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ORIGINAL RESEARCH

Quinolone resistance mechanisms among third-generation cephalosporin resistant isolates of *Enterobacter* spp. in a Bulgarian university hospital

This article was published in the following Dove Press journal:
Infection and Drug Resistance

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Background: There have been no reports in Bulgaria about quinolone resistance determinants among *Enterobacter* spp.

Aims: To investigate plasmid and chromosomal quinolone resistance rates among 175 third-generation cephalosporin resistant *Enterobacter* spp. isolates (167 *Enterobacter cloacae* complex and eight *Enterobacter aerogenes* isolates) collected at a university hospital in Varna, Bulgaria, as well as to reveal their association with ESBL/AmpC production and a carriage of specific plasmid replicon types.

Methods: PCR, isoelectric focusing, replicon typing, sequencing, and epidemiology typing were carried out.

Results: A high level of combined third-generation cephalosporin and quinolone resistant *Enterobacter* spp. was found − 79.4%. The ESBL production rate was 87%, consisting mainly of CTX-M-15 among *E. cloacae* complex (in 76%) and CTX-M-3 among *E. aerogenes* (in 88%). Plasmid mediated quinolone resistance (PMQR) determinants were identified in 57% of the isolates. The most commonly detected PMQR determinants were *qnrB* (90%), consisting mainly of *qnrB1* (in 61%), and *qnrB9* (in 27%) of the isolates. Both alleles were transferred with CTX-M-15 genes; transconjugants showed HI2 replicons (for *qnrB1* positive transconjugants) and were non-typeable (for *qnrB9*). One *Enterobacter* spp. isolate produced *qnrB4. QnrA1, qnrS1,* and *aac(6')-Ib-cr* were detected in single isolates only. *QnrC, qnrD, qep*A, and *oqx*AB genes were not found. *QnrB* was associated with CTX-M-15 production, and *qnrS1* was linked to CTX-M-3. Alterations in 83 and 87 positions of *gyrB* in quinolone-resistance determining regions, and 80 position of *parC* were detected in high level quinolone resistant isolates. Among all the *Enterobacter* spp. isolates tested, one predominant clone A was identified (53%).

Conclusion: Our data showed the necessity of more prudent use of quinolones and third-generation cephalosporins, because of the risk of promoting dissemination, and selection of multiple resistance determinants (ESBL, PMQR) among *Enterobacter* spp. isolates in Bulgaria.

Keywords: quinolone resistance, *Enterobacter* spp., PMQR, Bulgaria

Introduction

Enterobacter spp. is a common cause of hospital infections such as urinary tract, blood-stream, lower respiratory tract, and soft tissues.[1] These organisms have been associated with treatment failure and high mortality rate, mainly in patents admitted to intensive care units.[2] Recently, a WHO expert group defined a Priority Pathogen List for research and development of new antimicrobials active against

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DovePress
http://doi.org/10.2147/IDR.S204199

multidrug- and extensively drug-resistant Gram-negative bacteria. Third-generation cephalosporin resistant *Enterobacter* spp. were included in the first priority list, named "Priority 1: Critical", which shows their significance.[3] The treatment of infections associated with *Enterobacter* spp. is difficult due to overexpression of chromosomal AmpC enzymes, as well as production of ESBL (most commonly CTX-M, but also SHV and TEM).[1] During the last decade, increasing numbers of carbapenemase producing *Enterobacter* isolates have been reported.[4] Quinolones and aminoglycosides are treatment alternatives for infections caused by ESBL/AmpC or carbapenemase producing *Enterobacter* spp. susceptible to these antimicrobials.[6] The quinolones such as ciprofloxacin and especially levofloxacin and moxifloxacin possess a broad spectrum of activity and can be used in a wide range of infections. The increased inappropriate usage of quinolones has led to emergence of chromosomal point mutations in the quinolone-resistance determining regions (QRDR) (*gyrA* and/or *parC* genes), which encode the subunits of gyrase and topoisomerase IV enzymes.[5,6] Over the last decades, plasmid mediated quinolone resistance (PMQR) mechanisms have appeared. They perform target protection (gyrase and type IV topoisomerases) by qnr family proteins, enzymatic target modification by the aminoglycoside modifying enzyme aac(6′)Ib-cr and by efflux mechanisms (qepA and oqxAB).[5–7] In Bulgaria, there have been no reports about quinolone resistance determinants in *Enterobacter* spp.

The aim of this study was to determine the plasmid and chromosomal mechanisms of quinolone resistance in *Enterobacter* isolates resistant to third-generation cephalosporins from the University Hospital "Saint Marina" - Varna, Bulgaria, as well as to assess their association with ESBL/AmpC presence and plasmid replicon types.

Materials and methods

Bacterial isolates

A total of 175 isolates of *Enterobacter* spp. resistant to at least one third-generation cephalosporin were collected between January 2014 and January 2017 from hospitalized patients in the University Multiprofile Hospital for Active Treatment (UMHAT) "Saint Marina"-Varna during routine hospital laboratory work. Species' identification was done by Phoenix (BD, Franklin Lakes, NJ, USA). A previously published DHA-1 producing *Enterobacter* spp. isolate were also included in this study.[8]

Antimicrobial susceptibility testing

The antimicrobial susceptibility was determined by the disc diffusion method according to EUCAST, 2017 guidelines (http://www.eucast.org/clinical_breakpoints/). The following antimicrobial agents were tested: amoxicillin-clavulanate, cefotaxime, ceftazidime, cefepime, piperacillin-tazobactam, imipenem, meropenem, tobramycin, gentamicin, amikacin, trimethoprim/sulfamethoxazole (Oxoid, Basingstoke, UK). MICs of nalidixic acid, ciprofloxacin, and levofloxacin were determined by MIC strips (Liofilchem, Roseto degli Abruzzi, Italy).

Transfer of resistance determinants and plasmid replicon typing

Conjugative plasmid transfer was performed on BBL™ Mueller-Hinton agar II (Becton Dickinson, Sparks, MD, USA) using *Escherichia coli* K12:W_{3110} lac^- resistant to rifampicin as recipient. Transconjugants were selected on MacConkey agar (Becton Dickinson, Sparks, MD, USA) containing 50 mg/L rifampicin and 2 mg/L cefotaxime. Plasmid replicon types were determined by the PCR-based replicon typing scheme described by Carattoli et al,[9] using whole-cell DNA extracted from transconjugants. The replicon types were detected using primers described by Garcia-Fernandes et al.[10]

PCR detection and sequencing of ESBL and AmpC genes

PCR was performed to detect the presence of bla_{SHV} and $bla_{CTX\text{-}M}$ genes as previously described.[11] Plasmid-mediated AmpC genes –bla_{CMY}, bla_{FOX}, $bla_{DHA,}$ and bla_{AAC} were screened as described by Perez-Perez et al.[12] For sequencing of entire genes, primers binding outside the coding region were used for bla_{SHV}, $bla_{CTX\text{-}M\text{-}1\text{-}group}$,[11] and bla_{DHA}[13] The amplicons were purified and sequenced with ABI 3130xl Genetic Analyzer. The nucleotide and deduced amino acid sequences were analyzed and multiple alignments were performed using Chromas Lite 2.01 (Technelysium Pty Ltd, Brisbane, Australia) and DNAMAN version 8.0 Software (Lynnon BioSoft, Vaudreuil-Dorion, Canada).

Isoelectric focusing (IEF) and bioassay

Beta-lactamase production of representative SHV and CTX-M positive isolates and all CTX-M and SHV negative

isolates was analyzed by IEF as described previously.[11] The isolates with known beta-lactamases (TEM-1, OXA-1, SHV-3, SHV-12, CTX-M-3, and CTX-M-15) were used as controls. The hydrolytic activity of individual beta-lactamase bands was assessed by bioassay.[11] Two consecutive agar overlays were laid on the gel: first 0.5% tryptic soy agar (Becton Dickinson) containing the respective beta-lactam (cefotaxime 2 mg/L or ceftazidime 1 mg/L), followed (after 2hours of incubation at 35°C) by a second tryptic soy agar overlay containing the susceptible indicator strain *E. coli* K12:W_{3110} (Rif^R lac-, 1.2×10^7 CFU/mL). After an overnight incubation at 35°C, the growth of the indicator strain on the gel was determined the bands with hydrolytic activity.

Epidemiological typing

Whole-cell DNA was prepared by the GFX Genomic DNA Purification Kit (GE Healthcare UK Ltd, Little Chalfont, UK) and was used in random amplified polymorphic DNA analysis with ERIC 1 and ERIC 2A primers.[11] The genetic similarity was determined using Dice coefficient as similarity measure and the unweighted pair group method with arithmetic mean (http://genomes.urv.cat/UPGMA/).

Quinolone resistance determining regions (QRDR) and PMQR detection

QRDR in *gyrA* and *parC* were amplified by PCR and sequenced as described previously.[14] Plasmid mediated quinolone resistant determinants *qnrA, qnrB, qnrC, qnr*D, *qnrS,* and *qepA* were amplified[14] and sequenced with ABI 3130xl Genetic Analyzer. PCRs for *qep*A, *aac(6')-Ib,*[14] and *oqx*AB[15] were carried out. The exact allele of aac(6′)-Ib enzymes was determined with restriction with BtsCI (New England Biolabs, UK). If the allele *Ib-cr* was present, the PCR product was cut into two segments –270 bp and 210 bp.

The nucleotide sequences were analyzed with Chromas Lite 2.01 (Technelysium Pty Ltd) DNAMAN version 8.0 Software (Lynnon BioSoft) and NCBI Blast tool (http://www.ncbi.nlm.nih.gov). Mutations in QRDR of *gyr*A and *par*C were identified with comparison with DNA sequence of QRDR regions of *E. cloacae* ATCC 13047 (GenBank accession numbers D88980 and D88981 for *gyrA* and *parC,* respectively).[16]

Statistical analysis

Differences were assessed with the chi-squared test or Fisher's exact test (https://www.graphpad.com/quickcalcs/contingency1.cfm).

Results

Bacterial isolates and antimicrobial susceptibility testing

During the period 2014–2017, a total of 167 *Enterobacter cloacae* complex and eight *Enterobacter aerogenes* isolates resistant to at least one third-generation cephalosporin were collected from patients hospitalized in different hospital wards: intensive care units (39), surgery wards (21), hemodialysis (eight), hematology (17), pediatric wards (13), nephrology/urology wards (31), and other internal wards (46). The isolates were recovered from different clinical samples: urine (46), blood (45), central venous catheters (five), wounds (35), tracheal secretions (14), bronchoalveolar lavage (two), sputum (eight), bile (one), drainage fluids (six), throat swabs (eight), and synovial fluid (one).

The results of the antimicrobial susceptibility testing exhibited high resistance rates (resistant and intermediately susceptible) to third-generation cephalosporins (selection criteria) (ceftazidime, 98.9%; cefotaxime; 100%), aminoglycosides (tobramycin, 89.7%; gentamicin, 82.3%), and fluoroquinolones (ciprofloxacin, 79.4%; levofloxacin, 39.4%). The resistance rates to trimethoprim/sulfamethoxazole and piperacillin/tazobactam were 58.2% and 72%, respectively. The isolates were highly susceptible to imipenem (100%), meropenem (100%), and amikacin (88%). Twenty four isolates (13.7%) were susceptible to cefepime. MIC_{50} and MIC_{90} of nalidixic acid, ciprofloxacin, and levofloxacin are shown in Table 1.

Beta-lactamase identification

The PCR study showed positive results for bla_{SHV} and $bla_{CTX\text{-}M}$ group specific genes. The sequence analysis identified $bla_{SHV\text{-}12}$, $bla_{CTX\text{-}M\text{-}3}$, and $bla_{CTX\text{-}M\text{-}15}$. ESBL producing isolates were identified in 87% (152/175). CTX-M-15 was the predominant ESBL, detected in 73% (128/175) of the isolates, predominantly in *E. cloacae* complex isolates – 76%. CTX-M-3 production was found in 18 isolates (10%) and SHV-12 was present in only six (3%) isolates. All *E. aerogenes* isolates (except one) produced CTX-M-3 ESBL – 88%. Twenty three isolates were negative for the major types of ESBLs and were assumed as probable AmpC hyperproducers. All but one isolates were negative for bla_{CMY}, bla_{FOX}, bla_{AAC}, and bla_{DHA}. A single isolate of *E.*cloacae complex, co-producer of CTX-M-3 and DHA-1, has been previously reported.[8]

Table 1 MICs of nalidixic acid, ciprofloxacin, and levofloxacin in 175 *Enterobacter* spp. isolates

Antimicrobial agent	MICs mg/L																		MIC_{50}	MIC_{90}
	≤0.094	0.125	0.19	0.25	0.38	0.5	0.75	1	1.5	2	3	6	8	12	16	24	≥32			
Ciprofloxacin	23	2	10	1	11	19	2	29	7	10	8	9	1	5	-	-	38		1	≥32
Levofloxacin	29	12	16	16	8	25	11	3	-	8	3	5	3	4	3	1	28		0.38	≥32
	MICs mg/L																			
	≤0.75	1	1.5	2	3	6	8	12	16	24	32	48	64	98	128	≥256			MIC_{50}	MIC_{90}
Nalidixic acid	10	-	3	1	2	7	32	12	9	3	2	1	-	-	-	93			≥256	≥256

IEF and bioassay

IEF was performed with 48 isolates, representative for the three detected enzyme groups (CTX-M-15, CTX-M-3, and SHV-12). In addition, eight isolates, negative for both CTX-M and SHV enzymes were also studied. Beta-lactamases with pIs 5.4, 7.4, 7.8, 8.2, 8.4, 8.8, and ≥9.0 were found. Considering their cefotaxime-hydrolyzing activity determined by bioassay, the enzymes were assigned to different groups of beta-lactamases. All tested isolates positive for $bla_{\text{CTX-M-15}}$ gave one band with cefotaxime hydrolytic activity at pI 8.8. The tested isolates with $bla_{\text{CTX-M-3}}$ showed band with cefotaxime hydrolytic activity at pI 8.4. We did not find bands corresponding to TEM type ESBLs. The beta-lactamase with pI 7.4, with no cefotaxime hydrolytic activity was assumed to be an OXA-type broad-spectrum beta-lactamase. The beta-lactamases (pI 5.4) which did not hydrolyze ceftazidime or cefotaxime were deemed broad-spectrum TEM-1. For CTX-M and SHV PCR negative isolates, single beta-lactamases with pI 7.8 or ≥9.0 and no cefotaxime or ceftazidime hydrolytic activity were detected. These isolates were considered as chromosomal type AmpC enzymes.

Conjugation experiments and replicon typing

The conjugation experiments were successful for 40 (28 positive for $bla_{\text{CTX-M-15}}$ and 12 positive for $bla_{\text{CTX-M-3}}$) of 175 donor isolates (23%). CTX-M-3 and CTX-M-15 producers transferred the ESBL determinants in 67% (12/18) and 22% (28/128), respectively. The resistotypes of the transconjugant strains are shown in Table 2. Plasmid replicon typing showed the presence of IncL/M replicon type in all transconjugants that carried $bla_{\text{CTX-M-3}}$ (Table 2).

Regarding $bla_{\text{CTX-M-15}}$ gene, according to the resistance profile, seven types of transconjugants were found: three of them were positive for F replicon type and two (with identical resistance profile) were HI2 positive (Table 2). The other transconjugants were not typeable. The $bla_{\text{SHV-12}}$ positive *Enterobacter* spp. did not produce transconjugants. The aminoglycoside resistant determinants were most commonly co-transferred with ESBL genes. Quinolone resistance was observed in 13 transconjugates (33%), which were separated into two groups on the basis of their replicon type. (Table 2).

Molecular typing

ERIC PCR typing assigned all *E. cloacae* complex isolates to 15 different types. One dominant clone (A, n=92),

Table 2 Resistotypes and replicon types of 40 transconjugant isolates of *Enterobater* spp.

Type of the donor strains	Number of the donors tested	Number transcongugants	Resistotype of transconjugants	Replicon type
CTX-M-15 producers	128	28	CTX,CAZ,AMK,TOB,GEN (11)	Frep
			CTX,CAZ,AMK,TOB,GEN,**CIP** (11)	nt
			CTX,CAZ,AMK,TOB,GEN,**CIP**, TET,SXT (2)	HI2
			CTX,CAZ,AMC,TOB,GEN,TET(1)	Frep
			CTX,TOB,GEN,TET,SXT,CHL(1)	nt
			CTX,CAZ(2)	nt
CTX-M-3 producers	18	12	CTX,TOB,GEN,AMK (7)	L/M
			CTX,TOB,GEN,AMK,SXT(3)	L/M
			CTX,GEN (2)	L/M
SHV-12 producers	6	0	-	
AmpC hyperproducers	23	0	-	

Abbreviations: CTX, cefotaxime; CAZ, ceftazidime; AMC, amoxicilin/clavulanic acid; TOB, tobramycin; GEN, gentamicin; AMK, amikacin; CIP, ciprofloxacin, TET, tetracyclin; SXT, trimethoprim/sulfamethoxazole.

consisting of three ERIC types (A, n=56; Aa, n=32; Ab, n=4) with similarity >0.8 was identified. ERIC types E (n=3) and V (n=19) also defined a separate clone (similarity 0.8). The other ERIC types represented different clones with similarity between 0.2 and 0.7: clone C (n=32), B (n=3), F (n=5), K (n=2), and L (n=6). ERIC types D, J, I, H, and P were represented by single *E. cloacae* complex isolates. *E. aerogenes* demonstrated three different ERIC profiles: g (n=6), m (n=1), and q (n=1) with similarity of 0.5–0.6.

Quinolone resistance determinants

PMQR determinants

All 175 isolates were tested for presence of PMQR determinants. Totally, 103 isolates (59%) had PMQR determinants. The frequency of PMQR determinants in the group of ciprofloxacin resistant isolates was significantly higher (69%, 99/143 isolates) than in the susceptible isolates (13%, 4/32 isolates, $p<0.0001$).

All 103 isolates harbored *qnr* determinants. Five of them (2%) were positive for *aac(6')-Ib-cr* variant. No *qnrC, qnrD, qep*A, and *oqx*AB gene positive isolates were found. Three different *qnr* families were identified – *qnrA, qnrB,* and *qnrS*. Sequencing showed three *qnrB* variants. The first *qnrB* variant was identical to the published sequence DQ351241 of *qnrB1*[17] and is number 1 in *qnr* nomenclature in Lachey.org (https://www.lahey.org/qnrstudies/); the second one was identical to published sequence EF526508 of *qnrB9* and the third one was similar to published sequence accession number DQ303921 of *qnrB4* allele[18] with one silent mutation difference. *QnrA* and *qnrS* amplicons were identical to *qnrA1* (accession number AY070235[19] and CP031576.1 (*Enterobacter hormaechei*)) and *qnrS1* (accession number AB187515).[20]

QnrB1 and *qnrB9* were detected in 63 and 28 isolates, respectively. Combinations of determinants were found: *qnrA1, qnrS1, aac(6')-Ib-cr* and *qnrB9, qnrS1* in two isolates (Table 3). One isolate produced *qnrB4*. Eight isolates were *qnrA1* positive and four of them also harbored *aac (6')-Ib-cr* variant (Table 3). Three isolates were positive only for *qnrS1*.

The association between ESBL and PMQR determinants in *Enterobacter* spp. isolates is presented on Table 3. CTX-M-15 ESBL was associated predominantly with *qnr* determinants, mostly *qnrB* alleles. Eighty-seven *qnrB* positive isolates (96%, 87/91) carried $bla_{\text{CTX-M-15}}$, while only a single *Enterobacter* spp. isolate from a group of 16 positive for other *qnr* alleles isolates (6%) was a CTX-M-15 producer ($p<0.0001$).

The presence of $bla_{\text{CTX-M-15}}$ was significantly lower in the group of PMQR negative isolates (56%; 40 from 72) in comparison with the PMQR positive group (Table 3). CTX-M-3 and AmpC hyperproducers were not associated with presence of PMQR determinants. The SHV-12 producers carried *qnrA1* alleles. The single *qnrB4* positive isolate was positive for $bla_{\text{CTX-M-3}}$ and $bla_{\text{DHA-1}}$.

QnrB1 was successfully transferred only in two conjugation experiments. The transconjugants demonstrated resistance to cefotaxime, ceftazidime, amikacin, tobramycin, gentamycin, ciprofloxacin, tetracycline, and co-

Table 3 Distribution of plasmid mediated quinolone resistance (PMQR) alleles in *Enterobacter* spp. isolates according to the ESBL/AmpC enzymes and the ERIC type

PMQRD	Number	Beta-lactam resistance determinants (percent)				ERIC type
		CTX-M-15	CTX-M-3	SHV-12	AmpC overproducers	
qnrB1	62	60*	2*	-	-	A_{38},V_{10}, C_5, L_5,F_1,K_1, m_1,g_1
qnrB4	1	-	1+DHA-1	-	-	C_1
qnrB9	27	26	-	-	1	A_8,B_2,C_9,E_2,F_2,H_1,I_1,L_1,V_1
qnrB9 + *qnrS1*	1	1	-	-	-	C_1
qnrS1	3	-	3	-	-	C_2, F_1
qnrA1	4	1	-	2	1	A_2, C_2
qnrA1 + *aac(6')-Ib-cr*	4	-	-	2	2	A_4
qnrA1 + *qnrS1*+ *aac (6')-Ib-cr*	1	-	-	1	-	A_1
PMQRD positive	103	88 **(85%)**	7 **(7%)**	5 (5%)	4 **(4%)**	A_{53},C_{20},V_{11},L_6,F_4,B_2,E_2,K_1,H_1,I_1, m_1,q_1
PMQRD negative	72	40 **(56%)**	12**(17)	1 (1%)	19 **(26%)**	A_{39},C_{12},V_8, E_3,B_1,F_1,D_1,J_1,K_1,$P_1$$g_6$
p		<0.0001	=0.048	0.4	<0.0001	
Total all	175	128	18	6	23	A_{92},C_{32},V_{19},L_6,F_5,B_3,E_3,K_2,H_1,I_1 D_1, J_1,P_1, g_6,m_1,q_1

Notes: Statistically significant differences are presented in bold. *The group includes one *E. aerogenes* isolate. **The group includes six *E. aerogenes* isolates.
Abbreviations: PMQRD – plasmid mediated quinolone resistance determinants.

trimoxazole. Replicon typing detected the presence of HI2 replicons. *QnrB9* alleles were successfully transferred in eleven conjugation experiments. Resistance to ceftazidime, amikacin, tobramycin, gentamycin, and ciprofloxacin was detected in the transconjugants and they were nontypable in replicon typing. Some *qnrB1* postive transconjugants showed elevated MICs of ciprofloxacin (0.25–0.5 mg/L) and levofloxacin (0.12–0.38 mg/L), which were slightly higher than those found in the *qnrB9* positive transconjugants ($MIC_{of\ ciprofloxacin}$ 0.12−0.25 mg/L; $MIC_{of\ levofloxacin}$ 0.06−0.12 mg/L). The MICs for nalidixic acid were in the range 16–24 mg/L. Six of the eight *E. aerogenes* isolates were CTX-M-3 producers and PMQR negative. PMQR determinants, represented by *qnrB1*, were detected in two *E. aerogenes* isolates only.

QRDR

QRDR were studied in 130 *Enterobacter* isolates (127 *E. cloacae* and three*E. aerogenes* isolates). Substitutions in the QRDR of *gyrA* or/and *par*C were found in 53% of them (Table 4). Fifteen isolates (all members of clone V) with the highest ciprofloxacin and levofloxacin MICs harbored two substitutions in the QRDR of *gyr*A (Ser83Tyr and Asp87Ala) and one in *parC* (Ser80Ile) (Table 4). Two substitutions (one in *gyrA* and one in *parC)* were detected in 15 isolates of *E. cloacae* complex (Table 4). These isolates were highly resistant to ciprofloxacin and those positive for *qnrB4, qnrS1,* and *qnrA1* were also highly resistant to levofloxacin. A single substitution in *gyrA* region (Ser83Phe) was found in 35 isolates (Table 4). In general, the presence of at least one GyrA substitution led to a higher MIC of nalidixic acid (>256 mg/L), while a higher level of levofloxacin resistance was associated with a presence of two or more substitutions. Three *E. aerogenes* isolates showed presence of threonine in 83 positions of *gyrA* gene, which is typical for the wild type of *E. aerogenes* strains.[21]

Discussion

Quinolones are among the most commonly used antimicrobials to treat bacterial infections including those associated with *Enterobacter* spp. The prolonged usage of third-generation cephalosporins can lead to AmpC overexpression in *Enterobacter* spp. The present study demonstrated a high level (79.4%) of combined third-generation cephalosporins and ciprofloxacin non-suceptibility.

PMQR determinants have been increasingly reported in various *Enterobacteriaceae* species, especially in *E. coli, Enterobacter* spp., *Klebsiella* spp. and *Salmonella* spp.[6] The published data greatly depend on the selection criteria and the number of investigated PMQR determinants. The present study demonstrated a high frequency of PMQR

Table 4 Distribution of 130 *Enterobacter* spp. isolates according to point mutations in quinolone-resistance determining regions (QRDR) of *gyrA* and *parC*, plasmid mediated quinolone resistance (PMQR), MICs of quinolones, ERIC types, and ESBLs

Mutations in QRDR				MICs mg/L				Other characteristics		PMQD positive
Group number	GyrA		ParC	Number	Nx mg/L	Cip mg/L	Levo mg/L	ERIC type	Associated ESBL/AmpC genes	
A n=15	Ser83Tyr	Asp87Ala	Ser80Ile	15	≥256	>32	>32	V_{15}	CTX-M-15_{14}; CTX-M-3_1	*qnr*B1_7; *qnr*B9_1
B n=15	Ser83Ile	-	Ser80Ile	5	≥256	>32	>32	C_4, F_1	CTX-M-3_5	*qnr*B4_1; *qnr*S1_3; *qnr*A1_1
				10	≥256	>32	3–8	C_3,E_3;A_2; L_1; I_1	DHA-1+ CTX-M-3_1; CTX-M-15_8; AmpC$_1$	*qnr*B1_2; *qnr*B9_7
C n=5	-	Asp87Gly	-	5	≥256	1–3	3–6	A_5	SHV-12_2; AmpC$_3$	*qnr*A1_1 *qnr*A1 + aac(6′)-Ib-cr$_4$
D n=34	Ser83Phe	-	-	9	≥256	1–3	2–3	A_9	CTX-M-15_9	*qnr*B1_6; *qnr*B9_1
				25	≥256	0.19–1	≤0.5	A_{22};K_1; F_1; J_1	CTX-M-15_{22}; AmpC$_3$	-
E n=61	-	-	-	35	6–48	0.38–2	0.12–0.75	A_{14};B_2;C_8; F_3L_5;H_1; K_1;m_1	CTX-M-15_{33};SHV-12_1 CTX-M-3_1;	*qnr*B21_1; *qnr*B9_{13}; *qnr*A1_1
				26	≤6	≤0.25	≤0.25	A_{12};C_{10}; D_1;P_1; g_3	CTX-M-15_7; CTX-M-3_5; AmpC$_{13}$; SHV-12_1	-

Note: *E. aerogenes* ERIC types are shown in small letters.
Abbreviations: Nx, nalidixic acid; Cip, ciprofloxacin; Levo, levofloxacin; QRDR – quinolone resistance determining regions.

positive *Enterobacter* spp. (59%) in a large collection of third-generation cephalosporin resistant clinical isolates of *Enterobacter* spp. Similar results were reported for ESBL producing *Enterobacter* spp. isolates from Tunisia (50%), Mexico (61%), and Argentina (66%),[22,23] but lower rates for isolates from Cote d'Ivoire (42.9%).[24]

PMQR determinants typically induce low-level quinolone resistance with ciprofloxacin MIC of ≥0.25 µg/mL. They facilitate the selection of chromosomal mutants with higher level quinolone resistance and promote treatment failure.[5,7] In previous investigations, the presence of PMQR determinants in *E. coli* isolates was found to reduce ciprofloxacin activity in urinary[25] and respiratory tract[26] infections in a murine model.

The aac(6′)-Ib-cr enzyme and the qnr proteins are the most widely distributed PMQR determinants worldwide.[5,7] In the present study, the *qnrB* was the most common PMQR determinant, detected in 88% of all PMQR positive isolates (n=103). This is in concordance with other studies which reported *qnrB* determinant as the most prevailing PMQR determinant among *Enterobacter* spp. isolates. A survey from France showed that *qnr*, especially *qnrB* determinants, was predominant in carbapenem resistant *E. cloacae* isolates.[27] The same finding was reported from authors in Tunisia and Mexico.[22,23]In a recent survey from Iran, *qnr* genes were the predominant PMQR determinants in *E. cloacae* (60.3%). The authors found *qnrB1, qnrS1,* and *qnrB4* alone or in combinations, to be the most common genes.[28]

In our study, three variants of *qnrB* alleles were detected: predominantly *qnrB1* (61%; 63/103), followed by *qnrB9* (27%; 28/103), and *qnrB4* in a single isolate only. In addition, one *qnrB9* allele was found in a combination with *qnrS1. QnrB1* genes were commonly detected in *Enterobacter* spp. isolates. They prevailed in isolates from Iran,[28] Tunisia,[22] Italy,[29] and Algeria[30] In our study, *qnrB4* was found in one isolate only. This is in contrast with reports from some European countries, where *qnrB4* is the main detected allele.[31,32] *QnrB4* gene was recently detected in two Bulgarian NDM-1 producing isolates of *Klebsiella pneumoniae*.[33] Other *qnrB* alleles *(qnrB10, qnrB13,* and *qnrB18*) were found in *Citrobacter freundii* isolates from Bulgaria.[34]

Until now, 94 *qnrB* alleles (https://www.lahey.org/qnrstudies/) have been reported with *qnrB1, qnrB2, qnrB4, qnrB5, qnrB6,* and *qnrB19* being the most common.[5–7] In addition to this allele group, the present study has added *qnrB9* as the second most commonly detected gene (27%). This allele has been rarely reported and found mostly in *E. coli*[35] and in environmental and fecal carriage isolates of *C. freundii*.[36–38] Very recently, *qnrB9* was detected in *Enterobacter* spp. clinical isolates.[39]

The attempts to transfer the quinolone resistance determinants by conjugation experiments were successful. *QnrB1* gene was transferred rarely than *QnrB9* and the *qnrB1* transconjugants showed presence of replicon type HI2. In all cases the transconjugants were $bla_{\text{CTX-M-15}}$ positive and demonstrated resistance to aminoglycosides. *QnrB* alleles have been found often on plasmids carrying TEM, CTX-M (especially CTX-M-15), SHV, VEB, IMP, DHA, OXA-48, and KPC-3.[5,6] The results from the epidemiological typing revealed that the *qnrB* positive isolates belonged to different clones. We did not find any association between a particular *qnrB* allele and a specific clone. However, almost half of the isolates belonged to the predominant clone A (53%). We may conclude that the *qnrB* distribution in this study was mediated by both plasmid and clonal dissemination.

In concordance with other reports, *qnrA1* and *qnrS1* genes were rarely found in our study.[6,22,28] Similar to *qnrB*, all isolates with *qnrA1* determinants belonged to the main clone A. This fact showed the possibility for this clone to acquire different PMQR determinants. *QnrS1* was predominantly detected in clone C isolates.

Interestingly, we revealed a very low number of *aac(6')-Ib-cr* positive isolates. The acetyltransferase *aac(6')-Ib-cr* was produced only in combination with *qnrA1* (n=4) or *qnrA1* and *qnrS1* (n=1). It has been reported commonly in *E. coli* isolates, less frequently in *K. pneumoniae,* and rarely in *E. cloacae.*[5,6] However, some studies among *Enterobacter* spp. isolates showed higher rates for this enzyme.[6,27,31] *Aac(6')-Ib-cr* enzyme has been previously reported in Bulgaria, mainly in *E. coli*, but also in *E. aerogenes, K. pneumoniae,* and *C. freundii*.[34]

To the best of our knowledge, the present study is the first report of *qnrB1, qnrB9, qnrA,* and *qnrS* in Bulgaria. Similar to other surveys, we did not find *oqxAB, qepA, qnrD,* and *qnrC*.[6,22]

The present study investigated 175 third-generation cephalosporin resistant clinical isolates of *Enterobacter* spp. ESBL production was identified in 87%. Only 23 isolates were possible AmpC overproducers. CTX-M-15 was the predominant ESBL type in *E. cloacae* complex isolates. *E. aerogenes* mostly produced CTX-M-3 enzymes. These results confirm the findings of our previous report in 2014[40] and demonstrate a significant increase in the rate of CTX-M-15 producing *E. cloacae* isolates (45% in 2011/2012 vs 76% in the present study) ($p<0.0001$).

In the present study, a significant association between CTX-M-15 production and the presence of PMQR determinants was found: 88% of all PMQR positive isolates were CTX-M-15 producers vs 56% of all PMQR negative isolates ($p<0.0001$). CTX-M-15 was associated with *qnrB1* or *qnrB9*. The single *qnrB4* positive isolate detected in this study was a co-producer of DHA-1 and CTX-M-3 enzyme. The association between *qnrB4* and $bla_{\text{DHA-1}}$ has been reported for *K. pneumoniae*.[41] In addition, Potron et al[31] found an association between *qnrB4* and SHV-12 ESBL in *Enterobacter* spp. isolates. In our study, *qnrS1* was associated with CTX-M-3 production. SHV-12 ESBL producers predominantly showed the presence of *qnrA1* allele (five *Enterobacter* spp. from all six had *qnrA1)*, although this association is not significant due to the small number of isolates. Similar data were reported from Korea and Japan.[41,42]

In addition to the PMQR determinants, substitutions in QRDR were detected in 53% of all ciprofloxacin resistant isolates (n=103). The most frequent substitutions in *gyrA* were Ser83Phe (49%), followed by Ser83Ile (22%), Ser83Tyr (22%), Asp87Ala (22%), and Asp87Gly (7%) (Table 4). For *ParC,* the Ser80Ile substitution was the single type mutation identified in 44% of all isolates (Table 4). Ser83Phe and Ser83Ile have been reported as common mutations in *gyrA* among *E. cloacae* isolates from France[21,27] and Tunizia[22]

In our study, Ser83Phe mutation (Group D, Table 4) was associated with isolates from clone A (31 of 34 members). The isolates positive for this mutation could be divided into two groups: with and without PMQR determinants (Table 4). For the *qnr* positive group, slightly increased MICs to ciprofloxacin were observed, but both groups demonstrated levofloxacin susceptibility.

Asp87Gly mutation was found in five *qnrA1* positive isolates from clone A. These isolates showed slightly elevated MICs to both ciprofloxacin and levofloxacin.

The substitutions Ser83Ile (*gyrA*) and Ser80Ile (*parC*) were identified in 15 isolates (Group B, Table 4) with higher MICs for nalidic acid (>256 mg/L) and

ciprofloxacin (>32 mg/L). The MICs to levofloxacin were slighly increased (3–8 mg/L) and were higher in PMQR positive isolates. Interestingly, this group was presented predominantly by CTX-M-3 producers and the single DHA-1 positive isolate.

Three substitutions – two in *GyrA* (Ser83Tyr, Asp87Ala) and one in *ParC* (Ser80Ile) were identified in 15 isolates with very high MICs to the three tested quinolones (Group A, Table 4). Isolates with three substitutions and respectively higher resistance rates were associated with only one clone – V. In this group, only seven isolates were *qnr* positive.

In addition, *ParC* mutations were found in combination with GyrA substitutions. This is in agreement with other studies which demonstrated that the bacterial gyrase is the primary affected enzyme, while topoisomarase IV is the secondary target.[5,7]

The present results showed that a single mutation in QRDR resulted in the increase in the MICs for nalidixic acid only, while the higher level of quinolone resistance was associated with two or more mutations. This finding is in concordance with those of other authors.[5–7] The relatively small number of isolates with two and more mutations is in concordance with not very high resistance to levofloxacin, which gave more therapeutic options.

In conclusion, a high proportion of combined third-generation cephalosporin and quinolone resistant *Enterobacter* spp. was detected. The rate of ESBL producers in the isolates was high (87%), CTX-M-15 being the major enzyme identified. The predominant PMQR determinant was *qnrB* (*qnrB1* and *qnrB9*). They were co-transferred with $bla_{\text{CTX-M-15}}$ gene, showing possibility of both beta-lactams and quinolones to select resistant strains. The alterations in 83 and 87 positions of *gyrB* in QRDR, and in 80 positions of *parC* gene were associated with a high level of quinolone resistance. The results showed the need for more prudent use of quinolones and third-generation cephalosporins because of the risk of promoting dissemination and selection of multiple resistance determinants (ESBL, PMQR) among *Enterobacter* spp. isolates.

Acknowledgments

This study was funded by grant number 8383/07.12.2016 and contract number D-59/2.05. 2017 from the Medical University of Sofia, Sofia, Bulgaria.

Disclosure

The authors report no conflicts of interest in this work.

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