

Emergence of *Klebsiella pneumoniae* ST307 Co-Producing CTX-M with SHV and KPC from Paediatric Patients at Shenzhen Children's Hospital, China

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Aim: We investigated the clonal diversity of carbapenemase-producing *Klebsiella pneumoniae* isolates from the Shenzhen Children's Hospital, China, and drew conclusions on the clinical and public health impact of these isolates as multidrug-resistant.

Methods: From January 2014 to December 2018, a total number of 36 unique carbapenemase-producing clinical isolates of *Klebsiella pneumoniae* were collected out of 900 clinical isolates in paediatric patients from the Shenzhen Children's Hospital, China. After carbapenemase production confirmation, antimicrobial susceptibility, resistance determinants and phylogenetic relationship were determined.

Results: The isolates showed resistance to ceftazidime, ertapenem, ampicillin, cefazolin, ceftriaxone, cefotetan, ticarcillin, cefaclor, cefpodoxime, azlocillin, cefcapene, mezlocillin and ampicillin-sulbactam. Of the 36 *Klebsiella pneumoniae* carbapenemase genes coding isolates, *bla*_{NDM} was the mostly detected 50% (n=18) followed by *bla*_{KPC} and *bla*_{IMP} 19% (n=7), *bla*_{VIM} 17% (n=6), *bla*_{OXA-48-like} 8% (n=3) and *bla*_{SME} 5% (n=2), whereas extended-spectrum β-lactamase (*bla*_{SHV}) was predominantly detected 92% (n=33) followed by *bla*_{CTX-M} 53% (n=19) and *bla*_{CMY} 28% (n=10). Pulsed-field gel electrophoresis typing showed eight different patterns, and twenty-five distinct sequences types were observed with ST307 being predominantly identified 11% (n=4), followed by ST2407 8% (n=3). Plasmid replicon typing results indicated that IncFIS, IncHI2, IncFIC and IncFIA plasmids carry *bla*_{CTX-M}, *bla*_{SHV} and *bla*_{NDM} genes.

Conclusion: This study reports on the occurrence and spread of carbapenemase and extended-spectrum β-lactamase encoding genes co-existence in sporadic *Klebsiella pneumoniae* ST307 in paediatric patients from the Shenzhen Children's Hospital, China.

Keywords: *Klebsiella pneumoniae*, carbapenemase, ESBLs, antimicrobial susceptibility, molecular characterization

Introduction

The rise and spread of antimicrobial resistance bacteria are universal symbolic challenges for healthcare due to the restricted treatment choices.¹ In the past year, carbapenem-resistant *Klebsiella pneumoniae* (CRKP) infections have become a growing of global public health concern, particularly in paediatric patients, due to high morbidity and mortality.² Carbapenemase enzymes encoded by alleles of the *bla*_{KPC} gene, depict one of the five substantial carbapenemase families, others being the VIM, IMP and New Delhi metallo-β-lactamase (MBL) (NDM), also, the OXA-48-like oxacillinases have

mezlocillin, trimethoprim, aztreonam, and ciprofloxacin. Colistin susceptibility was performed by the disc diffusion method. To further ascertain the antimicrobial susceptibility, we used CIM disc to detect carbapenemase enzyme, where the disc was removed from the suspension and placed onto a Mueller-Hinton agar (MHA) plate, seeded with an ATCC25922 indicator organism, followed by overnight incubation. The results were construed according to the Clinical and Laboratory Standards Institute (CLSI) guideline (CLSI, 2019)¹⁶ and EUCAST 2016.¹⁸

Detection of Carbapenemase Encoding Genes

The standard PCR was used to detect the presence of carbapenemase encoding genes. Class-A includes *bla*_{IMI}, *bla*_{GES}, *bla*_{SME} and *bla*_{KPC}, while Class-B consists of *bla*_{IMP}, *bla*_{VIM}, *bla*_{GIM}, *bla*_{SIM} and *bla*_{NDM} and Class-D made up of *bla*_{OXA-48} like using specific primers as previously described.¹⁹⁻²¹ In addition, PCR assay was carried out for other β -lactamase encoding genes: *bla*_{CTX-M-(variant)}, *bla*_{SHV}, *bla*_{CMY}, *bla*_{TEM} and *bla*_{VEB} by using specific primers as described earlier.²² Control strain, which was selected from the characterized strain collection of our laboratory. The private company (Sangon Biotech-Shanghai, China) sequenced the purified PCR products. DNA sequences were analyzed using the following URLs <https://blast.ncbi.nlm.nih.gov/Blast.cgi>, <http://www.bldb.eu:4567/> and <https://bigsdtpasteur.fr/klebsiella/klebsiella.html>.

PFGE and Multi-Locus Sequence Typing (MLST)

We performed PFGE to check whether there is a presence of any clonal transmission within the Hospital. Furthermore, we used the MLST to assess the genetic relatedness of the identified isolates.

DNA Extraction Details

Post-extraction DNA was digested with 45U *Xba*I (Takara Biotech) for 2 hours at 37°C. We used CHEFDRIII apparatus (Bio-Rad Laboratories, Hercules, CA, USA) to perform PFGE for *K. pneumoniae* isolates as previously described.²³ PCR assay was performed to amplify internal portions of the seven housekeeping genes of *K. pneumoniae* (*gapA*, *infB*, *mdh*, *pgi*, *phoE*, *rpoB*, and *tonB*) with specific primers.²⁴ Amplified products were sequenced from private enterprise (Sangon Biotech-Shanghai, China <http://www.pas>

[teur.fr/recherche/genopole/PF8/mlst/Kpneumoniae](http://www.pas-teur.fr/recherche/genopole/PF8/mlst/Kpneumoniae)) and were referred to assign sequence types (STs).

Plasmid Transferability

Streptomycin-resistant *E. coli* C₆₀₀ was used as the recipient strain in conjugation experiments to analyze the horizontal genes transformation of plasmid-borne β -lactamase encoding genes in CRKP isolates, using liquid mating assay as previously described.¹⁴ Transconjugants were selected using Luria Bertani agar containing streptomycin 2000 (μ g/mL), ampicillin (100 μ g/mL) and cefotaxime (32 μ g/mL). Therefore, we further tested them using PCR for β -lactamase encoding genes after performing a phenotypic combination disc test.

PCR-Based Replicon Typing

PCR-based replicon typing was performed for both plasmids from parental and transconjugant isolates. The Inc (incompatibility) groups were determined by using a specific primer as previously described by Carattoli et al 2005.²⁵

Results

Antimicrobial Resistance Profile of *K. pneumoniae*

All the 36 isolates were identified as *K. pneumoniae* using API20E (Biomérieux, Ref. No. 27530/275660) automated system and were further confirmed using 16s RNA gene sequencing. Antimicrobial susceptibility tests were found in all the 36 CRKP isolates (100%) and were all resistant to ceftazidime, ertapenem, ampicillin, cefazolin, ceftriaxone, cefotetan, ticarcillin, cefaclor, cefpodoxime, azlocillin, cefcapene, mezlocillin and ampicillin-sulbactam. However, aztreonam showed 89% (n=32), piperacillin 86% (n=31), cefepime 83% (n=30), imipenem 80% (n=29), nitrofurantoin 47% (n=17), trimethoprim 44% (n=16), ciprofloxacin, gentamicin, levofloxacin 30% (n=11), tobramycin 25% (n=9), amikacin 11% (n=4). All isolates were susceptible to colistin (Figure 1), and the 36 CRKP isolates showed a multi-drug resistant phenotype, hence designated as “superbugs”.

Molecular Analysis of Drug Resistance Genes

All the 36 CRKP isolates were carrying carbapenemase encoding genes, with the most common being *bla*_{NDM} 50% (n=18) which include *bla*_{NDM-1} (n=13), *bla*_{NDM-6} (n=3) and *bla*_{NDM-5} (n=2); followed by *bla*_{IMP} 19%

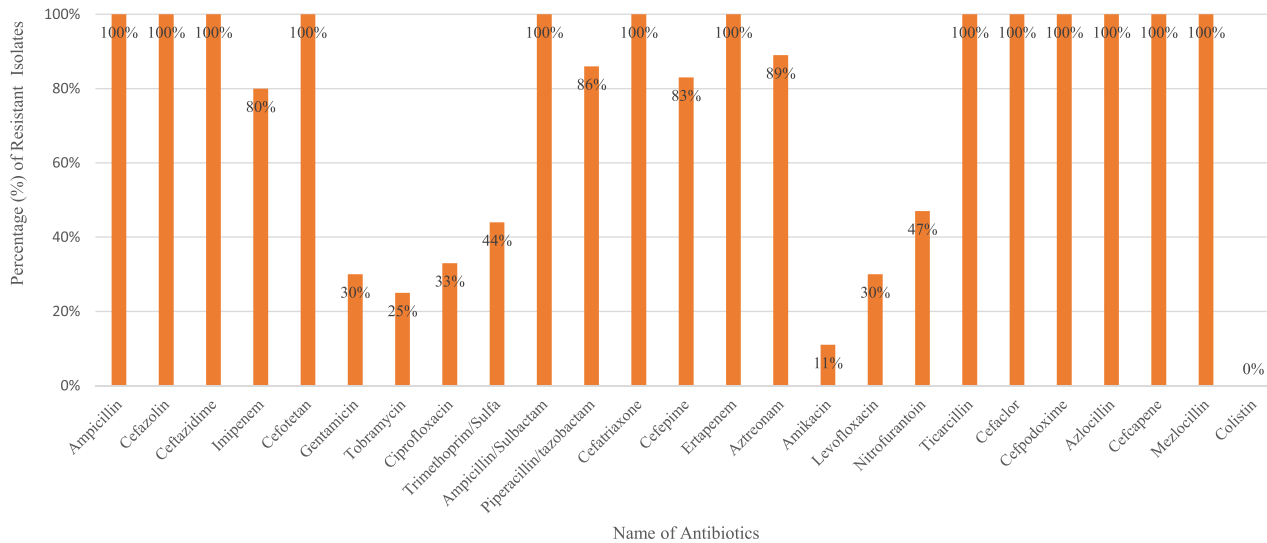


Figure 1 Antimicrobial resistance patterns of 25 commonly used antibiotics against 36 carbapenemase-producing *Klebsiella pneumoniae* isolates from paediatric clinical cases.

(n=7) including *bla*_{IMP-38} (n=5) and *bla*_{IMP-4} (n=2), *bla*_{KPC-2} 19% (n=7), *bla*_{VIM-2} 17% (n=6), *bla*_{OXA-48} and *bla*_{SME-1} 8% (n=3) each. Additionally, co-existences of other β-lactamases encoding genes were detected in *bla*_{SHV} 92% (n=33), contains *bla*_{SHV-11}

(n=15), *bla*_{SHV-1} (n=13), *bla*_{SHV-27} (n=3), *bla*_{SHV-26} and *bla*_{SHV-33} (n=1), *bla*_{CTX-M} (n=19), *bla*_{CTX-M-3} (n=11), *bla*_{CTX-M-15} (n=5), *bla*_{CTX-M-14}, 26, 40, (n=1 each), *bla*_{CMY-2} 28% (n=10) (Figure 2). The *bla*_{IMI}, *bla*_{GES}, *bla*_{GIM}, *bla*_{SIM} carbapenemase encoding genes

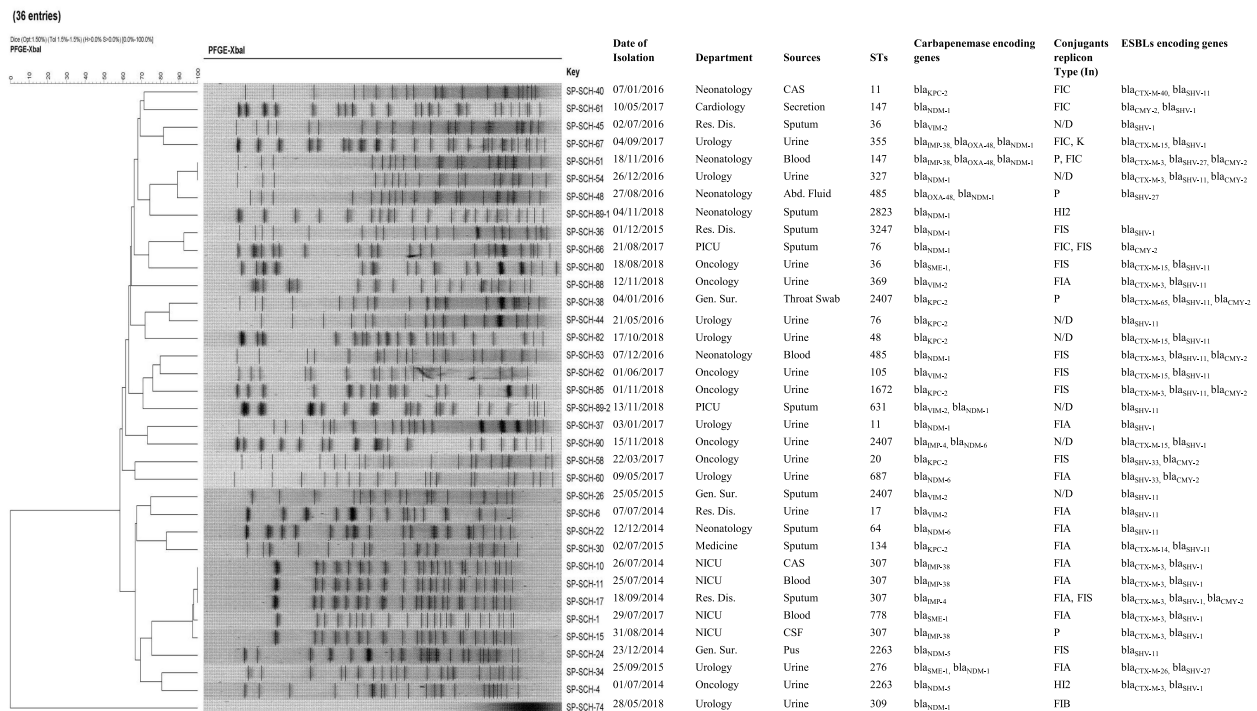


Figure 2 Dendrogram of the 36-PFGE-XbaI identified CRKP isolates collected from paediatric patients showing their genetic relatedness by date of isolation, department of isolation, sources of specimen, sequences types, replicon type, resistant determinants and clonal relatedness.

and ESBLs encoding genes *bla*_{TEM}, *bla*_{VEB} were not observed in this study. It is interesting that approximately 53% (n=19) of CRKP strains co-harboring ESBLs encoding genes *bla*_{CTX-M-variant} were found in *bla*_{SHV-variant}, with this, at least 50% of strains were carrying *bla*_{NDM-variant}.

Multi-Locus Sequences Typing and PFGE

Extensive diversity of MLST was recorded from CRKP isolates. In 25 different STs, we found that ST307 isolates (11%) were recovered from the neonatal intensive care unit (NICU). ST2407 (8%) was found to be highly prevalent and were collected from the general surgery department (GSD). In addition, we found that CRKP ST307 was dominant in NICU and in a reservoir of *bla*_{CTX-M-3} and *bla*_{SHV-11}. However, ST2407 was predominantly in GSD, which is a key transporter for *bla*_{CTX-M-15}, and *bla*_{SHV-11} gene and ST2263 a key transporter for *bla*_{NDM-5}. Nevertheless, *bla*_{KPC-2} was reported in diverse STs (Figure 2). Our particular concern is that the CRKP co-harboring ESBLs encoding genes *bla*_{CTX-M-variant} and *bla*_{SHV-variant} were reported in seventeen different STs in this hospital. This observation suggests that CRKP strains carrying ESBLs encoding genes might have spread to the Shenzhen region and may be widespread in Southern China. These 36 CRKP isolates were allocated to eight distinct PFGE clusters, sharing $\geq 80\%$ of similar bands. The PFGE results showed that the clonal transmission was often observed within different departments of the Hospital (Figure 2).

Plasmid Profiling

In total, 18 out of 36 successful transconjugants were selected using Luria Bertani agar. PCR-based replicon typing assay results showed that Inc plasmids groups lead was IncFIA 55% (n=10), followed by IncFIS 50% (n=9), IncFIC 27% (n=5), IncP 22% (n=4), IncHI2 11% (n=2), while IncK and IncFIB showed 6% (n=1) (Figure 2).

Discussion

CRKP is a serious threat in paediatric patients, particularly newborns, due to limited therapeutic options.^{26,27} This pathogen is now considered as a reservoir for virulent and resistant genes, due to the acquisition of β -lactamase (carbapenemase and ESBLs) and the recently reported colistin resistance *mcr-1* encoding genes; which make it a serious threat to human and

animal.^{28–30} These data revealed for the first time that NDM carbapenemase is widely spread among CRKP, while CTX-M and SHV were the most prevalent β -lactamase in same isolates in Shenzhen's children Hospital, China. So far, there are no data available on molecular analysis of CRKP in paediatric clinical cases, particularly those caused by IMP or NDM co-production of CTX-M and SHV. Here, we first explored the genetic background of CRKP isolates obtained from the paediatric samples. Data showed that CRKP isolates were highly resistant to commonly used antibiotics, except for colistin. We also found that IMP-38 producing *K. pneumoniae* isolates are significantly sensitive to Imipenem, which is in agreement with studies reported in Australia, however further investigation is required.³¹ *bla*_{NDM-1} was found to be the leading genotype of carbapenemase followed by *bla*_{KPC-2}, *bla*_{VIM-2}, *bla*_{IMP-4}, *bla*_{NDM-6}, *bla*_{SME-1}, *bla*_{oxa-48}, *bla*_{IMP-2}, and *bla*_{NDM-5}. A previous study reported the presence of NDM-1 dominant carbapenemase in carbapenem-resistant *K. pneumoniae* over China, which is comparable to our results.³² There were no cases with co-harboring *bla*_{NDM-1} and *bla*_{IMP-4} strain, which is in contrast with Liu et al's finding.³³ Interestingly, nineteen CRKPs were found to contain *bla*_{CTX-M} encoding determinants. To the best of our knowledge, this is the first report on an MDR CRKP isolates co-harboring *bla*_{NDM}, *bla*_{CTX-M} and *bla*_{SHV} has flagged concerns about the spread of such superbugs in the Shenzhen region, China; but also, studies have reported similar results from other provinces of China, Chongqing and Shanghai.^{34,35} The MLST results revealed that *K. pneumoniae* ST307 and ST2407 were highly dominant in Shenzhen area, which encodes carbapenemase and ESBLs genes. Several countries such as Italy, Korea, USA, Mexico, and China have reported CRKP ST307 with ESBLs production.^{36–40} No study has yet reported that the isolate CRKP belonged to ST307 in the Southern region of China. The emergence of this isolate indicates the rapid spread of this isolate. Also, studies have reported the existence of CRKP belonged to ST2407. Data also report the presence of CRKP belonged to ST2407; to the best of our knowledge, no study has yet reported the presence of CRKP ST2407 isolates that exist with ESBLs in Southern China. Our finding of CRKP belonged to ST307 and ST2407 isolates, identify a substantial public health concern.

Clonal dissemination within the hospital corresponded with a previous study by Tian et al 2018 in Shanghai Province, China.⁴¹ We did not analyze isolates from other hospitals to observe whether there was clonal transmission between the hospitals. Plasmid replicon typing and conjugation experiment results conferred that IncFIA, IncFIS, IncFIC, IncHI2, IncFIB, IncK and IncP replicons existed in the transconjugants and carbapenemase coding genes (*bla*_{KPC-2}, and *bla*_{NDM-variants}) co-transferred with ESBLs encoding genes (*bla*_{CTX-M-variant} and *bla*_{SHV-variant}). No apparent relationship between replicon and sequence type was observed in the current isolates. Also, data of Figure 2 show the presence of some previously published isolates with co-production of carbapenemases, which requires further analysis as these isolates could be of clinical concern. Previously published study has done successful clone for KPC such as the clone group GC258,⁴² nevertheless from our 36 KPC isolates reported in our study, none of them corresponded to the clone group GC258. And we did not find the dissemination of any particular clones at the hospital in Shenzhen, China. Our finding stresses out the importance of continuous monitoring to detect multi-drug resistant isolates to promote therapeutic strategies for infections in paediatric patients. Future studies may assess the presence of other resistance-related determinants by using WGS, such as the outer-membrane permeability and to augment sample size from different areas for the molecular study. It is also worth reporting here that although the methods used in our study are adequate, one of the potential limitations of this study is the lack of use of broth micro-dilution susceptibility testing method or the Clinical and Laboratory Standards Institute recommended disk elution method for colistin.

Conclusion

This study reports, for the first time, the emergence of CPKP ST307 co-producing CTX-M with SHV and KPC in paediatric patients from the Shenzhen's Children Hospital in China. Also, our results identify the occurrence of CRKP ST2407 belongs to co-producing CTX-M with SHV and KPC. The emergence of CPKP in our study highlights a substantial global concern, both within hospitals and the wider community. Continued appraisal of clinical experience and monitoring of the spread of CPKP will provide further important information on the emergence of CPKP ST307.

Abbreviations

Res. Dis., respiratory diseases; PICU, paediatric intensive care unit; Gen. Sur., general surgery; NICU, neonatal intensive care unit; CAS, catheter associated secretion; Abd., abdominal; CSF, cerebral spinal fluid; STs, sequences type; In, Incompatibility; N/D, not detected.

Data Sharing Statement

All data files mentioned in this manuscript have been submitted and are available.

Ethics Approval and Consent to Participate

The present study was approved by the Shenzhen Children's Hospital, Research Ethical Committee, reference number: 2018 (013).

Consent for Publication

The clinical isolate samples used in this research were part of the routine Hospital Laboratory procedure. We do not use patients' name or personal information, so in the publication, no written consent was required. Verbal consent was freely taken from the patients' parents after being duly informed of its nature.

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Author Contributions

All authors made a significant contribution to the work reported, whether that is in the conception, study design, execution, acquisition of data, analysis and interpretation, or in all these areas; took part in drafting, revising or critically reviewing the article; gave final approval of the version to be published; have agreed on the journal to which the article has been submitted; and also agree to be accountable for all aspects of the work.

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Disclosure

The authors report no conflicts of interest in this work.

References

- Munoz-Price L, Poirel L, Bonomo R, et al. Clinical epidemiology of the global expansion of *Klebsiella pneumoniae* carbapenemases. *Lancet Infect Dis.* 2013;13(9):785–796. doi:10.1016/S1473-3099(13)70190-7
- Zhu J, Sun L, Ding B, et al. Outbreak of NDM-1-producing *Klebsiella pneumoniae* ST76 and ST37 isolates in neonates. *Eur J Clin Microbiol Infect Dis.* 2016;35(4):611–618. doi:10.1007/s10096-016-2578-z
- Chang-Ro L, Jung L, Kwang P, Young K, Byeong J, Sang L. Global dissemination of carbapenemase-producing *Klebsiella pneumoniae*: epidemiology, genetic context, treatment options, and detection methods. *Front Microbiol.* 2016;7:895. doi:10.3389/fmicb.2016.00895
- Eva H, Hasan E, Josefin S, et al. Resistance mechanisms and population structure of highly drug resistant *Klebsiella* in Pakistan during the introduction of the carbapenemase NDM-1. *Sci Rep.* 2019;9(1):2392. doi:10.1038/s41598-019-38943-7
- Zhou J, Li G, Ma X, Yang Q, Yi J. Outbreak of colonization by carbapenemase-producing *Klebsiella pneumoniae* in a neonatal intensive care unit: investigation, control measures and assessment. *Am J Infect Control.* 2015;43(10):1122–1124. doi:10.1016/j.ajic.2015.05.038
- Hasan E, Nancy W, Jonathan J, et al. Phylogenetic analysis of *Klebsiella pneumoniae* from hospitalized children, Pakistan. *Emerg Infect Dis.* 2017;23(11):1872–1875. doi:10.3201/eid2311.170833
- Patrice N, Thierry N, Poirel L. Global spread of carbapenemase producing *Enterobacteriaceae*. *Emerg Infect Dis.* 2011;17(10):1791–1798. doi:10.3201/eid1710.110655
- Poirel L, Hombrouk-Alet C, Freneaux C, Bernabeu S, Nordmann P. Global spread of New Delhi metallo- β -lactamase. *Lancet Infect Dis.* 2010;10(12):832. doi:10.1016/S1473-3099(10)70279-6
- Cuzon G, Ouanich J, Gondret R, Naas T, Nordmann P. Outbreak of OXA-48-positive carbapenem-resistant *Klebsiella pneumoniae* isolates in France. *Antimicrob Agents Chemother.* 2011;55(5):2420–2423. doi:10.1128/AAC.01452-10
- Zhang X, Li X, Wang M, et al. Outbreak of NDM-1-producing *Klebsiella pneumoniae* causing neonatal infection in a teaching hospital in mainland China. *Antimicrob Agents Chemother.* 2015;59(7):4349–4351. doi:10.1128/AAC.03868-14
- Hu F, Guo Y, Zhu D, et al. Resistance trends among clinical isolates in China reported from CHINET surveillance of bacterial resistance, 2005–2014. *Clin Microbiol Infect.* 2016;22:S9–S14. doi:10.1016/j.cmi.2016.01.001
- Findlay J, Hopkins L, Loy R, et al. OXA-48-like carbapenemases in the UK: an analysis of isolates and cases from 2007 to 2014. *J Antimicrob Chemother.* 2017;72(5):1340–1349. doi:10.1093/jac/dkx012
- Yin D, Dong D, Li K, et al. Clonal dissemination of OXA-232 carbapenemase-producing *Klebsiella pneumoniae* in neonates. *Antimicrob Agents Chemother.* 2017;61(8):e00385–17. doi:10.1128/AAC.00385-17
- Robert C. An overview of harms associated with β -lactam antimicrobials: where do the carbapenems fit in? *Crit Care.* 2008;12(S4):S3. doi:10.1186/cc6819
- Haiyan L, Yu F, Ke M, Lu L, Alan M, Zhiyong Z. The co-transfer of plasmid-borne colistin-resistant genes *mcr-1* and *mcr-3.5*, the carbapenemase gene *bla_{NDM-5}* and the 16S methylase gene *rmtB* from *Escherichia coli*. *Sci Rep.* 2019;9(1):696. doi:10.1038/s41598-018-37125-1
- Kim Z, Angela H, Gerlinde P, Hester B, Albert N, Leo S. The Carbapenem Inactivation Method (CIM), a simple and low-cost alternative for the carba NP test to assess phenotypic carbapenemase activity in gram-negative rods. *PLoS One.* 2015;10(3):e0123690. doi:10.1371/journal.pone.0123690
- Patel JB, Cockerill FR, Bradford PA. M100-S25 performance standards for antimicrobial susceptibility testing; Twenty-fifth informational supplement. 2019.
- The European Committee on Antimicrobial Susceptibility Testing and Clinical and Laboratory Standards Institute. Recommendations for MIC determination of colistin (polymyxin E) as recommended by the joint CLSI-EUCAST Polymyxin Breakpoints Working Group. 2016.
- Poirel L, Walsh T, Cuvillier V, Nordmann P. Multiplex PCR 344 for detection of acquired carbapenemase genes. *Diagn Microbiol Infect.* 2011;70(1):119–123. doi:10.1016/j.diagmicrobio.2010.12.002
- Ejaz H, Ahmad M, Younas S, et al. Molecular epidemiology of extensively-drug resistant *Acinetobacter baumannii* sequence type 2 co-harboring *bla_{NDM}* and *bla_{OXA}* from clinical origin. *Infect Drug Resist.* 2021;14:1931–1939. doi:10.2147/IDR.S310478
- Naas T, Vandel L, Sougakoff W, Livermore D, Nordmann P. Cloning and sequence analysis of the gene for a carbapenem-hydrolyzing class A beta-lactamase, Sme-1, from *Serratia marcescens* S6. *Antimicrob Agents Chemother.* 1994;38(6):1262–1270. doi:10.1128/AAC.38.6.1262
- Dallenne C, Da A, Decre D, Favier C, Arlet G. Development of a set of multiplex PCR assays for the detection of genes encoding important β -lactamases in *Enterobacteriaceae*. *J Antimicrob Chemother.* 2010;65(3):490–495. doi:10.1093/jac/dkp498
- Hui H, Haijian Z, Haishan L, et al. Optimization of pulse-field gel electrophoresis for subtyping of *Klebsiella pneumoniae*. *Int J Environ Res Public Health.* 2013;10(7):2720–2731. doi:10.3390/ijerph10072720
- Andersson P, Tong YC, Bell JM, Turnidge JD, Giffard PM, Mokrousov I. Minim typing – a rapid and low cost MLST based typing tool for *Klebsiella pneumoniae*. *PLoS One.* 2012;7(3):e33530. doi:10.1371/journal.pone.0033530
- Carattoli A, Bertini A, Villa L, Falbo V, Hopkins L, Threlfall J. Identification of plasmids by PCR-based replicon typing. *J Microbiol Methods.* 2005;63(3):219–228. doi:10.1016/j.mimet.2005.03.018
- Almogbel M, Altheban A, Alenezi M, et al. CTX-M-15 positive *Escherichia coli* and *Klebsiella pneumoniae* outbreak in the neonatal intensive care unit of a maternity hospital in Ha’il, Saudi Arabia. *Infect Drug Resist.* 2021;14:2843–2849. doi:10.2147/IDR.S317079
- Berberian G, Brizuela M, Rosanova T, et al. Multidrug resistant gram-negative infections in neonatology. *Arch Argent Pediatr.* 2019;117(1):6–11. doi:10.5546/aap.2019.eng.6
- Hasan E, Badr A, Mutaz H, et al. Molecular analysis of the antibiotic resistant NDM-1 gene in clinical isolates of *Enterobacteriaceae*. *Clin Lab.* 2020;60:XXX. doi:10.7754/Clin.Lab.2019.190727
- Hasan E, Sonia Y, Muhammad Q, et al. Molecular epidemiology of extensively drug-resistant *mcr* encoded colistin-resistant bacterial strains co-expressing multifarious β -lactamases. *Antibiotic.* 2021;10(4):46. doi:10.3390/antibiotics.10040467
- Kelly L, Kathryn E. *Klebsiella pneumoniae* as a key trafficker of drug resistance genes from environmental to clinically important bacteria. *Curr Opin Microbiol.* 2018;45:131–139. doi:10.1016/j.mib.2018.04.004

31. Monika D, Martina M, Hana D, et al. High prevalence of *Salmonella* and IMP-4-producing *Enterobacteriaceae* in the silver gull on Five Islands, Australia. *J Antimicrob Chemother.* 2016;71(1):63–70. doi:10.1093/jac/dkv306
32. Cailin L, Shangshang Q, Hui X, et al. New Delhi Metallo- β -Lactamase 1(NDM-1), the dominant carbapenemase detected in carbapenem-resistant *Enterobacter cloacae* from Henan Province, China. *PLoS One.* 2015;10(8):e0135044. doi:10.1371/journal.pone.0135044
33. Liu Y, Wan L, Deng Q, Cao X, Yu Y, Xu F. First description of NDM-1-, KPC-2-, VIM-2- and IMP-4-producing *Klebsiella pneumoniae* strains in a single Chinese teaching hospital. *Epidemiol Infect.* 2015;143(2):376–384. doi:10.1017/S0950268814000995
34. Jinrong Y, Shuli P, Xiaojiong J, et al. Multidrug resistance mechanisms of carbapenem resistant *Klebsiella pneumoniae* strains isolated in Chongqing, China. *Ann Lab Med.* 2017;37(5):398–407. doi:10.3343/alm.2017.37.5.398
35. Shudan C, Fupin H, Xiaogang X, et al. High prevalence of KPC-2-type carbapenemase coupled with CTX-M-type extended-spectrum β -lactamases in carbapenem-resistant *Klebsiella pneumoniae* in a teaching hospital in China. *Antimicrob Agents Chemother.* 2011;55(5):2493–2494. doi:10.1128/AAC.00047-11
36. Bonura C, Giuffrè M, Aleo A, et al. An update of the evolving epidemic of blaKPC carrying *Klebsiella pneumoniae* in Sicily, Italy, 2014: emergence of multiple non-ST258 clones. *PLoS One.* 2015;10(7):e0132936. doi:10.1186/cc6819
37. Yoon E, Yang J, Kim J, et al. Carbapenemase-producing *Enterobacteriaceae* in South Korea: a report from the National Laboratory Surveillance System. *Future Microbiol.* 2018;13:771–783. doi:10.2217/fmb-2018-0022
38. Castanheira M, Farrell SE, Wanger A, et al. Rapid expansion of KPC-2- producing *Klebsiella pneumoniae* isolates in two Texas hospitals due to clonal spread of ST258 and ST307 lineages. *Microb Drug Resist.* 2013;19(4):295–297. doi:10.1089/mdr.2012.0238
39. Paola B, Elvira G, Magaly P, et al. The successful containment of a hospital outbreak caused by NDM-1-producing *Klebsiella pneumoniae* ST307 using active surveillance. *PLoS One.* 2019;14(2):e0209609. doi:10.1371/journal.pone.0209609
40. Lu L, Yu F, Guangmin T, et al. Carbapenem-resistant isolates of the *Klebsiella pneumoniae* complex in Western China: the common ST11 and the surprising hospital-specific types. *Clin Infect Dis.* 2018;67(S2):S263–S265. doi:10.1093/cid/ciy662
41. Dongxing T, Fen P, Chun W, Yan S, Hong Z. Resistance phenotype and clinical molecular epidemiology of carbapenem-resistant *Klebsiella pneumoniae* among pediatric patients in Shanghai. *Infect Drug Resist.* 2018;11:1935–1943. doi:10.2147/IDR.S175584
42. Rémy B, Agnès J, Adriana C, et al. Emergence of new non-clonal group 258 high-risk clones among *Klebsiella pneumoniae* carbapenemase-producing *K. pneumoniae* isolates, France. *Emerg Infect Dis.* 2021;26(6):1212–1220. doi:10.3201/eid2606.191517

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