Extended-spectrum beta-lactamase-producing *Klebsiella pneumoniae* isolated from an abattoir worker in Cameroon

To the Editor: Extended-spectrum beta-lactamase (ESBL)-producing Enterobacteriaceae are a serious public health concern globally.[1] Beta-lactamases are chromosomal and plasmid-mediated enzymes that are able to inactivate beta-lactam antibiotics. They represent an important mechanism of antibiotic resistance among Enterobacteriaceae such as *Klebsiella pneumoniae*.[2] The latter is among the foremost causative agents of both hospital- and community-acquired difficult-to-treat infections in humans, and has serious consequences.[1] However, the extent to which this bacterium could represent a public health threat through its spread from food animals such as pigs to humans has yet to be elucidated despite the well-established animal reservoir, emergence of resistant strains, and probable dissemination through the food chain.

During a multicentre study carried out from March to October 2016, nasal and rectal swabs were collected from 432 pigs in five abattoirs, three in Cameroon and two in South Africa (SA). Nasal and hand swabs were also collected from 82 humans in Cameroon (n=53) and SA (n=29). All samples were cultured overnight on MacConkey agar supplemented with 2 mg/L cefotaxime at 37°C, and putative ESBL producers were phenotypically confirmed via the Vitek 2 System and Vitek 2 Gram Negative Susceptibility card (AST-N255) (BioMérieux, France). The results were interpreted according to the Clinical and Laboratory Standards Institute (CLSI)[3] guideline, with the exception of colistin, amoxicillin + clavulanic acid, piperacillin/tazobactam and amikacin, which were based on European Committee on Antimicrobial Susceptibility Testing (EUCAST)[4] breakpoints. The genetic backbone of closely related isolates was molecularly characterised through whole-genome sequencing (WGS) on an Illumina MiSeq platform (Illumina Inc., USA) with 100× coverage. The bacterial analysis pipeline GoSeqIt tool (GoSeqIt, Denmark) was used to annotate and identify resistance genes, virulence factors and plasmids, respectively. The multi-locus sequence type was also determined through WGS.

One ESBL-producing *K. pneumoniae*, HH516E4IA (GenBank accession no. PCFF00000000), isolated from a hand swab of a slaughterer working in a pig abattoir in Yaoundé, Cameroon, displayed phenotypic resistance to several antibiotic classes (Table 1). This isolate was assigned to sequence type (ST) 39 with 100% identity among the seven housekeeping genes. *In silico* analysis using ResFinder with 90% identity as threshold corroborated the phenotypic resistance and revealed several genes encoding for resistance to beta-lactams ($bla_{CTX\text{-}M\text{-}15}$, $bla_{SCO\text{-}1}$, $bla_{SHV\text{-}11}$ and $bla_{TEM\text{-}1B}$), aminoglycosides (*aac(3)-IIa* and *aadA1*), fluoroquinolones (*oqxA* and *oqxB*), fosfomycin (*fos*A), tetracyclines (*tet*(A)) and sulphonamides (*sul1* and *dfrA15*) (Table 1). It additionally harboured one replicon (colRNAI) along with two plasmid incompatibility groups, namely IncFIB(K) and IncHI1B.

ESBL-producing *K. pneumoniae* ST39 strains have been associated with severe outbreak situations and nosocomial infections worldwide, although there is limited information on their evolutionary emergence in the developing world. Our findings concur with a recent study which showed that ESBL-producing *K. pneumoniae* are actively disseminating in pigs and abattoir workers in Cameroon and are probably underestimated in the absence of molecular epidemiological studies.[2] The concomitant presence of genes encoding resistance to several antibiotic classes suggests that resistant commensal bacteria could contribute to the emergence/dissemination of antibiotic resistance and represent a serious public health threat, as few therapeutic options remain available. The presence of IncFIB(K) and IncHI1B plasmid incompatibility groups highlights the horizontal transfer of resistance genes that may occur within and between commensal and pathogenic bacteria of the same species or genus. Detection of this ST has always prompted the implementation of stringent infection, prevention and control measures and ongoing surveillance of antibiotic resistance in hospital settings. Likewise, strict food safety measures should be implemented in the farm-to-plate continuum if we are to successfully contain the clonal spread of ESBL-producing *K. pneumoniae* in the food chain in developing countries, and especially in Cameroon.

Acknowledgements. We thank the abattoir owners/co-ordinators for granting access to their structures and for their great hospitality. We are grateful to the National Center for Biotechnology Information GenBank submission staff for help with genome upload, decontamination and deposition procedures.

Table 1. Antimicrobial susceptibility results of selected beta-lactam and non-beta-lactam antibiotics

Isolate name	Beta-lactam antibiotics								Non-beta-lactam antibiotics						Antibiotic resistance genes	Plasmids
	AMP	AMC	TZP	CXM	CTX	CAZ	FEP	ETP	MEM	IMP	GEN	AN	CIP	TGC	FT	CS	TMP/SXT	
HH516E4IA	R	S	S	R	I	R	I	S	S	S	S	S	S	S	I	R	S	$bla_{TEM\text{-}1B}$, $bla_{CTX\text{-}M\text{-}15}$, $bla_{SCO\text{-}1}$, $bla_{SHV\text{-}11}$, *aac(3)-IIa*, *aadA1*, *oqxA*, *oqxB*, *fosA*, *tet*(A), *dfrA*15, *sul1*	ColRNAI IncFIB(K), IncHI1B

AMP = ampicillin; AMC = amoxicillin plus clavulanic acid; TZP = piperacillin plus tazobactam; CXM = cefuroxime; CTX = cefotaxime; CAZ = ceftazidime; FEP = cefepime; ETP = ertapenem; MEM = meropenem; IMP = imipenem; GEN = gentamicin; AN = amikacin; CIP = ciprofloxacin; TGC = tigecycline; FT = nitrofurantoin; CS = colistin; TMP/SXT = trimethoprim plus sulfamethoxazole; R = resistant; S = susceptible; I = intermediate.

Funding. LLF and RCF are funded by the Antimicrobial Research Unit and College of Health Sciences of the University of KwaZulu-Natal. The National Research Foundation (NRF) funded this study through the NRF Incentive Funding for Rated Researchers (grant no. 85595), the NRF Competitive Grant for Rated Researchers (grant no. 106063) and the DST/NRF South African Research Chair in Antibiotic Resistance and One Health (grant no. 98342) awarded to SYE. The South African Medical Research Council also funded the study through the Self-Initiated Researcher (SIR) Grant awarded to SYE. Any opinions, findings and conclusions, or recommendations expressed in this review are those of the authors and do not represent the official position of the funders. The funders had no role in the study design, preparation of the manuscript or the decision to submit the work for publication.

Conflicts of interest. SYE is a member of the Global Respiratory Infection Partnership, sponsored by an unrestricted educational grant from Reckitt Benckiser, UK. All the other authors declare that they have no competing financial interests.

Luria Leslie Founou
Antimicrobial Research Unit, College of Health Sciences, University of KwaZulu-Natal, Durban, South Africa; and Department of Food Safety and Environmental Health, Centre of Expertise and Biological Diagnostic of Cameroon, Yaoundé, Cameroon
luriafounou@gmail.com

Raspail Carrel Founou
Antimicrobial Research Unit, College of Health Sciences, University of KwaZulu-Natal, Durban, South Africa; and Department of Clinical Microbiology, Centre of Expertise and Biological Diagnostic of Cameroon, Yaoundé, Cameroon

Mushal Allam, Arshad Ismail
Sequencing Core Facility, National Health Laboratory Service, Johannesburg, South Africa

Sabiha Yusuf Essack
Antimicrobial Research Unit, College of Health Sciences, University of KwaZulu-Natal, Durban, South Africa

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S Afr Med J 2019;109(11):820-821. https://doi.org/10.7196/SAMJ.2019.109i11.14378