

Molecular characterization of multidrug-resistance in Gram-negative bacteria from the Peshawar teaching hospital, Pakistan

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Abstract

Extended-spectrum β -lactamases, carbapenemases, 16S rRNA methylases conferring pan-drug aminoglycoside resistance and colistin resistance were investigated among Gram-negative bacteria recovered from clinical samples (infections) from 200 individuals hospitalized at the Khyber Teaching Hospital of Peshawar, north Pakistan, from December 2017 to March 2018. Out of 65 isolates recovered, 19% were carbapenem resistant and 16% carried a *bla*_{NDM-1} gene, confirming the widespread distribution of NDM producers in this country. The association of the NDM carbapenem-resistance determinant, together with the extended-spectrum β -lactamase CTX-M-15 and 16S rRNA methylases, was frequent, explaining the multidrug-resistance pattern observed. All isolates remained susceptible to colistin.

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methylases conferring pan-aminoglycoside resistance, and colistin resistance (plasmid-mediated *mcr* genes) from a series of clinical isolates obtained in acute-care facilities from Peshawar, Pakistan.

Introduction

The increasing occurrence of resistance to carbapenems is a major issue for global public health. Resistance to carbapenems is often mediated by carbapenemases, with NDM-1 (New Delhi metallo- β -lactamase) being one of the most commonly identified carbapenemases worldwide, its main reservoir corresponding to the Indian subcontinent [1]. Accordingly, several studies reported a high occurrence of NDM-1 producers in India and Pakistan [2,3]. Most of the carbapenemase producers are co-resistant to other antibiotic families, so it is interesting to obtain further characterization about those co-resistance markers [4]. Our aim was to characterize the carbapenemases, extended-spectrum β -lactamases (ESBLs), 16S rRNA

Materials and methods

Bacterial isolates

A total of 200 samples were collected from 200 individuals between December 2017 and March 2018 at the Khyber Teaching Hospital of Peshawar, north Pakistan. Those samples included urine, blood, pus and broncheal lavage specimens. Samples were plated on URSelect-4™ medium (Bio-Rad, Cressier, Switzerland) and identification was performed using the API-20E system (bioMérieux, La Balme-les-Grottes, France). Antimicrobial susceptibility testing was performed using the disc diffusion method and interpreted according to the CLSI recommendations [5], except for colistin. Resistance to colistin was evaluated first by using the Rapid Polymyxin test

[6], and then by determination of MIC values of colistin by broth microdilution, as recommended by European Committee on Antimicrobial Susceptibility Testing (EUCAST) (www.eucast.org). Carbapenemase and ESBL activities were detected using the Carba NP test [7] and the ESBL NP test [8], respectively.

Molecular analysis

A series of acquired resistance genes were searched by PCR, including those encoding ESBLs (*bla*_{TEM}, *bla*_{SHV} and *bla*_{CTX-M}-like genes), carbapenemases (*bla*_{KPC}, *bla*_{NDM}, *bla*_{VIM}, *bla*_{IMP}, *bla*_{OXA-48}, *bla*_{OXA-181}), 16S rRNA methylases genes (*armA*, *rmtA* to *rmtH* and *npmA*), and *mcr*-like genes (*mcr*-I to *mcr*-8) [9–14]. The obtained amplicons were sent for sequencing (Microsynth®, Balgach, Switzerland).

Clonal diversity

Clonal relationship of the isolates was evaluated by pulsed-field gel electrophoresis (PFGE) [15]. Total DNA from *Escherichia coli*, *Klebsiella pneumoniae* and *Enterobacter* spp. were digested using the *Xba*I enzyme (New England Biolabs, Ipswich, MA, USA). The generated fragments were separated by PFGE using a CHEF-DR III System (Bio-Rad) creating a unique PFGE profile for each clonal strain. Multilocus sequencing typing was performed for pan-drug aminoglycoside-resistant strains belonging to the species *E. coli* (strain no. 31) and *K. pneumoniae* (strain no. 62) [16]. Sequence types (STs) were investigated using the online databases (<http://genomicepidemiology.org/>).

Results

A total of 65 Gram-negative bacteria were recovered including 46 *E. coli*, 10 *Enterobacter* spp. (9 *Enterobacter cloacae*, 1 *Enterobacter sakazakii*), 6 *K. pneumoniae*, 2 *Alcaligenes faecalis* and 1 *Citrobacter freundii*.

Thirty-eight of the 65 Gram-negative bacteria produced a carbapenemase, as assessed by the results of the Rapid Carba NP test, whereas 32 of those 65 isolates produced an ESBL according to the results of the ESBL NP test. Among the 46 *E. coli* isolates, 12 produced NDM-I, 5 co-produced NDM-I and CTX-M-15, 2 co-produced NDM-I and OXA-181, 2 isolates co-producing OXA-181 and CTX-M-15, a single isolate producing OXA-48. Twelve *E. coli* isolates produced CTX-M-15 without any carbapenemase associated. A single *bla*_{NDM-I}-positive *E. coli* isolate produced the 16S rRNA methylase RmtB.

Among the six *K. pneumoniae* isolates, one isolate co-produced NDM-I and CTX-M-15, another co-produced NDM-I, OXA-181 and CTX-M-15, and a single isolate co-

produced NDM-I, OXA-232 and CTX-M-15 together with the 16S rRNA methylase RmtB (see Table 1).

The ten *Enterobacter* spp. isolates (nine *Enterobacter cloacae*, one *Enterobacter sakazakii*) co-produced NDM-I and CTX-M-15.

Two *Alcaligenes faecalis* isolates were identified, both producing a carbapenemase VIM-4.

The single *C. freundii* isolate did not produce any carbapenemase but was positive for CTX-M-15. None of the isolates was resistant to colistin. PFGE analysis showed a very high clonal diversity for all those isolates producing a carbapenemase, except among *Enterobacter* spp. with a single clone being identified among six patients (EC-1) that may have resulted from an outbreak.

By using MLST, we showed that the *bla*_{NDM-I} and *rmtB*-positive *E. coli* clone belonged to ST215 (strain no. 31) and that the multidrug-resistant *K. pneumoniae* isolate belonged to ST231 (strain no. 62).

Discussion

Here we evaluated the occurrence of multidrug resistance from infecting strains (not colonizers) from individuals hospitalized at the Khyber Teaching Hospital, Peshawar, north Pakistan from November 2017 to March 2018. A rate of 19% of carbapenem-resistant *Enterobacteriaceae* (38/200) was identified, among which 16% harboured the *bla*_{NDM-I} gene. This overall rate of 16% of NDM producers is in accordance with the estimated rate of NDM producers in *Enterobacteriaceae* in Pakistan (8.7%–18.5%). Actually, 18.5% stool samples were found to contain *bla*_{NDM-I}-positive strains (mostly *E. coli* and *Enterobacter cloacae*) in military hospitals of Rawalpindi (Combined Military Hospitals and Military Hospital at Rawalpindi) [17], 8.7% of the isolates were NDM-I positive (*K. pneumoniae*, *E. coli*, *Pseudomonas aeruginosa*) from two tertiary-care hospitals (Pakistan Institute of Medical Science, Islamabad and Mayo Hospital, Lahore) [18] and 14.6% of the strains carried *bla*_{NDM-I} (*E. coli*, *Enterobacter cloacae*, *Pseudomonas putida* and *K. pneumoniae* from three children's hospitals (The Children's Hospital, Islamabad, The Children's Hospital Multan and Nishtar Hospital, Multan) [19].

Interestingly, some strains were found to harbour two unrelated carbapenemase genes (*bla*_{NDM-I} and *bla*_{OXA-181}), as observed previously in Singapore [20], Nigeria [21] and Romania [22].

In our study, co-resistance to multiple antibiotics was commonly observed among those carbapenem-resistant isolates, with 60% of them harbouring at least two other resistance genes (ESBL, or 16S rRNA methylase gene). A single

TABLE 1. Information and genetic features of samples isolated in Peshawar teaching hospital, Pakistan

Patient/strain no.	Site of isolation	Residence	Treatment	Strains	Carbapenemase	ESBL	16S RNA methyltransferase	Clonality
1	Pus	Peshawar	Ciprofloxacin	<i>Alcaligenes faecalis</i>	VIM-4	None	None	None
2	Urine	Mardan	Ofloxine	<i>Alcaligenes faecalis</i>	VIM-4	None	None	None
3	Urine	Batkhela	Unknown	<i>Citrobacter freundii</i>	None	CTX-M-15	None	EsC-7
4	Pus	Peshawar	Ciprofloxacin	<i>Enterobacter cloacae</i>	NDM-I	None	None	EC-I
5	Urine	Peshawar	Unknown	<i>Enterobacter cloacae</i>	NDM-I	CTX-M-15	None	EC-I
6	Urine	Kohat	Unknown	<i>Enterobacter cloacae</i>	NDM-I	CTX-M-15	None	EC-I
7	Blood	Unknown	Cefixime	<i>Enterobacter cloacae</i>	NDM-I	CTX-M-15	None	EC-I
8	Urine	Mardan	Ofloxine	<i>Enterobacter cloacae</i>	NDM-I	CTX-M-15	None	EC-I
9	Urine	Afghanistan	Unknown	<i>Enterobacter cloacae</i>	NDM-I	CTX-M-15	None	EC-I
10	Urine	Afghanistan	Unknown	<i>Enterobacter cloacae</i>	NDM-I	CTX-M-15	None	EC-I
11	Urine	Peshawar	Levofloxacin	<i>Enterobacter cloacae</i>	NDM-I	CTX-M-15	None	None
12	Urine	Peshawar	Levofloxacin	<i>Enterobacter cloacae</i>	NDM-I	CTX-M-15	None	None
13	Urine	Peshawar	Unknown	<i>Enterobacter sakazakii</i>	NDM-I	CTX-M-15	None	None
14	Fluid	Peshawar	Ciprofloxacin	<i>Escherichia coli</i>	NDM-I	None	None	None
15	Pus	Charsada	Ciprofloxacin	<i>Escherichia coli</i>	NDM-I	None	None	None
16	Pus	Dir	Amoxicillin	<i>Escherichia coli</i>	NDM-I	None	None	None
17	Pus	Peshawar	Levofloxacin	<i>Escherichia coli</i>	NDM-I	None	None	None
18	Pus	Peshawar	Levofloxacin	<i>Escherichia coli</i>	NDM-I	None	None	None
19	Pus	Peshawar	Unknown	<i>Escherichia coli</i>	NDM-I	None	None	None
20	Pus	Peshawar	Unknown	<i>Escherichia coli</i>	NDM-I	None	None	None
21	Urine	Peshawar	Ceftriaxone	<i>Escherichia coli</i>	NDM-I	None	None	None
22	Urine	Peshawar	Ciprofloxacin	<i>Escherichia coli</i>	NDM-I	None	None	None
23	Urine	Peshawar	Unknown	<i>Escherichia coli</i>	NDM-I	None	None	None
24	Urine	Peshawar	Unknown	<i>Escherichia coli</i>	NDM-I	None	None	None
25	Unknown	Peshawar	Cefixime	<i>Escherichia coli</i>	NDM-I	None	None	None
26	Blood	Mardan	Unknown	<i>Escherichia coli</i>	NDM-I	CTX-M-15	None	None
27	Blood	Peshawar	Unknown	<i>Escherichia coli</i>	NDM-I	CTX-M-15	None	EsC-15
28	Urine	Peshawar	Unknown	<i>Escherichia coli</i>	NDM-I	CTX-M-15	None	None
29	Urine	Peshawar	Unknown	<i>Escherichia coli</i>	NDM-I	CTX-M-15	None	None
30	Urine	Peshawar	Unknown	<i>Escherichia coli</i>	NDM-I	CTX-M-15	None	None
31	Unknown	Unknown	Unknown	<i>Escherichia coli</i>	NDM-I	None	rmtB	ST 215
32	Urine	Peshawar	Ciprofloxacin	<i>Escherichia coli</i>	NDM-I; OXA-181	None	None	EsC-10
33	Urine	Peshawar	Unknown	<i>Escherichia coli</i>	NDM-I; OXA-181	None	None	None
34	Urine	Peshawar	Ciprofloxacin	<i>Escherichia coli</i>	OXA-48	None	None	EsC-1
35	Blood	Peshawar	Ciprofloxacin	<i>Escherichia coli</i>	OXA-181	CTX-M-15	None	EsC-5
36	Blood	Peshawar	Unknown	<i>Escherichia coli</i>	OXA-181	CTX-M-15	None	EsC-1
37	Blood	Kohat	Unknown	<i>Escherichia coli</i>	None	CTX-M-15	None	EsC-14
38	Pus	Dir	Unknown	<i>Escherichia coli</i>	None	CTX-M-15	None	EsC-2
39	Pus	Peshawar	Ofloxine	<i>Escherichia coli</i>	None	CTX-M-15	None	EsC-2
40	Urine	Peshawar	Amoxicillin-Clavulanate	<i>Escherichia coli</i>	None	CTX-M-15	None	EsC-2
41	Urine	Peshawar	Levofloxacin	<i>Escherichia coli</i>	None	CTX-M-15	None	EsC-2
42	Bronchial lavage	Peshawar	Levofloxacin	<i>Escherichia coli</i>	None	CTX-M-15	None	EsC-3
43	Pus	Peshawar	Cefixime	<i>Escherichia coli</i>	None	CTX-M-15	None	EsC-3
44	Urine	Peshawar	Unknown	<i>Escherichia coli</i>	None	CTX-M-15	None	EsC-3
45	Urine	Kohat	Unknown	<i>Escherichia coli</i>	None	CTX-M-15	None	EsC-3
46	Urine	Peshawar	Ciprofloxacin	<i>Escherichia coli</i>	None	CTX-M-15	None	EsC-9
47	Urine	Peshawar	Levofloxacin	<i>Escherichia coli</i>	None	CTX-M-15	None	EsC-12
48	Urine	Afghanistan	Levofloxacin	<i>Escherichia coli</i>	None	CTX-M-15	None	None
49	Blood	Peshawar	Cefixime	<i>Escherichia coli</i>	None	None	None	EsC-16
50	Blood	Unknown	Cefixime	<i>Escherichia coli</i>	None	None	None	EsC-13
51	Pus	Afghanistan	Unknown	<i>Escherichia coli</i>	None	None	None	EsC-11
52	Pus	Charsada	Ciprofloxacin	<i>Escherichia coli</i>	None	None	None	None
53	Pus	Peshawar	Ciprofloxacin	<i>Escherichia coli</i>	None	None	None	None
54	Pus	Peshawar	Linezolid	<i>Escherichia coli</i>	None	None	None	EsC-18
55	Urine	Afghanistan	Unknown	<i>Escherichia coli</i>	None	None	None	EsC-17
56	Urine	Peshawar	Cefixime	<i>Escherichia coli</i>	None	None	None	EsC-4
57	Urine	Peshawar	Unknown	<i>Escherichia coli</i>	None	None	None	EsC-4
58	Urine	Peshawar	Unknown	<i>Escherichia coli</i>	None	None	None	EsC-6
59	Urine	Peshawar	Cefixime	<i>Escherichia coli</i>	None	None	None	EsC-8
60	Blood	Peshawar	Unknown	<i>Klebsiella pneumoniae</i>	NDM-I	CTX-M-15	None	KP-1
61	Pus	Dir	Amoxicillin	<i>Klebsiella pneumoniae</i>	NDM-I; OXA-181	None	None	KP-1
62	Blood	Mardan	Unknown	<i>Klebsiella pneumoniae</i>	NDM-I; OXA-232	CTX-M-15	rmtB	ST 231
63	Pus	Peshawar	Ciprofloxacin	<i>Klebsiella pneumoniae</i>	None	None	None	KP-2
64	Urine	Noweshehra	Ciprofloxacin	<i>Klebsiella pneumoniae</i>	None	None	None	KP-2
65	Unknown	Afghanistan	Levofloxacin	<i>Klebsiella pneumoniae</i>	None	None	None	None

Abbreviations: EC, *Enterobacter cloacae* clone X; ESBL, extended spectrum β -lactamase; EsC, *Escherichia coli* clone X; KP, *Klebsiella pneumoniae* clone X; ST, sequence type.

K. pneumoniae isolate carried two carbapenemase genes, namely *bla*_{NDM-1} and *bla*_{OXA-232}, along with the ESBL-encoding gene *bla*_{CTX-M-15} and the 16S rRNA methylase gene *rmtB*. That isolate was an ST231 clone, already described in South-East Asia [23,24] and Switzerland [25], and associated with OXA-232.

Among the 16S rRNA methylase genes, the methylase gene *rmtB*, rather than *rmtF*, was mostly identified here, which is not

surprising owing to the spread of *rmtB*-positive strains in Pakistan [26]. Our study showed the frequent identification of the ESBL CTX-M-15 among those multidrug-resistant bacteria. It is possible that the spread of CTX-M-15 that is observed worldwide originated from the Indian subcontinent because we identified the first CTX-15 producers from India in 2001 [27]. Our study confirms the frequent association of those three important resistance markers that are NDM, ESBL of the CTX-

M-15 type and 16S rRNA methylases as a source of multidrug resistance. This combination complicates the treatment of infected patients.

We also identified two *A. faecalis* isolates producing a same VIM-4 metallo- β -lactamase. Occurrence of carbapenemase production in that bacterial species is rare. Only a single case of *A. faecalis* carrying *bla*_{VIM-4} has been described in Gaza, Palestine [28]. Further work may identify the genetic basis of such acquisition of carbapenemase. Other reports about ESBL in clinical isolates of *Alcaligenes* species have been described in Malaysia [29], France [30] and Italy [31].

Finally, no resistance to colistin was observed whereas MCR-I-mediated colistin resistance isolates was observed recovered from *E. coli* in animals [32,33] and from a single patient [34] in Pakistan. Lack of colistin resistance among those multidrug-resistant isolates is good news as it would indicate the availability to use that drug for treating infected patients in this country.

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Conflicts of interest

None to declare.

References

- [1] Dortet L, Poirel L, Nordmann P. Worldwide dissemination of the NDM-type carbapenemases in Gram-negative bacteria. *Biomed Res Int* 2014;2014:1–12.
- [2] Kumarasamy KK, Toleman MA, Walsh TR, Bagaria J, Butt F, Balakrishnan R, et al. Emergence of a new antibiotic resistance mechanism in India, Pakistan, and the UK: a molecular, biological, and epidemiological study. *Lancet Infect Dis* 2010;10:597–602.
- [3] Zahedi Bialvaei A, Samadi Kafil H, Ebrahimzadeh Leylabadlo H, Asgharzadeh M, Aghazadeh M. Dissemination of carbapenemases producing Gram-negative bacteria in the Middle East. *Iran J Microbiol* 2015;7:226–46.
- [4] Ain NU, Iftikhar A, Bukhari SS, Abrar S, Hussain S, Haider MH, et al. High frequency and molecular epidemiology of metallo- β -lactamase-producing Gram-negative bacilli in a tertiary care hospital in Lahore, Pakistan. *Antimicrob Resist Infect Control* 2018;7:1–9.
- [5] Clinical and Laboratory Standards Institute. Performance standards for antimicrobial susceptibility testing. 29th ed. Wayne, PA: Clinical and Laboratory Standards Institute; 2019. M100.
- [6] Nordmann P, Jayol A, Poirel L. Rapid detection of polymyxin resistance in *Enterobacteriaceae*. *Emerg Infect Dis* 2016;22:1038–43.
- [7] Poirel L, Nordmann P. Rapidec Carba NP test for rapid detection of carbapenemase producers. *J Clin Microbiol* 2015;23:3003–8.
- [8] Nordmann P, Dortet L, Poirel L. Rapid detection of extended-spectrum- β -lactamase-producing *Enterobacteriaceae*. *J Clin Microbiol* 2012;50:3016–22.
- [9] Nordmann P, Boulanger AE, Poirel L. NDM-4 metallo- β -lactamase with increased carbapenemase activity from *Escherichia coli*. *Antimicrob Agents Chemother* 2012;56:2184–6.
- [10] Poirel L, Dortet L, Bernabeu S, Nordmann P. Genetic features of *bla*_{NDM-1}-positive *Enterobacteriaceae*. *Antimicrob Agents Chemother* 2011;55:5403–7.
- [11] Lartigue MF, Zinsius C, Wenger A, Bille J, Poirel L, Nordmann P. Extended-spectrum β -lactamases of the CTX-M type now in Switzerland. *Antimicrob Agents Chemother* 2007;51:2855–60.
- [12] Poirel L, Walsh TR, Cu villier V, Nordmann P. Multiplex PCR for detection of acquired carbapenemase genes. *Diagn Microbiol Infect Dis* 2011;70:119–23.
- [13] Berçot B, Poirel L, Nordmann P. Updated multiplex polymerase chain reaction for detection of 16S rRNA methylases: high prevalence among NDM-I producers. *Diagn Microbiol Infect Dis* 2011;71:442–5.
- [14] Lescat M, Poirel L, Nordmann P. Rapid multiplex PCR for detection of *mcr-1* to *mcr-5* genes. *Diagn Microbiol Infect Dis* 2018;92:267–9.
- [15] Sharma-Kuinkel BK, Rude TH, Fowler Jr VG. Pulsed field gel electrophoresis. *Methods Mol Biol* 2016;1373:117–30.
- [16] Diancourt L, Passet V, Verhoef J, Grimont PA, Brisse S. Multilocus sequence typing of *Klebsiella pneumoniae* nosocomial isolates. *J Clin Microbiol* 2005;43:4178–82.
- [17] Perry JD, Naqvi SH, Mirza IA, Alizai SA, Hussain A, Gharardi S, et al. Prevalence of faecal carriage of *Enterobacteriaceae* with NDM-I carbapenemase at military hospitals in Pakistan, and evaluation of two chromogenic media. *J Antimicrob Chemother* 2011;66:2288–94.
- [18] Nahid F, Khan AA, Rehman S, Zahra R. Prevalence of metallo- β -lactamase NDM-I-producing multi-drug resistant bacteria at two Pakistani hospitals and implications for public health. *J Infect Public Health* 2013;6:487–93.
- [19] Qamar MU, Nahid F, Walsh TR, Kamran R, Zahra R. Prevalence and clinical burden of NDM-I positive infections in pediatric and neonatal patients in Pakistan. *Pediatr Infect Dis J* 2014;34:452–4.
- [20] Balm MND, La MV, Krishnan P, Jureen R, Lin RTP, Teo JWP. Emergence of *Klebsiella pneumoniae* co-producing NDM-type and OXA-181 carbapenemases. *Clin Microb Infect* 2013;19:421–3.
- [21] Uwaezuoke NS, Kieffer N, Iregbu KC, Nordmann P. First report of OXA-181 and NDM-I from a clinical *Klebsiella pneumoniae* isolate from Nigeria. *Int J Infect Dis* 2017;61:1–2.
- [22] Székely E, Damjanova I, Jánvári L, Vas KE, Molnár S, Bilca DV, et al. First description of *bla*_{NDM-1}, *bla*_{OXA-48}, *bla*_{OXA-181} producing *Enterobacteriaceae* strains in Romania. *Int J Med Microbiol* 2013;303:697–700.
- [23] Abdul Momin MHF, Liakopoulos A, Phee LM, Wareham DW. Emergence and nosocomial spread of carbapenem-resistant OXA-232-producing *Klebsiella pneumoniae* in Brunei Darussalam. *J Glob Antimicrob Resist* 2017;9:96–9.
- [24] Teo JWP, Kurup A, Lin RTP, Hsien KT. Emergence of clinical *Klebsiella pneumoniae* producing OXA-232 carbapenemase in Singapore. *N Microbe N Infect* 2013;1:13–5.
- [25] Mancini S, Poirel L, Tritten M-L, Lienhard R, Bassi C, Nordmann P. Emergence of an MDR *Klebsiella pneumoniae* ST231 producing OXA-232 and RmtF in Switzerland. *J Antimicrob Chemother* 2018;73:821–3.
- [26] Habeeb MA, Haque A, Nematzadeh S, Iversen A, Giske CG. High prevalence of 16S RNA methylase RmtB among CTX-M extended-spectrum β -lactamase-producing *Klebsiella pneumoniae* from Islamabad, Pakistan. *Int J Antimicrob Agents* 2013;41:524–6.
- [27] Karim A, Poirel L, Nagarajan S, Nordmann P. Plasmid-mediated extended-spectrum β -lactamase (CTX-M-3-like) from India and gene

- p association with insertion sequence ISEcpI. FEMS Microbiol Lett 2001;201:237–41.
- [28] Al Laham N, Chavda KD, Cienfuegos-Gallet AV, Kreiswirth BN, Chen L. Genomic characterization of VIM metallo- β -lactamase-producing *Alcaligenes faecalis* from Gaza, Palestine. Antimicrob Agents Chemother 2017;61(11). pii:e01499-17.
- [29] Puah SM, Puthucheary SD, Chua KH. First report of TEM-116 and OXA-10 extended-spectrum β -lactamase in clinical isolates of *Alcaligenes* species from Kuala Lumpur, Malaysia. Jpn J Infect Dis 2019;72:266–9.
- [30] Dubois V, Arpin C, Coulangue L, Andre C, Noury P, Quentin C. TEM-21 extended-spectrum β -lactamase in a clinical isolate of *Alcaligenes faecalis* from a nursing home. J Antimicrob Chemother 2006;57:368–9.
- [31] Pereira M, Perilli M, Mantengoli E, Luzzaro F, Toniolo A, Rossolini GM, Amicosante G. PER-1 extended-spectrum β -lactamase production in an *Alcaligenes faecalis* clinical isolate resistant to expanded-spectrum cephalosporins and monobactams from a hospital in Northern Italy. Microb Drug Resist 2000;6:85–90.
- [32] Azam M, Ehsan I, Sajjad-Ur-Rahman, Saleemi MK, Javed MR, Mohsin M. Detection of the colistin resistance gene *mcr-1* in avian pathogenic *Escherichia coli* in Pakistan. J Glob Antimicrob Resist 2017;11:152–3.
- [33] Lv J, Mohsin M, Lei S, Srinivas S, Wigar RT, Lin J, Feng Y. Discovery of a *mcr-1*-bearing plasmid in commensal colistin-resistant *Escherichia coli* from healthy broilers in Faisalabad, Pakistan. Virulence 2018;9:994–9.
- [34] Mohsin M, Raza S, Roschanski N, Guenther S, Ali A, Schierack P. Description of the First *Escherichia coli* clinical isolate harboring the colistin resistance gene *mcr-1* from the Indian subcontinent. Antimicrob Agents Chemother 2016;61:1–2.