

Detection Of Plasmid Mediated Quinolone Resistance Among Isolates From Cirrhotic Patients With Spontaneous Bacterial Peritonitis In A University Hospital

¹Rana M. Elshamy, ¹Mervat S. Oda, ²MaysaaA.Saeed, ¹RaghdAA. Ramadan

¹Medical Microbiology and Immunology Department, Faculty of Medicine, Zagazig University, Zagazig, Egypt

²Tropical Medicine Department, Faculty of Medicine, Zagazig University, Zagazig, Egypt

Corresponding author:

RanaElshamy

Medical Microbiology and Immunology Department, Faculty of Medicine, Zagazig University, Egypt.

Email: ranaelshamy5@gmail.com

Abstract

Introduction: Spontaneous bacterial peritonitis in advanced liver cirrhosis and its treatment have a global burden in healthcare management especially in our locality. Fluoroquinolones are widely used as prophylaxis in that group of patients. Data concerning the prevalence of PMQR determinants in SBP are quite limited.

Purpose: To study prevalence of PMQR determinants in isolates from ascetic fluid of cirrhotic patients with SBP and the relation to ESBL production.

Patients and Methods: Ascetic fluid culture was performed; Identification and antimicrobial susceptibility of isolates were done by conventional methods. FQ resistant isolate are subjected to double disc synergy test for phenotypic detection of ESBL and Polymerase chain reaction for detection of PMQR determinants.

Results: Among total of 145 Ecoli, 21 Klebsiella pneumonia and 31 gram positive cocci, we found that 70 Ecoli (48.2%), 10 K pneumonia (47.6%) and 10 (32.2%) Gram positive isolates were FQ-resistant. All tested FQ-Resistant Gram negative isolates (100%) harbored at least one of studied PMQR genes. *acc6-Ib-cr* is most frequent (87.5%) followed by *qnrS* (81.2%), while *qnrB* frequency was 12.5% and *qepA* was detected in 10% of gram negative bacilli. In Gram positive cocci 6 isolates showed PMQR (*acc6-Ib-cr* & *qnrS* only). A statistically significant association was found between ESBL producers and *acc6-Ib-cr* gene, an association was also found with *qnrS* gene.

Conclusion: PMQR determinants and ESBLs prevalence is high among FQ-resistant isolates from ascetic fluid of cirrhotic patients diagnosed with spontaneous bacterial peritonitis. The PMQR genes and their association with ESBL-producing plasmids have a great effect on multidrug resistance spread, thus might lead to serious problems. Judicious use of quinolones as prophylaxis in SBP patients is essential.

Keywords: Spontaneous bacterial peritonitis, Fluoroquinolone resistance, PMQR determinants, extended spectrum beta lactamases.

INTRODUCTION:

Spontaneous bacterial peritonitis is frequent and life threatening complication in cases have advanced liver cirrhosis with hospital mortality that reaches up to 80% [1]. Intestinal bacterial translocation through gut wall is the cause, so decreasing the burden of intestinal pathogenic bacteria and consequently its translocation is effective in preventing SBP [2]. Secondary antibiotic prophylaxis

for avoidance of recurrence in cirrhotic cases with ascites and primary antibiotic prophylaxis with elevated-risk profile is recommended by recent guidelines [3].

Quinolones are widely used as a prophylactic therapy in that patient group; unfortunately quinolone prophylaxis had been related to overgrowing of intestinal gram positive bacteria as *Staphylococcus aureus* and *Enterococcus* spp., and also related to increased prevalence of quinolone-resistant gram negative bacteria (QR-GNB) [4]. Resistance to quinolones has emerged over the last years due to extensive use of quinolones in human and veterinary medicines; They have been prescribed to treat UTI infections as well as respiratory tract, intra-abdominal and skin infections [5, 6].

Plasmid mediated quinolone resistance genes (PMQR) changed quinolone resistance pattern. PMQR was first described in 1990s [7,8]. First PMQR, *qnrA*, was described in 1998 [9] and, to date, about 100 *Qnr* variants have been identified, being classified to 6 families as: *QnrA*, B, S, C, D and VC. The *Qnr* protein belong to pentapeptide-repeat protein and confer quinolone resistance throughout physical protection of DNA gyrase and topoisomerase IV from inhibition by quinolones [10]. PMQR have been mainly detected in transposons and/or integrons, meanwhile; these genes have also been reported with a certain frequency in chromosomal locations, reflecting the plasticity of PMQR-related mobile genetic elements [11].

Horizontal transmission of these mobile elements represents a major clinical problem due to easy dissemination with wide geographical distribution [12]; In addition, co-location of PMQR with multiple resistance determinants (frequently extended spectrum β -lactamases, carbapenemase and Amp-C-type β lactamase genes) in MDR plasmids represents an alarm [13]. Actual prevalence of these determinants is not precisely known. Incidences varying <1% to <50% have been reported, depending on the bacterial species and resistance mechanism [14]. Due to lacking data especially in our locality, we decided to investigate PMQR prevalence and their association with ESBL production in isolates from ascitic fluid in patients suffering from spontaneous bacterial peritonitis who have a high rate in Egypt. Extensive use of quinolones as prophylaxis among these patients had paid attention for that emerging problem.

Methods:

Cross sectional investigation conducted for 35 months (January 2017_November 2019) in Medical Microbiology and Immunology Department, Faculty of Medicine, Zagazig University. Specimens were collected from ICU of Tropical Medicine Department, Zagazig University Hospitals.

Bacterial Isolates

Isolates were collected from ascitic fluid of cirrhotic patients diagnosed clinically with spontaneous bacterial peritonitis with PML count of ascitic fluid ≥ 250 cells/mm³, who had not yet received antibiotics. A sterile syringe was used to withdraw 10 ml from ascitic fluid and inoculated immediately in the blood culture bottles (Inoculated at bedside). Foil cap of blood culture bottle was held cut and then the rubber cap was wiped using an ethanol swab, then perforated with the syringe containing the collected ascitic fluid, the top of culture bottle was wiped again with ethanol swab and foil cap was replaced, the sample was mixed with the broth without delay, bottles were labeled with the name, the number of case and the date of collection. Blood culture bottles incubated on 37°C and subculture was done after the first night incubation on blood agar and MacConkey agar plates and then were aerobically incubated on 37°C / 24 hours. The plates were examined after the incubation period for growth, Negative blood culture bottles were checked and sub cultured every other day, If there was no evidence of microbial growth after 10 days of incubation, the culture was considered negative [15,17]. Identification up to species level was done by conventional methods.

Phenotypic detection of FQ Resistance

Collected *Enterobacteriaceae* and Gram positive isolates subjected to phenotypic FQ resistance detections by disk diffusion using ciprofloxacin and levofloxacin antibiotic discs.

Disc Diffusion Method

Antimicrobial susceptibility was done by disc diffusion method (Modified Kirby-Bauer technique) using Muller Hinton agar according to Clinical Laboratory Standards Institute. [12] For

Enterobacteriaceae, in addition to FQ discs (ciprofloxacin (CIP) 5 µg and levofloxacin (LVX) 5 µg), we used antimicrobial discs including carbapenems (Imipenem (IMP) 10 µg, Meropenem (MEM) 10 µg), aminoglycosides (Amikacin (AK) 30 µg, gentamicin (GEN) 10 µg), penicillin/β-lactamase inhibitor (amoxicillin/clavulanic acid (AMC) 20/10 µg), monobactam (Aztreonam (ATM) 30 µg), broad-spectrum cephalosporins (cefoxitin (FOX) 30 µg, ceftazidime (CAZ) 30 µg, cefepime (FEP) 30 µg, cefotaxime (CTX) 30 µg and ceftriaxone (CRO) 30 µg), trimethoprim-sulfamethoxazole (SXT) 25 µg.

Gram positive isolates were subjected to FQ discs (ciprofloxacin (CIP) 5 µg and levofloxacin (LVX) 5 µg), in addition; we used penicillin (oxacillin (OX) 1 µg, fifth generation cephalosporin (ceftaroline (CPT) 30 µg), aminoglycosides (gentamycin (CN) 10 µg), carbapenems (imipenem (IPM) 10 µg, meropenem (MEM) 10 µg), clindamycin (CLI) 2 µg, doxycycline (DO) 5 µg, trimethoprim-sulfamethoxazole (SXT) 25 µg, quinopristin-dalfopristin (QDA) 15 µg, linezolid (LZD) 30 µg, vancomycin (VA) (E test strips).

Phenotypic Detection of ESBL

Enterobacteriaceae were subjected to initial screening for ESBL production by inhibition zones produced by ceftazidime (30 µg), ceftriaxone (30 µg), and cefotaxime (30 µg). Breakpoints indicative of ESBL suspicion were ≤22 mm for ceftazidime, ≤25 mm for ceftriaxone, and ≤27 mm for cefotaxime. Double-disk synergy test was used for phenotypic ESBL detection, Antibiotic disks were ceftriaxone (30 µg), cefotaxime (30 µg), ceftazidime (30 µg), aztreonam (30 µg), and amoxicillin/clavulanic acid (20/10 µg) [17] 4 antibiotic discs were placed at 20 mm edge to edge from amoxicillin/clavulanic acid disk which was placed in the middle. After one day incubation, if enhanced zone of inhibition between cephalosporin antibiotics and the amoxicillin/clavulanic acid disk occurred, test would be considered as ESBL positive. Multi-drug resistant bacteria was defined as resistance to at least three usually-active drugs from different classes, vancomycin-resistant enterococci, methicillin-resistant staphylococci, extended spectrum beta lactamase produced by Gram negative bacteria [18].

Genotypic Detection of FQ Resistance Determinants

Isolates found resistant to FQ were subjected for PCR (Polymerase Chain Reaction) amplification of PMQR.

Plasmid Extraction

For *Enterobacteriaceae*, extraction of bacterial plasmid was performed using QIAprep® Spin Miniprep Kit (Qiagen GmbH, Hilden, Germany).

DNA Extraction

DNA extraction was performed using QIAamp® DNA Mini kit (Qiagen GmbH, Hilden, Germany).

Simple PCR to Detect PMQR

5 PMQR genes detection was performed using simple PCR, for QnrA, B and S, aac(6')-Ib-cr and qepA genes. Amplification was performed using Taq PCR Master Mix (Qiagen GmbH, Hilden, Germany) and primers listed on Tab. 1. Following components were added for every 20 µL reaction: 10 µL of PCR Master Mix (2X), 2 µM of forward primer, 2 µM of reverse primer, (Table 1) 2 µg of template DNA, 4 µL of water (nuclease free). The Amplification was carried out under the following conditions: 30 sec at 96°C for denaturation, then annealing for 30 sec with temperature according to each primer as shown in table 1 and elongation at 72° for 60 sec [19] DNA fragments were analysed by electrophoresis in 2% agarose gel.

Our investigation was done in accordance with Declaration of Helsinki and approved by institutional review board (IRB) – Faculty of Medicine, Zagazig University.

Table I: Primers Sets Used for Detection of PMQR Genes[20, 21, 22]

Gene	Primer sequence (5' to 3')	Size of PCR product (bp)	Annealing temperature(°C)
qnrA-F	ATTTCTCACGCCAGGATTTG	516	53
qnrA-R	GATCGGCAAAGGTTAGGTCA		
qnrB-F	ATGACGCCATTACTGTATAA	469	53
qnrB-R	GATCGCAATGTGTGAAGTTT		
qnrS-F	ACG ACA TTC GTC AAC TGC AA	417	53
qnrS-R	TAA ATT GGC ACC CTG TAG GC		
aac(6')Ib-cr-F	TTGCGATGCTCTATGAGTGGCTA	482	54
aac(6')Ib-cr-R	CTCGAATGCCTGGCGTGTTT		
qepA-F	GCA GGT CCA GCA GCG GGT AG	199	60
qepA-R	CTT CCT GCC CGA GTA TCG TG		

Statistical analysis

Data was analyzed throughout using SPSS 20.0 for windows (SPSS Inc., Chicago, IL, USA). Qualitative data was expressed as numbers & percentage. Chi-square test or Fisher exact test were used to compare percent of categorical variables. Probability values (p) < 0.05 were considered statistically significant (S).

Results

During the study period, 145 Ecoli, 21 Klebsiella pneumonia and 31 gram positive cocci were collected from hospitalized cirrhotic patients diagnosed with SBP from ICU of Tropical medicine department, Zagazig University Hospitals. The Gram positive cocci included (16 staph aureus, 9 Enterococci, 3 CoNS and 3 Viridans streptococci). Among the isolates, 70 Ecoli (48.2%), 10 K pneumonia (47.6%) and 10 (32.2%) Gram positive isolates were FQ-resistant (resistant to ciprofloxacin and levofloxacin) and were included in investigation.

Antibiotic susceptibility results among FQ-resistant Ecoli isolates shown in **Table 1**. Out of 70 FQ-resistant Ecoli isolates, 55 (78.5%) expressed MDR phenotype; the highest rates of resistance were detected to cephalosporins (90% -100%), Aztreonam (87.1%), piperacillin-tazobactam (82.8%) and amoxicillin-clavulinate (68.5%). Meropenem and Imipenem showed good action with least resistance rates (5.7% and 7.1% respectively). Antibiotic susceptibility pattern among FQ-resistant K pneumonia are shown in **Table 2**. MDR phenotype was expressed in 6 (60%) of K pneumonia isolates. The highest resistance rates were also detected for cephalosporins (90-100%), Aztreonam (100%), amoxicillin-clavulinate (70%) and piperacillin-tazobactam (70%). Meanwhile, all isolates except one were sensitive to imipenem (90%) and meropenem (90%). ESβL phenotype was detected in 55 (68.7%) out of 80 FQ-resistant Enterobacteriaceae including 50 isolates Ecoli and 5 isolates K pneumoniae. Regarding FQ resistant Gram positive cocci, **Table 3** summarized their antibiotic susceptibility pattern. All *S. aureus* isolates were sensitive to ceftaroline, imipenem, vancomycin and linezolid; one MRSA was detected and was thus considered MDR. None of the gram positive isolates was vancomycin or linezolid resistant.

PCR for five PMQR determinants was performed, **Table 4** illustrated PMQR detection among 80 FQ-resistant Enterobacteriaceae isolates. All tested FQ-Resistant Gram negative isolates (100%) harbored at least one of the tested PMQR genes. We detected *acc6'-Ib-cr* gene with highest frequency (70/80 - 87.5%) followed by *qnrS* (65/80 - 81.2%) (**Figure 3,4**). Lower rates of *qnrB* (10/80 - 12.5%) and *qepA* (8/80 - 10%) were found while we found no *qnrA* gene. In Gram positive isolates, PMQR were detected in 6 out of 10 FQ-resistant isolates as summarized in **Table 5**. *qnrS* (6/10 - 60%) and *acc6'-Ib-cr* (5/10 - 50%) were the only found in Gram positive isolates, None of *qnrA*, *qnrB* or *qepA* were found in Gram positive isolates.

Concerning association between ES β L production and PMRQ genes, **Table 5** demonstrated statistically significant association between production of ES β L & *qnrS* gene carriage $p < 0.001$. Significantly association was also reported among *acc6* - *Ib-cr* gene detections and ES β L productions $p = 0.035$.

DISCUSSION

Spontaneous bacterial peritonitis in advanced liver cirrhosis and its treatment have a global burden in healthcare management especially in our locality. Fluoroquinolones constitutes an important line in the prophylaxis from SBP recurrence or in cirrhotic patients with high-risk profiles, These patients may take prophylaxis for entire life or till liver transplantation [3]; however, extensive use of FQ has led to and increased prevalence of quinolone-resistant strains especially in developing countries [23].

FQ resistances rates were found to be 48.2% of *E. coli* isolates, 47.6% of *K. pneumonia* isolates but was lower in Gram positive isolates (32.2%). This comes in consistent with a recent study in our locality that detected FQ resistance among 46.8% of uropathogenic *E. coli* [24]. A systemic review detected moderately high rate of quinolone resistance in Arab countries up to 31% - 38% in Tunisia and Lebanon respectively [25]. Globally, quinolone resistance rates varies from 35% to 57% in several geographical areas [26]. Higher rate observed in Iran (45.3–61.9%) and in Pakistan (84.2%) [27,28]. Egyptian studies had been previously reported high rates of quinolone resistance in isolates from SBP [29,30] nearly similar rates also detected by Ardolino E et al [31]. Lower rates of resistance among SBP patients were detected by other studies in Germany [32, 33]. Adequate antibiotic prescription policy followed in developed countries could be the cause of these variations.

Cirrhotic cases were frequently exposed to health care structure, and carrying higher probabilities of colonization by multidrug resistant germs. Fluoroquinolone exposure had led to higher rates of resistant microorganisms in enteric microbiota [34]. We detected MDR phenotype in 78.5% of FQ-resistant *E. coli* and 60% of FQ-resistant *klebsiella* isolates; this was in accordance with a systematic review by Foire et al., who reported an overall proportion of MDR bacteria in SBP from 22% to 73% of cases across several studies [35]. Piano et al found less prevalence of MDR (35%) [36]. While in Germany, no MDR organisms were isolated from SBP patients in a study by Lutz et al [32].

Several studies on FQ-resistant strains from urinary tract infection reported nearly similar results [24, 37, 38, 39], which was attributed to FQ resistance genes coexistence along with genetic determinants of other antimicrobials on mobile genetic elements.

The isolated FQ-resistant *E. coli* unfortunately give higher rates of resistance to cephalosporins (90%-100%), where are used as first line empirical treatment of SBP, There was also high resistance rates to amoxicillin clavulanic acid and piperacillin/tazobactam. *K. pneumonia* isolates also showed high resistance to cephalosporins, amoxicillin/clavulanic acid, piperacillin/tazobactam but fortunately, carbapenems, amikacin and gentamycin showed good action against gram negative isolates that was in accordance to the new guidelines by European Association for the Study of Liver (EASL) that recommended carbapenems for nosocomial SBP especially in localities with high frequency of ESBL [3]. Meanwhile, lower resistance levels among SBP patients were reported in Germany by Lutz et al. who detected 31% resistance to 3rd generation cephalosporin in, 35% to quinolones and 23% to piperacillin/tazobactam [32] while in Spain resistance was only 9% to 3rd generation cephalosporins [40]. In addition, our result comes similar to the findings of Majlesi et al who found that FQ-resistant Enterobacteriaceae isolates showed resistance to other antimicrobial agents like cefotaxime, ceftazidime, cefoxitin, cefepime, aztreonam, amoxicillin-clavulanic acid, tetracyclines, rifampicin, and trimethoprim-sulfamethoxazole, but remain susceptible to carbapenem antibiotics [41].

As regard to gram positive cocci in our study, 25% (4/16) of staph aureus, 66.6% (2/3) CoNS, 22.2% (2/9) of Enterococci and 33.3% (1/3) of streptococci were resistant to FQs, which was inconsistent to results of a previous study [42]. One MRSA was detected, that isolate was sensitive to carbapenems, vancomycin, linezolid and ceftaroline (the only fifth generation (anti MRSA) cephalosporin). All other staphylococcus isolates were sensitive to oxacillin; several studies reported isolation of MRSA in SBP [42,43]. Quinolone use was reported to be associated with a risk ratio of 3 of acquiring methicillin-resistant Staphylococcus aureus (MRSA) infection, the highest across different class of

antibiotics, with relevant consequences in infections other than SBP.[44] We found no vancomycin resistant cocci.

The Previous discrepancy in antimicrobial susceptibility pattern and frequency of MDR phenotype detection could be due to different study populations, different samples and variable antibiotic selective pressures so regional epidemiological studies are essential in order to design hospital antimicrobial stewardship programs.

Regarding ESBL production, we detected ESBL production in (55/80)68.7% of FQ-resistant Enterobacteriaceae, including 50 E. coli isolates and 5 Klebsiella isolates. Nearly consistent results were found in FQ-resistant Enterobacteriaceae isolated from patients with UTI [45], while other studies reported lower rates [46,47]. The co-resistance to ciprofloxacin and ESBL production demonstrated enormous impacts of antibiotic pressure and selection in intestine post susceptible bacteria had killed by many antibiotics [34].

Plasmid mediated quinolone resistance genes (PMQR) have changed the pattern of quinolone resistance. Patient group in our study are frequently exposed to quinolones as it is used as prophylaxis in those patients after a previous attack of SBP or GI bleeding. Regarding PMQR genes, All tested Enterobacteriaceae isolates (100%) were found carrying at least one of the PMQR with *acc(6)-Ib-cr* being the most prevalent (87.5%) followed by *qnrS* gene (81.2%) and less frequently *qnrB* gene (12.5%) and *qepA* (10%). No *qnrA* gene was detected.

The incidence and distribution of PMQR genes shows a great discrepancy. A study on *Klebsiella* in Egypt by Hammad et al. detected PMQR genes in all isolates but the highest prevalence of *qnrS* (81.3%) and lower percentage of *acc(6)-Ib-cr* (23.3%) than our results [48] while in accordance to our study, a recent study in our locality found *Acc(6)-Ib-cr* the most prevalent gene (80.1%) and less frequently *qnrS*, *qnrB* and *qepA* [24]. Several other studies also reported nearly similar rates of PMQR detection [30,45, 49].

In accordance to our results; no *qnrA* was detected in Egyptian study and in Iran [24,49] while Thai, Mexican and Korean studies showed no detection of *qepA* gene [50, 51,52]. *qepA* was documented in Japan, France and China [54]. Harboring more than one PMQR genes was frequently found in 58 isolates 72.5% carried both *acc(6)-Ib-cr* & *qnrS* while 7 isolates carried *acc(6)-Ib-cr* & *qnrS* & *qnrB* genes at the same time. Co-existence of *acc(6)-Ib-cr* & *qnr* were reported in other studies [24, 54].

In contrast, lower prevalence for PMQR than our finding (<1%) were observed [55, 56, 57, 58]. Probably geographical changes, different pattern of antibiotic resistance and infection control policies are causes of this discrepancy in the PMQR distribution.

Concerning association between ESBL production and PMQR genes detection, a study carried out by Khalil et al, found a prevalence of PMQR genes 85.7% among ESBLs producing Enterobacteriaceae clinical isolates [59]. In addition, Higher PMQR prevalence determinants was 93.1% [60]. Interestingly we found all ESBL positive Enterobacteriaceae isolates harbored PMQR, Statistically significant association was found between *qnrS* carriage and ESBL ($p < 0.001$). Additionally, there was significant association between *acc(6)-Ib-cr* and ESBL positive isolates, that was consistent with previous studies in Iran and Korea [49, 61]. Perhaps that is due to co-carriage of PMQR genes with other resistance determinants frequently ESBL, AmpC-type β -lactamase and carbapenemase genes on a plasmid [12].

Additionally, PMQR genes were sought in the gram positive isolates. Interestingly 6 of tested gram positive isolates that showed phenotypic resistance to quinolones harbored PMQR. Previous studies reported PMQR genes (*qnr* & *acc6-Ib-cr*) in gram positive bacteria carried on chromosomes [62].

Association between PMQRs and ESBLs is clinically important since treatment options for these isolates are limited and led to therapy failure; so more cautious use of quinolones as a prophylaxis in SBP should be considered with proper selection of cases and re-evaluation of antibiotic prophylaxis in case of selection of quinolone resistance [17].

The limitations in our study was not performing molecular epidemiology and typing, also PMQR in gram positive isolates need further investigations with larger number of isolates. The high prevalence of MDR, ESBL and quinolone resistance among patients with SBP should direct us to the correct and judicious use of fluoroquinolone.

CONCLUSION

PMQR determinants and ESBLs prevalence is high among FQ-resistant isolates from cirrhotic patients diagnosed with spontaneous bacterial peritonitis. The PMQR genes and their association with ESBL-producing plasmids have a great effect on spread of multidrug resistance and may lead to serious problems for treatment. This necessitates detection of PMQR determinants and ESBL genes among non-susceptible fluoroquinolone Enterobacteriaceae for appropriate empirical treatment and infection control.

Disclosure

No conflicts of interest in this work.

Conflict of Interest: none

Financial Disclosures: none

Table (1): Antibiotic Susceptibility Pattern of FQ Resistant *E. coli*.

Antibiotic Disks	E. coli Isolates (No=70)					
	Sensitive		Intermediate		Resistant	
	No	%	No	%	No	%
Ciprofloxacin	-	-	-	-	70	100%
Levofloxacin	-	-	-	-	70	100%
Amox./clav.	22	31.4%	-	-	48	68.5%
Piperacilintazobactam	5	7.1%	7	10%	58	82.8%
Cefoxitin	3	4.2%	17	24.2%	50	71.4%
Cefotaxime	-	-	-	-	70	100%
Ceftriaxone	-	-	-	-	70	100%
Ceftazidime	-	-	-	-	70	100%
Cefepime	2	2.8%	5	7.1%	63	90%
Aztreonam	2	2.8%	7	10%	61	87.1%
Meropenem	58	82.8%	8	11.4%	4	5.7%
Imipenem	55	78.5%	10	14.2%	5	7.1%
Gentamycin	49	70%	8	11.4%	13	18.5%
Amikacin	50	71.4%	6	8.5%	14	20%
Trimethoprim sulpha.	24	34.2%	18	25.7%	28	40%
MDR	-	-	-	-	55	78.5%
ESBL production	-	-	-	-	50	71.4%

Table (2): Antibiotic Susceptibility Pattern of FQ Resistant *K. pneumoniae* isolates.

Antibiotic Disks	<i>K. pneumoniae</i> Isolates (No=10)					
	Sensitive		Intermediate		Resistant	
	No	%	No	%	No	%
Ciprofloxacin	-	-	-	-	10	100%
Levofloxacin	-	-	-	-	10	100%
Amox./clav.	1	10%	2	20%	7	70%
Piperacilintazobactam	2	20%	1	10%	7	70%
Cefoxitin	-	-	-	-	10	100%
Cefotaxime	-	-	-	-	10	100%
Ceftriaxone	-	-	1	10%	9	90%

Ceftazidime	-	-	-	-	10	100%
Cefepime	-	-	-	-	10	100%
Aztreonam	-	-	-	-	10	100%
Meropenem	9	90%	-	-	1	10%
Imipenem	9	90%	1	10%	-	-
Gentamycin	5	50%	3	30%	2	20%
Amikacin	5	50%	-	-	5	50%
Trimethoprim sulpha.	5	50%	1	10%	4	40%
MDR	-	-	-	-	6	60%
ESBL production	-	-	-	-	5	50%

Table (3): Antibiotic Resistance Pattern among FQ Resistant Gram positive isolates

Antibiotic Disks	<i>S. aureus</i>		CoNS		Enterococci		v. streptococci	
	No=4	(%)	No=2	(%)	No=3	(%)	No=1	(%)
Ciprofloxacin	4	100%	2	100%	3	100%	1	100%
Levofloxacin	4	100%	2	100%	3	100%	1	100%
Oxacillin	1	25%	2	100%	3	100%	1	100%
Ceftaroline	0	0	0	0	-	-	-	-
Quinopristin/dalfopristin	3	75%	2	100%	2	66.6%	0	0
Meropenem	1	25%	0	0	-	-	0	0
Imipenem	0	0	0	0	-	-	0	0
Gentamycin	1	25%	2	100%	3	100%	1	100%
Doxycycline	1	25%	1	50%	3	100%	0	0
Clindamycin	2	50%	1	50%	-	-	1	100%
Trimethoprim sulpha	2	50%	2	100%	-	-	1	100%
Vancomycin	0	0	0	0	0	0	0	0
Linezolid	0	0	0	0	0	0	0	0

CoNS=coagulase negative staphylococci

(No=80)

<i>Isolate(n)</i>	<i>PMRQ gene</i>	<i>acc6'-Ib-cr</i>	<i>qnrS</i>	<i>qnrB</i>	<i>qepA</i>	<i>qnrA</i>
<i>E.coli</i> (70)		60	57	6	6	0
<i>K pneumonia</i> (10)		10	8	4	2	0
Total (%)		70 (87.5%)	65 (81.2%)	10 (12.5%)	8 (10%)	0

Table (5)PMRQ determinants detected in PCR tested Gram positive isolates (No=10)

<i>Isolate(n)</i>	<i>PMRQ gene</i>	<i>acc6'-Ib-cr</i>	<i>qnrA</i>	<i>qnrB</i>	<i>qnrS</i>	<i>qepA</i>
<i>S aureus</i> (4)		1	0	0	1	0
CoNS (2)		1	0	0	1	0
Viridansstrept (1)		1	0	0	1	0
Enterococci (3)		2	0	0	3	0
Total (%)		5 (50%)	0	0	6 (60%)	0

Table(6): Relation between ESBL and PMRQ gene among tested *Enterobacteriaceae*.

	ESBL (No=55)		Total number	*p
	Present(No=55)	Absent(No=25)		

	No	%	No	%	No=80	
<i>qnr S</i>						
Present	55	100%	10	40%	65	< 0.001(s)
Absent	0	0%	15	60%	15	
<i>acc(6`)-Ib-cr</i>						
Present	45		25	100%	70	0.035(s)
Absent	10		0	0%	10	
<i>qnr B</i>						
Present	5	9%	5	20%	10	0.31
Absent	50	90.9%	20	80%	70	
<i>qep A</i>						
Present	5	9%	3	12%	8	0.99
Absent	50	90.9%	22	88%	72	

*Fisher exact test S= significant



Figure (1) Double disk synergy test for 2 gram negative isolates showing positiveESβL (Key hole appearance) with enhanced zone of inhibition between AMC, ATM and CTX discs

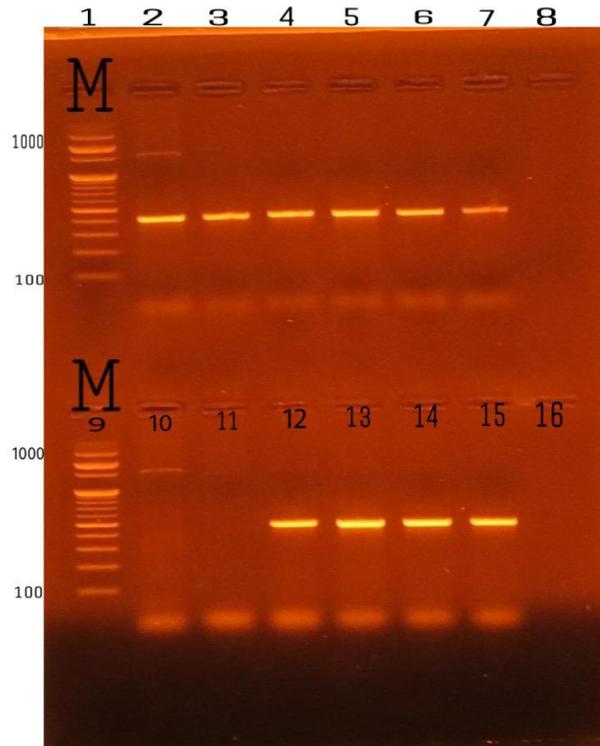


Figure (2): Agarose gel electrophoresis for *acc(6)-Ib-cr* gene. Positive samples showed bands at 482 bp.

Lane (1,9) showed Molecular weight marker from 100 to 1000 bp

Lanes (2, 3, 4, 5, 6, 7, 12, 13, 14, 15, 16) showed positive *acc(6)-Ib-cr* gene

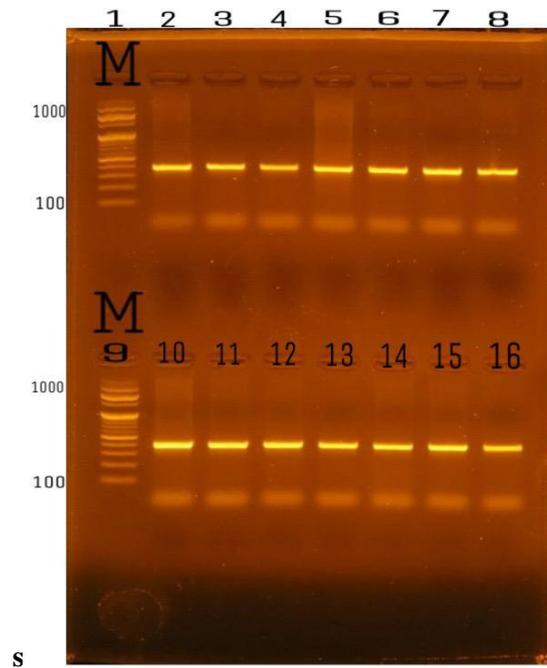


Figure (3): Agarose gel electrophoresis for *qnrS* gene. Positive samples showed bands at 417 bp

Lane (1,9) showed Molecular weight marker from 100 to 1000 bp

Lanes (2, 3, 4, 5, 6, 7, 8, 10, 11, 12, 13, 14, 15, 16) showed positive *qnrS* gene

REFERENCES

1. Karvellas CJ, Abraldes JG, Arabi YM et al. 2015. Cooperative Antimicrobial Therapy of Septic Shock (CATSS) Database Research Group. Appropriate and timely antimicrobial therapy in cirrhotic patients with spontaneous bacterial peritonitis-associated septic shock: a retrospective cohort study. *Aliment Pharmacol Ther*; 41(8):747-757.
2. Wiest R, Lawson M, Geuking M. 2014. Pathological bacterial translocation in liver cirrhosis. *J Hepatol*; 60:197–209.
3. European Association for the Study of the Liver EASL. 2018. Electronic address: easloffice@easloffice.eu, EASL clinical practice guidelines for the management of patients with decompensated cirrhosis. *J Hepatol*; 69(2):406–460.
4. Rimola A, Garcia-Tsao G, Navasa M et al. 2000. Diagnosis, treatment and prophylaxis of spontaneous bacterial peritonitis: a consensus document. *J Hepatol*; 32:142–153.
5. Aldred KJ, Kerns RJ and Osheroff N. 2014. Mechanism of quinolone action and resistance. *Biochemistry*; 53(10):1565–1574.
6. Kim ES and Hooper DC. 2014. Clinical importance and epidemiology of quinolone resistance. *Infect Chemother*; 46:226–238.
7. Martínez-Martínez L, Eliecer CM, Rodríguez-Martínez J et al. 2008. Plasmid-mediated quinolone resistance. *Expert Rev Anti Infect Ther*; 6:685–711.
8. Hooper DC and Jacoby GA. 2016. Topoisomerase inhibitors: fluoroquinolone mechanisms of action and resistance. *Cold Spring Harb Perspect Med*; 6:25-32.
9. Martínez-Martínez L, Pascual A and Jacoby GA. 1988. Quinolone resistance from a transferable plasmid. *Lancet*; 351:797–799.
10. Strahilevitz J, Jacoby GA, Hooper DC et al. 2009. Plasmid-mediated quinolone resistance: a multifaceted threat. *Clin Microbiol Rev*; 22:664–689.
11. Guan X, Xue X, Liu Y et al. 2013. Plasmid-mediated quinolone resistance—current knowledge and future perspectives. *J Int Med Res*; 41:20–30.
12. Jacoby GA, Hooper DC and Strahilevitz J. 2014. Plasmid-mediated quinolone resistance. *Microbiol Spectr*; 2:1–24.
13. Ruiz J., Pons M.J. and Gomes C. 2012. Transferable mechanisms of quinolone resistance. *Int. J. Antimicrob. Agents*; 40(3): 196-203.
14. Correia S, Hebraud M, Chafsey I et al. 2017. Mechanisms of quinolone action and resistance: where do we stand? *J. Med. Microbiol*; 66:551–559.
15. Runyon BA. 2010. Ascites and spontaneous bacterial peritonitis. In: *Gastrointestinal and Liver Disease*, Feldman M, Friedman LS and Brandt LJ (editors); 9th ed. Philadelphia: Saunders Elsevier; pp. 1517–1541.
16. Sajjad M, Khan ZA and Khan MS. 2016. Ascitic Fluid Culture in Cirrhotic Patients with Spontaneous Bacterial Peritonitis. *J Coll Physicians Surg Pak*; 26(8):658-561.
17. European Committee on Antimicrobial Susceptibility Testing EUCAST 2018: http://www.eucast.org/fileadmin/src/media/PDFs/EUCAST_files/Consultation/EUCAST_T_guidelines_detection_of_resistance_mechanisms.
18. Piroth L, Pechinot A, Di Martino V et al. 2014. Evolving epidemiology and antimicrobial resistance in spontaneous bacterial peritonitis: a two-year observational study. *BMC Infect Dis*; 14:287-293.
19. Domokos J, Kristof K and Szabo D. 2016. Plasmid-Mediated Quinolone Resistance 450 among Extended-Spectrum Beta-Lactamase producing Enterobacteriaceae from bloodstream infections. *Acta Microbiologica Et Immunologica Hungarica*; 452 (63):313 -323.
20. Robicsek, G, Jacoby A, and Hooper D.C. 2006. The worldwide emergence of plasmid-mediated quinolone resistance. *Lancet Infectious Diseases*; 6 (10): 629–640.
21. Park CH, Robicsek A, Jacoby GA et al. 2008. Prevalence in the United States of *aac(6)-Ib-cr* encoding a ciprofloxacin-modifying enzyme. *Antimicrob Agents Chemother*; 50:3953-3955.
22. Yamane K, Wachino JI, Suzuki S et al. 2008. Plasmid-mediated *qepA* gene among *Escherichia coli* clinical isolates, Japan. *Antimicrob Agents Chemother*; 52:1564–1566.

23. Fasugba O, Gardner A, Mitchell BG, Mnatzaganian G. 2015. Ciprofloxacin resistance in community- and hospital-acquired *Escherichia coli* urinary tract infections: a systematic review and meta-analysis of observational studies. *BMC Infect Dis*;15:545.
24. Ismaeel NE, Gerges MA, Hosny TA et al. 2020. Detection of Chromosomal and Plasmid-Mediated Quinolone Resistance Among *Escherichia coli* Isolated from Urinary Tract Infection Cases; Zagazig University Hospitals, Egypt, *Infect Drug Resist*; 154:134-142.
25. Yassin I, Rafie R, Osman M et al. 2019. Plasmid-mediated quinolone resistance: Mechanisms, detection, and epidemiology in the Arab countries. *Infect. Genet. Evol*;76: 104020
26. Tandogdu Z, Cek M, Wagenlehner F, et al. 2014. Resistance patterns of nosocomial urinary tract infections in urology departments: 8-year results of the global prevalence of infections in urology study. *World J Urol*;32(3):791–801.
27. Shenagari M, Bakhtiari M, Mojtahedi A, Roushan ZA. 2018. High frequency of mutations in *gyrA* gene associated with quinolones resistance in uropathogenic *Escherichia coli* isolates from the north of Iran. *Iran J Basic Med Sci*;21(12):1226–1231.
28. Muhammad I, Uzma M, Yasmin B, Mehmood Q, Habib B. 2011. Prevalence of antimicrobial resistance and integrons in *Escherichia coli* from Punjab, Pakistan. *Braz J Microbiol*;42(2):462–466.
29. Amer F, Monkez M, Ayaat M et al. 2016. Spontaneous bacterial peritonitis in the medical intensive care unit of a University Hospital in Egypt: frequency, bacteriological profile, risk factors and outcomes, *IAJAA*; 6(2):5.
30. . El-Badawy MF, Tawakol WM, El-Far SW, et al. 2017. Molecular identification of aminoglycoside-modifying enzymes and plasmid-mediated quinolone resistance genes among *Klebsiella pneumoniae* clinical isolates recovered from Egyptian Patients. *Int. J. Microbiol*;2017:12.
31. Ardolino E, Wang SS, Patwardhan VR et al. 2019. Evidence of Significant Ceftriaxone and Quinolone Resistance in Cirrhotic with Spontaneous Bacterial Peritonitis, *Dig. Dis. Sci*; 64:2359–2367
32. Lutz P, Nischalke HD, Krämer B et al. 2017. Antibiotic resistance in healthcare-related and nosocomial SBP. *Eur J Clin Invest*; 47(1):44–52
33. Mücke MM, Mayer A, Kessel J et al. 2019. Quinolone and Multidrug Resistance Predicts Failure of Antibiotic Prophylaxis of Spontaneous Bacterial Peritonitis. *Clin Infect Dis*; 15:70(9):1916-1924.
34. Lombardi A, Zuccaro V, Faggioli S et al. 2019. Prophylaxis of spontaneous bacterial peritonitis: Is there still room for quinolones? *J. Hepatol*;70: 1027-1028.
35. Fiore M, Chiodini P and Pota V. 2017. Risk of spontaneous fungal peritonitis in hospitalized cirrhotic patients with ascites: a systematic review of observational studies and meta-analysis. *Minerva Anestesiol*; 83(12):1309–1316
36. Piano S, Singh V, Caraceni P et al. 2019. Epidemiology and effects of bacterial infections in patients with cirrhosis worldwide. *Gastroenterology Int*; 156(5):1368-1375.
37. El-Mahdy RH, Saleh MA, Aboelnour A. 2017. *GyrA* mutations in nosocomial ciprofloxacin-resistant *Escherichia coli* isolates associated with urinary tract infections. *Int J Curr Microbiol App Sci*; 6 (2):1902–1907.
38. Karlowsky JA, Hoban DJ, DeCorby MR et al. 2006. Fluoroquinolone-resistant urinary isolates of *Escherichia coli* from outpatients are frequently multidrug resistant: results from the North American Urinary Tract Infection Collaborative Alliance-Quinolone Resistance study. *Antimicrob Agents Chemother*;50 (6):2251–2254.
39. Niranjani V, Malini A. 2014. Antimicrobial resistance pattern in *Escherichia coli* causing urinary tract infection among inpatients. *Indian J Med Res*;139(6):945–948.
40. Ariza X, Castellote J, Lora-Tamayo J et al. 2012. Risk factors for resistance to ceftriaxone and its impact on mortality in community, healthcare and nosocomial spontaneous bacterial peritonitis. *J Hepatol*; 56:825–832.
41. Majlesi A, Kakhki RK, Nejad ASM, et al. 2018. Detection of plasmid-mediated quinolone resistance in clinical isolates of Enterobacteriaceae strains in Hamadan, West of Iran. *Saudi J Biol Sci*;25(3):426–430.

42. Alexopoulou A, Papadopoulos N, Eliopoulos DG et al. 2013. Increasing frequency of gram-positive cocci and gram-negative multidrug-resistant bacteria in spontaneous bacterial peritonitis. *Liver Int*;33(7):975-81.
43. Li YT, Yu CB, Huang JR et al. 2015. Pathogen profile and drug resistance analysis of spontaneous peritonitis in cirrhotic patients. *World J Gastroenterol*; 21(36):409–417.
44. Tacconelli E, De Angelis G, Cataldo M et al., 2008. Does antibiotic exposure increase the risk of methicillin-resistant *Staphylococcus aureus* (MRSA) isolation? A systematic review and meta-analysis, *Journal of Antimicrobial Chemotherapy*; 61(1): 26–38.
45. Azargun R, Sadeghi MR, SoroushBarhaghi MH, et al. The prevalence of plasmid-mediated quinolone resistance and ESBL-production in *Enterobacteriaceae* isolated from urinary tract infections. *Infect Drug Resist*. 2018;11:1007-1014.
46. Kantele A, Mero S, Kirveskari j et al., Fluoroquinolone antibiotic users selectfluoroquinolone-resistant ESBL-producing *Enterobacteriaceae* (ESBL-PE) – Data of a prospective traveller study. *Travel Med Infect Dis*.2017;16:23-30.
47. Reuland EA, Sonder G.J.BM, Stolte I et al. 2016. Travel to Asia and traveller's diarrhoea with antibiotic treatment are independent risk factors for acquiring ciprofloxacin-resistant and extended spectrum β -lactamase-producing *Enterobacteriaceae*—a prospective cohort study. *Clin. Microbiol. Infect*;22:1-7.
48. Hammad A, Hadiya S, EL-Feky MA et al. 2017. Co-occurrence of Plasmid-mediated Quinolone Resistance and Carbapenemases in *Klebsiellapneumoniae* Isolates in Assiut, Egypt. *EJMM*; 26(4):1-7.
49. Shams E, Firoozeh F, Moniri R et al. 2015. Prevalence of plasmid-mediated quinolone resistance genes among extended-spectrum β -Lactamase-producing *Klebsiellapneumoniae* human isolates in Iran, *J Pathog*; 43:132-140.
50. Park KS, Kim KS, Nam YS et al. 2012. Prevalence of the plasmid-mediated quinolone resistance genes, *aac(6')-Ib-cr*, *qepA*, and *oqxAB* in clinical isolates of extended-spectrum β -lactamase, *Ann Clin Lab Sci*; 42(2):191-197.
51. Silva-Sánchez J, Cruz-Trujillo E, Barrios H et al. 2013. Characterization of plasmid-mediated quinolone resistance (PMQR) genes in extended-spectrum β -lactamase-producing *Enterobacteriaceae* pediatric clinical isolates in Mexico, *PLoS ONE*; 8:10-18.
52. Pasom W, Chanawong A, Lulitanond A et al. 2013. Plasmid-mediated quinolone resistance genes, *aac(6')-Ib-cr*, *qnrS*, *qnrB* and *qnrA*, in urinary isolates of *Escherichia coli* and *Klebsiellapneumoniae* at a teaching hospital, Thailand, *Jpn J Infect Dis*; 66(5):428-432.
53. Wang D, Huang X, Chen J et al. 2015. Characterization of genetic structures of the *QepA3* gene in clinical isolates of *Enterobacteriaceae*, *Front. Microbiol*; 6:1147.
54. Le TM, Baker S, Le TP, et al. 2009. High prevalence of plasmid-mediated quinolone resistance determinants in commensal members of the *Enterobacteriaceae* in Ho Chi Minh City, Vietnam. *J Med Microbiol*; 58(pt12):1585–1592.
55. Jacoby GA and Bush, K. 2005. Amino acid sequences for TEM, SHV and OXA extended-spectrum and inhibitor resistant β -lactamases. *N Engl J Med*; 355:270-281.
56. Xue G, Li J, Feng Y, et al. 2017. High prevalence of plasmid-mediated quinolone resistance determinants in *Escherichia coli* and *Klebsiellapneumoniae* isolates from pediatric patients in China. *Microb Drug Resist*;23(1):107–114.
57. Wang M, Tran JH, Jacoby GA. 2003. Plasmid-mediated quinolone resistance in clinical isolates of *Escherichia coli* from Shanghai, China. *Antimicrob Agents Chemother*;47(7):2242–2248.
58. Jeong J-Y, Yoon HJ, Kim ES, et al. 2005. Detection of *qnr* in clinical isolates of *Escherichia coli* from Korea. *Antimicrob Agents Chemother*;49(6):2522–2524.
59. Khalil M, Elsherif R, Ghaith D, et al. 2017. Quinolone resistance detection by PCR-RFLP and multiplex-PCR among extended-spectrum β -lactamase producing *Enterobacteriaceae*. *Int J Clin Med Microbiol*;2:119.
60. El-sayedMarei Y, MohamedAboul-Ola O, Zakaria El-Azab S et al. 2019. Detection of plasmid-mediated quinolone resistance determinants in ESBLs and non-ESBLs producing *Enterobacteriaceae* from urinary tract infections. *Ann ClinImmunolMicrobiol*;1(2):1008.

61. Jeong HS, Bae IK and Shin et al JH. 2011. Prevalence of plasmid mediated quinolone resistance and its association with extended-spectrum beta-lactamase and AmpC beta-lactamase in Enterobacteriaceae. *J Lab Med*; 31(4):257–264.
62. Correia S, Hebraud M, Chafsey I et al. 2016. Impacts of experimentally induced and clinically acquired quinolone resistance. *J Proteomics*; 145:46–49.