate), with ResFinder 4.1 (https://cge.cbs.dtu.dk/services/ResFinder/) and PlasmidFinder 2.1 (https://cge.cbs.dtu.dk/services/PlasmidFinder/) databases, and Kleborate (https://github.com/kathit/Kleborate) were used for prediction of resistome, plasmidome, species confirmation, multilocus sequence type (ST), virulence loci, and K (capsule) and O antigen (LPS) serotypes (Lam et al., 2018; Wick et al., 2018; Wyres et al., 2016). The nucleotide sequences of K. pneumoniae strain PVT01 were deposited at GenBank under accession number JABSUB000000000.1.

3 | RESULTS AND DISCUSSION

The PVT01 strain exhibited a multidrug-resistant (MDR) profile (Magiorakos et al., 2012) to amoxicillin/clavulanic acid, aztreonam, ceftriaxone, ceftazidime, cefotaxime, cefepime, cefidiomor, ertapenem, imipenem, meropenem, amikacin, gentamicin, sulfamethoxazole/trimethoprim, enrofloxacin, ciprofloxacin, nalidixic acid and chloramphenicol, remaining susceptible to tetracycline and colistin (Table 1). ESBL and carbapenemase production were confirmed by the phenotypic tests. Additionally, the PVT01 strain displayed a hypermucoviscous phenotype, as defined by a positive string test (i.e. viscous filament ≥ 5 mm in length).

Resistome analysis revealed a MDR genotype to β-lactams, quinolones, aminoglycosides, sulfamethoxazole/trimethoprim, fosfomycin, macrolides and chloramphenicol (Table 1). Moreover, genes encoding for yersiniabactin siderophore synthesis (ybt, fyuA and irp genes) (Paczoza & Mecsas, 2016), and KL15 (wzi50 and O4 loci were identified (Wyres et al., 2016).
Hybrid assembly revealed three resistance plasmids: IncFIB(K) (168-kb), IncN (54-kb) and Col4401-like (76-kb). The IncFIB(K) plasmid, named pPVT01_P1, harboured blaCTX-M-15, aac(3)-Ia, aadA2, aph(3')-Ia, mphpA, sul1 and dfrA12, whereas Col4401(76-kb)-like plasmid (pPVT01_P2) harboured blaOXA-1, blaLAP-2, qnrS1 and aac(6')-Ib-cr resistance genes. Specifically, the blaKPC-2 gene was carried by the 54-kb IncN plasmid (named pPVT01_P3) assigned to ST15 by pMLST typing and located on a Tn4401 transposon > 99% identical to Tn4401b isoform (GenBank accession number: EU176012). The plasmid pPVT01_P3 (GenBank accession number: JABSUB010000003.1) shared 99.8 and 96.8% pairwise identity with pKPC_FCF/3SP and pKP148 IncN-pST15 plasmids (GenBank accession numbers: CP004367.2 and KX062091.1), previously identified in human and environmental K. pneumoniae strains belonging to ST442 (Pérez-Chaparro et al., 2014) and ST437, respectively (Oliveira et al., 2014) (Figure 1). Strikingly, all these K. pneumoniae strains come from an area with high endemicity of KPC-2 (Sampaio & Gales, 2016), highlighting the widespread and adaptation of IncN-pST15 plasmids carrying blaKPC-2 at the human-animal-environment interface (Rada et al., 2020), and addressing a One-Health implication to the problem of rapid dissemination of KPC-2-producing K. pneumoniae. In fact, K. pneumoniae PVT01 belonged to ST11/CG258, recognized as an international high-risk clone linked to the epidemiological success of pandemic KPC carbapenemases in nosocomial settings (Bialek-Davenet et al., 2014; Kelly et al., 2017; Rojas et al., 2017; Wyres & Holt, 2018). Worryingly, adaptation of ST11 to veterinary settings has been documented in European and Asian countries (Donati et al., 2014; Hidalgo et al., 2013; Loncaric et al., 2016; Mairi et al., 2020; Ovejero et al., 2017; Pilo et al., 2015; Schmidt et al., 2020; Wang et al., 2020; Wohlwend et al., 2015; Zhang et al., 2019), with KPC-2-positive ST11 only being reported in horse (Wang et al., 2020) and swine (Zhang et al., 2019) in China, so far.

In summary, to the best of our knowledge, this is the first report of KPC-positive K. pneumoniae ST11/CG258 isolated from a pet. The emergence of KPC-2-producing bacteria in companion animals is an important public health issue that denotes that pets are a neglected reservoir for critical priority pathogens in the community, and susceptible hosts for acquisition of untreatable or difficult-to-treat infections (Abraham et al., 2014; Sürek et al., 2018; Pomba et al., 2017; Sellera & Lincopan, 2019). In this regard, IncN-pST15 plasmids conferring carbapenem resistance can play as important a role as clonal transmission of K. pneumoniae, representing another major challenge for One Health. Therefore, surveillance studies should investigate similarities of plasmids circulating at the human-environment-animal interface in addition to clonal transmission.

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**CONFLICT OF INTEREST**

The authors have no conflict of interest to declare.

**ETHICAL APPROVAL**

The authors confirm that the ethical policies of the journal, as noted on the journal's author guidelines page, have been adhered to. No ethical approval was required for this specific study.

**DATA AVAILABILITY STATEMENT**

All data generated or used during the study appear in the submitted article. The data that support the findings of this study are available from the corresponding author upon reasonable request. The whole genome nucleotide sequence of the K. pneumoniae PVT01 strain is available in the GenBank database under accession number JABSUB000000000.1. Genomic data of K. pneumoniae strain PVT01 is also available on the OneBR platform (http://onehealthbr.com/) under the number ID ONE247.

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**REFERENCES**

Abraham, S., Wong, H. S., Turnidge, J., Johnson, J. R., & Trott, D. J. (2014). Carbapenemase-producing bacteria in companion animals: A public health concern on the horizon. *Journal of Antimicrobial Chemotherapy, 69*, 1155–1157. [https://doi.org/10.1093/jac/dkt158](https://doi.org/10.1093/jac/dkt158)

Arredondo-Alonso, S., Rogers, M. R. C., Braat, J. C., Verschuuren, T. D., Top, J., Corander, J., Willems, R. J. L., & Schürch, A. C. (2018). Mlplasmids: A user-friendly tool to predict plasmid-and chromosome-derived sequences for single species. *Microbial Genomics, 4*, e000224. [https://doi.org/10.1099/mgen.0.000224](https://doi.org/10.1099/mgen.0.000224)

Baquero, F., Coque, T. M., Martínez, J. L., Aracil-Gisbert, S., & Lanza, V. F. (2019). Gene transmission in the One Health microbiosphere and the channels of antimicrobial resistance. *Frontiers in Microbiology, 10*, 2892. [https://doi.org/10.3389/fmicb.2019.02892](https://doi.org/10.3389/fmicb.2019.02892)

Bialek-Davenet, S., Criscuolo, A., Ailloud, F., Passet, V., Jones, L., Delannoy-Vieillard, A. S., & Brisse, S. (2014). Genomic definition of hypervirulent and multidrug-resistant *Klebsiella pneumoniae* clonal groups. *Emerging Infectious Diseases, 20*, 1812–1820. [https://doi.org/10.3201/eid2011.140206](https://doi.org/10.3201/eid2011.140206)

Brandt, C., Viehweger, A., Singh, A., Pletz, M. W., Wibberg, D., Kalinowski, J., Lerch, S., Müller, B., & Makarewicz, O. (2019). Assessing genetic diversity and similarity of 435 KPC-carrying plasmids. *Scientific Reports, 9*, 11223. [https://doi.org/10.1038/s41598-019-47758-5](https://doi.org/10.1038/s41598-019-47758-5)

Clinical and Laboratory Standards Institute (2018). *Performance standards for antimicrobial disk and dilution susceptibility tests for bacteria isolated from animals*. CLSI Supplement VET08, 4th ed. CLSI.

Clinical and Laboratory Standards Institute (2020). *Performance standards for antimicrobial susceptibility testing: Fifteenth informational supplement*. CLSI document M100-S30. CLSI.
in Akfadou Forest, Algeria. *Journal of Global Antimicrobial Resistance*, 22, 515–518. https://doi.org/10.1016/j.jgar.2020.04.027

Oliveira, S., Moura, R. A., Silva, K. C., Pavez, M., McCulloch, J. A., Dropa, M., Matte, M. H., Mamizuka, E. M., Sato, M. I. Z., Pestana de Castro, A. F., & Lincopan, N. (2014). Isolation of KPC-2-producing *Klebsiella pneumoniae* strains belonging to the high-risk multiresistant clonal complex 11 (ST437 and ST340) in urban rivers. *Journal of Antimicrobial Chemotherapy*, 69, 849–852. https://doi.org/10.1093/jac/dkt431

Ovejero, C. M., Escudero, J. A., Thomas-Lopez, D., Hoefer, A., Moyano, G., Montero, N., Martin-Espada, C., & Gonzalez-Zorn, B. (2017). Highly tigecycline-resistant *Klebsiella pneumoniae* sequence type 11 (ST11) and ST147 isolates from companion animals. *Antimicrobial Agents and Chemotherapy*, 61, e02640–e2716. https://doi.org/10.1128/AAC.02640-16

Paccosa, M. K., & Mecساس, J. (2016). *Klebsiella pneumoniae*: Going on the offense with a strong defense. *Microbiology and Molecular Biology Reviews*, 80, 629–661. https://doi.org/10.1128/MMBR.00078-15

Perez-Chaparro, P. J., Cerdeira, L. T., Queiroz, M. G., de Lima, C. P. S., Levy, C. E., Pavez, M., Lincopan, N., Goncalves, E. C., Mamizuka, E. M., Sampaio, J. L. M., Nunes, M. R. T., & McCulloch, J. A. (2014). Complete nucleotide sequences of two bla<sub>KPC</sub>-bearing IncN plasmids isolated from sequence type 442 *Klebsiella pneumoniae* clinical strains four years apart. *Antimicrobial Agents and Chemotherapy*, 58, 2958–2960. https://doi.org/10.1128/AAC.02341-13

Pilo, P., Vogt, D., Origg, F. C., Endimiani, A., Peterson, S., & Perreten, V. (2015). First report of a multidrug-resistant *Klebsiella pneumoniae* of sequence type 11 causing sepsis in a free-ranging beaver (Castor fiber). *Environmental Microbiology Reports*, 7, 351–353. https://doi.org/10.1111/1758-2229.12257

Pomba, C., Rantalata, M., Greko, C., Baptiste, K. E., Catry, B., van Duijkeren, E., Mateus, A., Moreno, M. A., Pyöälä, L., Ružauskas, M., Sanders, P., Teale, C., Threlfall, E. J., Kunsagi, Z., Torren-Edo, J., Jukes, H., & Törnke, K. (2017). Public health risk of antimicrobial resistance transfer from companion animals. *Journal of Antimicrobial Chemotherapy*, 72, 957–968. https://doi.org/10.1093/jac/dkw481

Rada, A. M., De La Cadena, E., Agudelo, C., Capataz, C., Orozco, N., Pallares, C., & Restrepo, E. (2020). Dynamics of bla<sub>KPC2</sub> dissemination from non-CG258 *Klebsiella pneumoniae* to other Enterobacteriales via IncN plasmids in an area of high endemicity. *Antimicrobial Agents and Chemotherapy*, 64, e01743–e1820. https://doi.org/10.1128/AAC.01743-20

Rojas, L. J., Weinstock, G. M., De La Cadena, E., Díaz, L., Rios, R., Hanson, B. M., Brown, J. S., Vats, P., Phillips, D. S., Nguyen, H., Hujer, K. M., Correa, A., Adams, M. D., Perez, F., Sodergren, E., Narechania, A., Planet, P. J., Villegas, M. V., Bonomo, R. A., & Arias, C. A. (2017). An analysis of the epidemic of *Klebsiella pneumoniae* carbapenemase-producing *K. pneumoniae*: Convergence of two evolutionary mechanisms creates the “perfect storm”. *Journal of Infectious Diseases*, 217, 82–92. https://doi.org/10.1093-infdis/jix524

Sampaio, J. L., & Gales, A. C. (2016). Antimicrobial resistance in *Enterobacteriaceae* in Brazil: Focus on β-lactams and polymyxins. *The Brazilian Journal of Microbiology*, 47, 31–37. https://doi.org/10.1016/j.bjm.2016.10.002

Schmidt, J. S., Kuster, S. P., Nigg, A., Dazio, V., Brilhante, M., Rohrbach, H., Bernasconi, O. J., Büdel, T., Campos-Madueno, E. I., Gobelli Bravand, S., Schuller, S., Endimiani, A., Perreten, V., & Willi, B. (2020). Poor infection prevention and control standards are associated with environmental contamination with carbapenemase-producing Enterobacteriales and other multidrug-resistant bacteria in Swiss companion animal clinics. *Antimicrobial Resistance and Infection Control*, 9, 93. https://doi.org/10.1186/s13756-020-00742-5

Sellera, F. P., Fernandes, M. R., Ruiz, R., Falleiros, A. C. M., Rodrigues, F. P., Cerdeira, L., & Lincopan, N. (2018). Identification of KPC-2-producing *Escherichia coli* in a companion animal: A new challenge
for veterinary clinicians. Journal of Antimicrobial Chemotherapy, 73, 2259–2261. https://doi.org/10.1093/jac/dky173

Sellera, F. P., & Lincopan, N. (2019). Zooanthroponotic transmission of high-risk multidrug-resistant pathogens: A neglected public health issue. Journal of Infection and Public Health, 12, 294–295. https://doi.org/10.1016/j.jiph.2018.12.013

Shon, A. S., Bajwa, R. P., & Russo, T. A. (2013). Hypervirulent (hypemucoviscous) Klebsiella pneumoniae: A new and dangerous breed. Virulence, 4, 107–118. https://doi.org/10.4161/viru.22718

Tsakris, A., Themeli-Digalaki, K., Poulou, A., Vrioni, G., Voulgaris, E., Kounaki, V., Agodi, A., Pournaras, S., & Sofianou, D. (2011). Comparative evaluation of combined-disk tests using different boronic acid compounds for detection of Klebsiella pneumoniae carbapenemase-producing Enterobacteriaceae clinical isolates. Journal of Clinical Microbiology, 49, 2804–2809. https://doi.org/10.1128/JCM.00666-11

van Duin, D., & Doi, Y. (2017). The global epidemiology of carbapenemase-producing Enterobacteriaceae. Virulence, 8, 460–469. https://doi.org/10.1080/21505594.2016.1222343

Wang, H., Li, X., & Liu, B. T. (2020). Occurrence and characterization of KPC-2-producing ST11 Klebsiella pneumoniae isolate and NDM-5-producing Escherichia coli isolate from the same horse of equestrian clubs in China. Transboundary and Emerging Diseases, [Epub ahead of print]. https://doi.org/10.1111/tbed.13614

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Wick, R. R., Heinz, E., Holt, K. E., & Wyres, K. L. (2018). Kaptive web: User-friendly capsule and lipopolysaccharide serotype prediction for Klebsiella genomes. Journal of Clinical Microbiology, 56, e00197-e218. https://doi.org/10.1128/JCM.00197-18

Wohlwend, N., Endimiani, A., Francey, T., & Perreten, V. (2015). Third-generation-cephalosporin-resistant Klebsiella pneumoniae isolates from humans and companion animals in Switzerland: Spread of a DHA-producing sequence type 11 clone in a veterinary setting. Antimicrobial Agents and Chemotherapy, 59, 2949–2955. https://doi.org/10.1128/AAC.04408-14

Wyres, K. L., & Holt, K. E. (2018). Klebsiella pneumoniae as a key trafficker of drug resistance genes from environmental to clinically important bacteria. Current Opinion in Microbiology, 45, 131–139. https://doi.org/10.1016/j.mib.2018.04.004

Wyres, K. L., Wick, R. R., Gorrie, C., Jenney, A., Follador, R., Thomson, N. R., & Holt, K. E. (2016). Identification of Klebsiella capsule synthesis loci from whole genome data. Microbial Genomics, 2, e000102. https://doi.org/10.1099/mgen.0.000102

Zhang, W., Zhu, Y., Wang, C., Liu, W., Li, R., Chen, F., & Liu, S. (2019). Characterization of a multidrug-resistant porcine klebsiella pneumoniae sequence type 11 strain cohaboring blaKPC-2 and fosA3 on two novel hybrid plasmids. mSphere, 4, e00590-e619. https://doi.org/10.1128/mSphere.00590-19