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High prevalence of qnrA and qnrB genes among fluoroquinolone-resistant *Escherichia coli* isolates from a tertiary hospital in Southern Nigeria

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Abstract

Background: This study was aimed to determine the prevalence of qnr genes among fluoroquinolone-resistant *Escherichia coli* (FREC) isolates from Nigeria. Antimicrobial susceptibility testing was performed by disc diffusion technique. Polymerase chain reaction was used to identify *Escherichia coli* (*E. coli*) and for the detection of qnr genes.

Results: A total of 206 non-duplicate *E. coli* were isolated from 300 clinical specimens analyzed. In all, 30 (14.6%) of these isolates were FREC; the resistance to fluoroquinolones among these 30 FREC showed 80% (24), 86.7% (26), 86.7% (26), 100% (30), 86.7% (26), 93.3% (28) and 86.7% (26) were resistant to pefloxacin, ciprofloxacin, sparfloxacin, levofloxacin, nalidixic acid, ofloxacin and moxifloxacin, respectively. The distribution of FREC among the various sample sources analyzed showed that 14%, 10%, 13.3%, 16.7% and 20% of the isolates came from urine, stool, high vaginal swab, endo cervical swab and wound swab specimens, respectively. More FREC were isolated from female samples 73.3% (22) compared to male samples 26.7% (8) and were more prevalent among the age group 26–35 years (40%). Twenty eight out of the 30 (93.3%) FREC isolates possessed at least one fluoroquinolone resistance gene in the form of qnrA 10 (33.3%) and qnrB 18 (60%), respectively; qnrS was not detected among the FREC isolates analyzed and 13.5% of the isolates possessed both the qnrA and qnrB genes. Phylogenetic analysis showed that these isolates were genetically diverse.

Conclusions: These findings suggest a possible resistance to fluoroquinolone is of high interest for better management of patients and control of antimicrobial resistance in Nigeria.

Keywords: *Escherichia coli*, Fluoroquinolone-resistant genes, Nigeria

Background

Since it was discovered in 1885, *Escherichia coli* has been subjected to comprehensive studies and become one of the best understood and characterized organisms (Kuhnert et al. 2000). Despite the vast knowledge accumulated throughout the last decades, *E. coli* is still one of the major causes of infection in humans. In addition to

urinary tract infection (UTI), where it is responsible for most of the reported cases, *E. coli* has been associated with a number of other diseases including gastrointestinal diseases, pneumonia and meningitis (Kaper et al. 2004).

The fluoroquinolones comprise one of the most widely used groups of antibacterial agents in Nigeria (Alade et al. 2018); however, concerns have developed about the emergence of bacteria resistant to these broad-spectrum antibiotics. *E. coli* uses different mechanisms to provide resistance to quinolones, including (1) the accumulation of mutations in the genes encoding quinolone target

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DNA gyrase and topoisomerase IV; (2) a decrease of intracellular concentration of fluoroquinolones by porins down-regulation or modification of the efflux pumps activity; and (3) the acquisition of plasmid quinolone resistance genes (Zhao et al. 2015). Studies have shown that the emergence of plasmid-mediated quinolone resistance (PMQR) may contribute by several means to the rapid increase in bacterial resistance to quinolones. Plasmid-mediated quinolone resistance genes *qnrA*, *qnrB* and *qnrS* encode pentapeptide repeat protein and have ability to protect DNA gyrase from quinolone inhibition (Kurnia et al. 2018). About 100 *qnr* genes variants have been described mainly from Enterobacteriaceae and grouped into five distinct families: *qnrA*, *qnrB*, *qnrC*, *qnrD* and *qnrS* (Strahilevitz et al. 2009; Salah et al. 2019).

Hospital wards, especially those in low-income countries such as Nigeria, where infection prevention and control protocols are lacking, have become the main foci for developing multidrug resistance in bacteria such as *E. coli* (Nsofor and Iroegbu 2013). Increasing rates of *E. coli* resistance to fluoroquinolone class of antibiotics are of great concern not only to healthcare workers (HCWs) but to the public. This is because they are the drug of choice for the treatment of very stubborn infection. The poor screening of these multidrug resistance (MDR) pathogens in the hospitals coupled with poor antibiotic stewardship and surveillance systems has increased their burden in the country. The traditional antibiotic susceptibility testing protocol being used currently in many clinical laboratories in Nigeria may not adequately detect bacteria harboring fluoroquinolone resistance genes. Therefore, this study was aimed to determine the prevalence of *qnr* genes among fluoroquinolone-resistant *E. coli* (FREC) clinical isolates from Madonna University Teaching Hospital, a tertiary health institution in Southern Nigeria. The findings from this work will help to better understand and potentially predict trends in antibiotic resistance patterns, as well as establish adequate infection control measure in the region.

Methods

Bacterial isolates

A total of 206 consecutive non-duplicate *E. coli* were isolated from 300 various clinical specimens at Madonna University Teaching Hospital Elele, a tertiary hospital in Rivers State, Southern Nigeria, from October 2018 to March 2019. The specimens included urine, stool, high vaginal swab, endo cervical swab and wound swab. Criteria used to decide the suitability of patients for sample collection were as follows: (1) outpatients, emergency patients or inpatients who were admitted with infections within 48 h of diagnosis; (2) patients not hospitalized for the preceding 90 days; (3) individuals with no long-term

indwelling catheters; and (4) patients who received antimicrobial agents for ≤ 72 h. Standard microbiological methods were used to isolate and purify bacterial isolates on MacConkey or eosin methylene blue (EMB) media (Cheesbrough 2000). No antibiotic was included in the agar plates used for the cultivation. *E. coli* strains were fully identified by 16s rRNA PCR and stored at -20°C in a nutrient agar slant prior to molecular characterization. All sampling procedures were in accordance with guidelines of the National Health Research Ethics Committee, Nigeria (www.nhrec.net), and the protocol of this study was approved by the Ethics Committee of Madonna University Elele, Nigeria. The patients gave oral consent for their specimens to be used in the study. The sampling and phenotypic characterization was carried out at Madonna University Nigeria, while molecular characterization was carried out at Niger Delta University Nigeria.

Antibiotics susceptibility testing

The antibiotics susceptibility pattern of the isolates was determined using the disc diffusion method on Mueller–Hinton agar (Oxoid, England). Inhibition zone diameter values were measured and interpreted using the European Committee on Antimicrobial Susceptibility Testing breakpoint (EUCAST 2018). The isolates were tested against nine antibiotics, namely pefloxacin, ciprofloxacin, sparfloxacin, levofloxacin, nalidixic acid, ofloxacin, moxifloxacin, oxacillin and erythromycin (Oxoid, England). *E. coli* ATCC 25922 strain was used as a control for antibiotic susceptibility testing.

Extraction of bacterial DNA

DNA extraction was performed using a boiling technique. Briefly, overnight broth culture of the bacterial isolate in Luria–Bertani (LB) medium was transferred into 1.5-ml Eppendorf tube and was centrifuged at 14,000 rpm/min for 3 min. The supernatant was discarded, and 1000 μl of 0.5% normal saline was added to the pellet for cell wall weakening and was vortexed on eltech XH-B vortexer. The cells were re-suspended in 500 μl of normal saline and heated at 95°C for 20 min to release bacterial nucleic acid. The heated bacterial suspension was cooled on ice and centrifuged at 14,000 rpm/min for 3 min. DNA was then precipitated in 250 μL of absolute ethanol, washed twice in 1000 μL of ethanol 75%, dried and re-suspended in 100 μL of sterile water. The extracted genomic DNA was quantified using the NanoDrop 1000 spectrophotometer.

Molecular detection of *qnr* genes

PCR assays were performed for the detection of *qnr* resistance genes including *qnrA*, *qnrB* and *qnrS*. The primers used to detect *qnr* genes were selected from

previously described sequences by Cattoir et al. (2007). PCR was done in a total volume of 25 µL containing 3 µL DNA template, 2.5 µL PCR buffer (1X), 1 µL deoxyribonucleotide triphosphates solution (dNTPs, 200 µM), 1.5 µL MgCl₂ (1.5 mM), 0.25 µL Taq DNA polymerase (1 unit) and 1 µL each specific primer (1 µM). PCR amplifications were carried out on a T100™ thermal cycler (Bio-Rad, Hercules, CA, USA). The cycling conditions were as follows: 95 °C for 5 min (step 1), 95 °C for 1 min (step 2), annealing for 45 s (step 3), 72 °C for 1 min (step 4) and 72 °C for 5 min (step 5); steps 2–4 were repeated for 30 cycles. DNA fragments were analyzed by electrophoresis in a 1.5% agarose gel at 130 V for 25 min in 1X TBE buffer containing ethidium bromide using 1100-bp DNA ladder (Promega, USA) as a size marker and visualized on a blue light transilluminator. The primer sequences used in this are listed in Table 1.

Sequencing

Sequencing was done using the BigDye Terminator kit on a 3510 ABI sequencer at Inqaba Biotechnological, Pretoria South Africa. The sequencing was done at a final volume of 10ul; the components included 0.25 µL BigDye® terminator v1.1/v3.1, 2.25 µL of 5× BigDye sequencing buffer, 10 µM primer PCR primer, and 2–10 ng PCR template per 100 bp. The sequencing conditions were as follows: 32 cycles of 96 °C for 10 s, 55 °C for 5 s and 60 °C for 4 min. The primer sequences used to detect qnr genes are listed in Table 1. The basic local alignment search tool (BLAST) program was used to compare DNA sequences against those in the National Center for Biotechnology Information (NCBI) database.

Phylogenetic analysis

Obtained sequences were edited using the bioinformatics algorithm Trace edit, and similar sequences were downloaded from the NCBI database using BLAST. These sequences were aligned using multiple alignment using fast Fourier transform (MAFFT). The evolutionary history was inferred using the neighbor-joining method in MEGA 6.0 (Saitou and Nei 1987). The bootstrap consensus tree inferred from 500 replicates (Felsenstein 1985)

was taken to represent the evolutionary history of the taxa analyzed. The evolutionary distances were computed using the Jukes–Cantor method (Jukes and Cantor 1969).

Statistical analysis

The statistical analyses were performed using SPSS software version 21.0 (IBM Corp., USA). The results were presented as descriptive statistics in terms of relative frequency. Categorical variables were expressed as counts and percentages. The Chi-square (χ²) or Fisher’s exact tests were performed to analyze significant differences; P value < 0.05 was considered as statistically significant.

Results

Bacterial isolates

Out of the 300 various clinical specimens analyzed in this study, 206 (68.7%) yielded *E. coli*; only one *E. coli* strain was picked per specimen. The distribution of the strains according to sample sources is as follows: urine 100 (48.5%), stool 20 (9.7%), high vaginal swab 30 (14.6%), endo cervical swab 36 (17.5%) and wound swab 20 (9.7%). Specimen from female patients yielded more *E. coli* isolates 142 (68.9%) when compared to male patients 64 (31.1%) as shown in Table 2.

Antibiotic susceptibility profile

Among the 206 *E. coli* strains isolated, 30 (14.6%) were found to be fluoroquinolone-resistant *E. coli* (FREC). The detailed resistance profile of the 30 FREC to individual fluoroquinolones and other antibiotics tested showed 80% (24), 86.7% (26), 86.7% (26), 100% (30), 86.7% (26), 93.3% (28), 86.7% (26), 66.7% (20) and 60.0% (18) were resistant to pefloxacin, ciprofloxacin, sparfloxacin, levofloxacin, nalidixic acid, ofloxacin, moxifloxacin, oxacillin and erythromycin, respectively, as shown in Table 3. The distribution of FREC among the various sample sources analyzed showed that 14%, 10%, 13.3%, 16.7% and 20% of the isolates came from urine, stool, high vaginal swab, endo cervical swab and wound swab specimens, respectively (Table 4). More

Table 1 Primers used for PCR amplification of qnr genes

Target gene	Primer sequence (5'-3')	Size (bp)
qnrA	F: GATAAAGTTTTTCAGCAAGAGG R: ATCCAGATCCGCAAAGGTTA	823
qnrB	F: ATGACGCCATTACTGTATAA R: GATCGCAATGTGTGAAGTTT	408
qnrS	F: ATGGAAACCTACAATCATAC R: AAAAACACCTCGACTTAAGT	428

Table 2 The distribution of the *E. coli* isolates according to sample sources and gender

Sample source	Male (%)	Female (%)	Total (%)
Urine	32(15.5)	68(33.0)	100(48.5)
Stool	20(9.7)	–	20(9.7)
High vaginal swab	–	30(14.6)	30(14.6)
Endo cervical swab	–	36(17.5)	36(17.5)
Wound swab	12(5.8)	8(3.9)	20(9.7)
Total	64(31.1)	142(68.9)	206(100)

Table 3 The antibiotics susceptibility pattern of the 30 fluoroquinolone-resistant *E. coli*

Antibiotics	Susceptible (%)	Resistance (%)
Quinolones		
Pefloxacin	6(20.0)	24(80.0)
Ciprofloxacin	4(13.3)	26(86.7)
Sparfloxacin	4(13.3)	26(86.7)
Levofloxacin	0(0.00)	30(100)
Nalidixic acid	4(13.3)	26(86.7)
Ofloxacin	2(6.7)	28(93.3)
Moxifloxacin	4(13.3)	26(86.7)
Penicillin		
Oxacillin	10(33.3)	20(66.7)
Aminoglycosides		
Erythromycin	12(40.0)	18(60.0)

Table 4 The distribution of fluoroquinolone-resistant *E. coli* among the various sample sources

Sample source	FREC	
	Positive (%)	Negative (%)
Urine	14(14.0)	86(86.0)
Stool	2(10.0)	18(90.0)
High vaginal swab	4(13.3)	26(86.7)
Endo cervical swab	6(16.7)	30(83.3)
Wound swab	4(20.0)	16(80.0)
Total	30(14.6)	176(85.4)

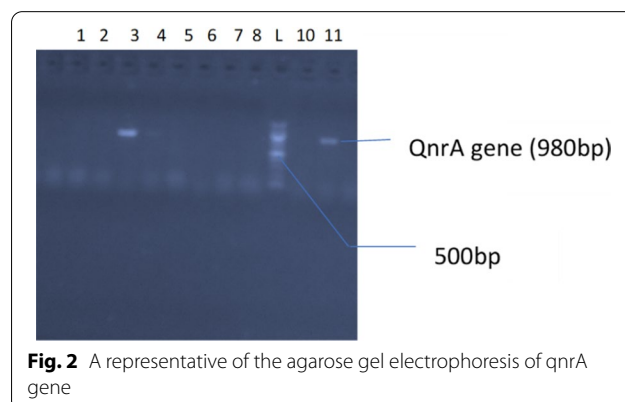
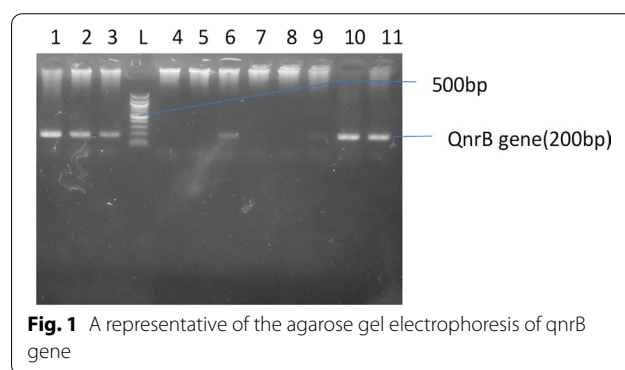
FREC were isolated from female samples 73.3% (22) compared to male samples 26.7% (8) and were more prevalent among the age group 26–35 years (40%).

Distribution of qnr genes

Electrophoresis analysis revealed that 28 out of the 30 (93.3%) FREC isolates harbored at least one fluoroquinolone resistance gene: qnrA 10 (33.3%) and qnrB 18 (60%), respectively; qnrS was not detected among the FREC analyzed. The concomitant presence of two qnr genes (qnrA and qnrB) was detected in 13.5% of the isolates. *E. coli* strains from urine specimen harbored the highest number qnr genes, 16, while strains from wound swab had 6 genes and those from stool, HVS and ECS had 2 qnr genes, respectively (Table 5). A representative of the agarose gel electrophoresis of each of the qnr genes is shown in Figs. 1, 2, 3. Phylogenetic analysis showed that these isolates were not clonally related and were genetically diverse (Fig. 4).

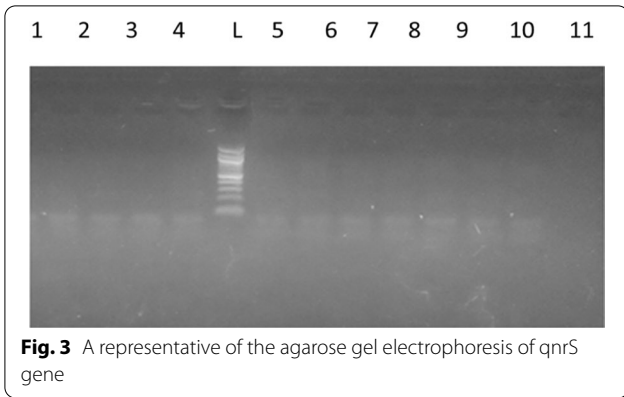
Table 5 The distribution of fluoroquinolone-resistant genes, qnrA and qnrB among the sample sources

Sample source	qnrA Number positive (%)	qnrB Number positive (%)	Total (%)
Urine	6(37.5)	10(62.5)	16(100.0)
Stool	0	2(100.0)	2(100.0)
HVS	0	2(100.0)	2(100.0)
ECS	2(100.0)	0	2(100.0)
Wound	2(33.3)	4(66.7)	6(100.0)
Total	10(35.7)	18(64.3)	28(100.0)



Discussion

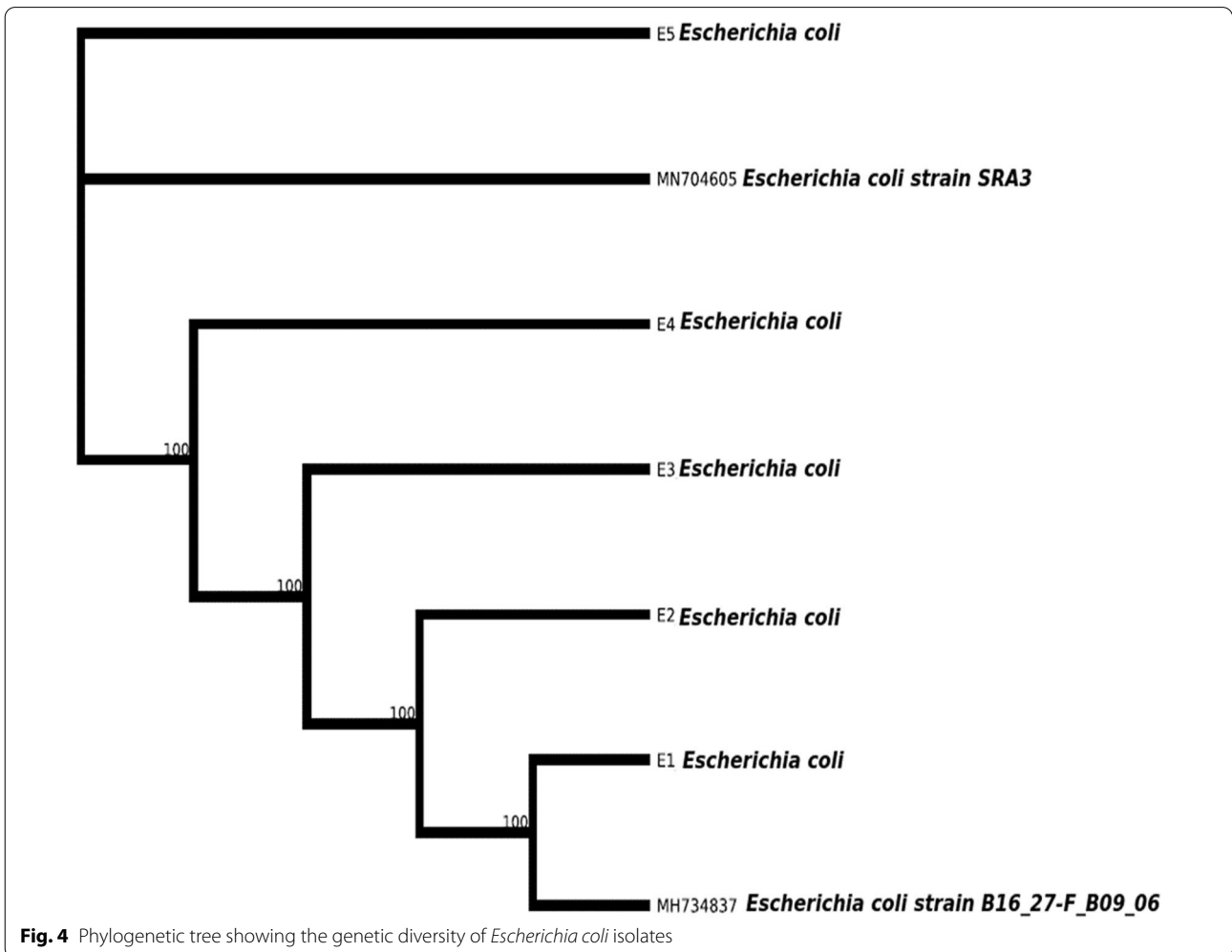
The extensive use of fluoroquinolone antibiotics in human medicine is associated with increasing emergence of quinolone resistance strains (Correia et al. 2017). Here, we investigated the fluoroquinolone resistance among a collection of clinical isolates from Madonna University Teaching Hospital Nigeria. In all, 14.6% of the isolates were found to be FREC, while 93.3% of the isolates harbored at least one fluoroquinolone resistance genes: qnrA 33.3% and qnrB 60%, respectively; qnrS was not detected among the FREC analyzed. This indicates low



rate of qnr genes in *E. coli* (qnrB 47.74%, qnrS 47.10% and qnrA 2.58%), while Guessennd et al. (2008) reported 31.2% with 14.6% for qnrB, 9.9% for qnrA and 2.7% for qnrS in Côte d'Ivoire. In a study conducted in Niger, Moumouni et al. (2017) showed a 44.4% occurrence of qnr genes in *E. coli* with 64.3% for qnrS, 26.2% for qnrB and 9.5% for qnrA, while Jamali et al. (2014), showed that the prevalence of qnr gene was 2.6% (1.7% qnrS and 0.9% qnrB) in a Moroccan community. Studies conducted in some Asian countries showed that the frequencies of qnr genes are considerably low; in China, Wang et al. (2008) reported the incidences of qnr as 7.5% among ciprofloxacin-resistant *E. coli*, with qnrA, qnrB and qnrS detected either alone or in combination in 3.8%, 4.7% and 3.8% of these isolates, respectively. In Korea, Shin et al. (2008) reported that 5.6% of *E. coli* ciprofloxacin-resistant isolates contained only qnrB. Jeong et al. (2005) reported that the prevalence of qnrA in Korea was 0.8% in *E. coli* isolates (ciprofloxacin susceptible and resistant) between 2001 and 2003. These data show that the distribution of

level resistance to fluoroquinolones but high rate of qnr genes among the FREC.

The occurrence of qnr genes observed in this study is higher than those reported in other neighboring African countries; in Togo, Salah et al. (2019) reported 67.03%



qnr genes in *E. coli* varies from one region to the other. The regionally diverse and wide distribution of qnr genes in *E. coli* suggests that resistance evolved independently on many occasions. However, the rational and controlled use of fluoroquinolone antibiotics is an effective way to control the development of higher levels of resistance.

Though similar studies usually detect the three major qnr genes (qnrA, qnrB, qnrS), our study did not detect qnrS in any of the isolates; however, it is in agreement with some studies (Seo et al. 2010; Yang et al. 2014; Moghadasi et al. 2016), which has shown that qnrB is most common qnr genes; our findings showed highest occurrence of qnrB (60%). The mobile characteristic of PMQR genes allows them to move across plasmids or spread from one species to another via moving elements. Although they provide a low level of quinolone resistance, they can promote mutations of target enzymes such as DNA gyrase and topoisomerase IV. The horizontal transmission of these plasmids to susceptible bacteria should be of concern, particularly in its ability to aid in the dissemination of antibiotic resistances (Lamikanra et al. 2011). Various reasons have been adduced for this spread, of which the high level of quinolones use in human medicine has been considered an important factor (Poirel et al. 2012). As reported by various researchers, another factor of concern associated with the advent of quinolone resistance is their close relation with other agents, especially the expression of extended-spectrum beta lactamases (ESBLs) and aminoglycosides (Zhang et al. 2012; Andres et al. 2013; Liu et al. 2013). It is quite unfortunate that this biologic relationship among these agents has caused a suitable opportunity for dissemination of multidrug resistance among the Enterobacteriaceae, thus resulting in restrictions on treatment choices. Therefore, this should be of concern to the physicians when prescribing quinolones that the resistance to cephalosporins and aminoglycosides and other resistance forms which are associated with PMQRs may occur as well (Robicsek et al. 2006).

The antibiotic resistance profile of the isolates encoding qnr genes showed 80%, 86.7%, 86.7%, 100%, 86.7%, 93.3% and 86.7% resistance to pefloxacin, ciprofloxacin, sparfloxacin, levofloxacin, nalidixic acid, ofloxacin and moxifloxacin, respectively. These rates are similar to those observed in Togo (90.48% for nalidixic acid and 93.46% for ciprofloxacin) (Salah et al. 2019) but higher than those observed in Morocco (57% for nalidixic acid and 78% for ciprofloxacin) (Jamali et al. 2014) and in Mexico (41.1% for nalidixic acid and 29.4% for ciprofloxacin) (Silva-Sanchez et al., 2013). The higher resistance rate of the qnr-positive strains observed in this study could be explained by the concomitant presence of two qnr gene groups, thus inducing an additive effect on the

minimal inhibiting concentrations (MICs) of these different molecules. In addition, qnr-positive isolates showed more resistance to erythromycin (60.0%). This may be explained by the fact that plasmid-mediated quinolone resistance is associated with integrons bearing resistance determinants to several other antibiotics such as beta lactams and aminoglycosides (Minh Vien et al. 2009, Iabadene et al. 2008). It is worthy to note that in this study, no qnr genes were detected in 6.7% of the FREC isolates; this can suggest the presence of another mechanism of resistance to quinolones such as mutations in the gyrase and topoisomerase IV genes (Jacoby et al. 2014, Redgrave et al. 2014).

Phylogenetic analysis showed that the FREC isolates exhibited genetic diversity. As the phylogenetic tree did not show any major clusters among the isolates, the clonal transfer of resistant strains cannot be inferred from this study. As whether the resistance genes could be transmitted horizontally in vehicles such as plasmids, further studies should be conducted.

Conclusions

In conclusion, our result revealed a high rate of qnrA and qnrB among FREC isolates from Southern Nigeria. These qnr gene-positive strains were highly resistant to pefloxacin, ciprofloxacin, sparfloxacin, levofloxacin, nalidixic acid, ofloxacin and erythromycin. The plasmid-mediated quinolone resistance genes and their association with aminoglycoside resistance contribute to the spread of multidrug resistance due to their easy transfer between bacteria. Their wide dissemination impairs treatment outcome of common infections in community and hospital settings. These findings suggest the strengthening of the public health policies in Nigeria in order to prevent, monitor and control antimicrobial resistance through the implementation of an antibiotic resistance surveillance system. Further studies on plasmid profiling and conjugation experiments or hybridization to confirm the presence of target genes on plasmid are recommended.

Abbreviations

MDR: multidrug resistance; PCR: polymerase chain reaction; BLAST: basic local alignment search tool; NCBI: National Center for Biotechnology Information; MAFFT: multiple alignment using fast Fourier transform.

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Authors' contributions

This paper is part of M.Sc. research project of CMN at Madonna University Nigeria. MYT and CMN designed the work; CMN performed the experiments; CMN, MYT and CAN analyzed and interpreted the data; CMN and CAN wrote the paper. All authors have read and approved the manuscript.

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Availability of data and materials

Supporting data are available on request.

Ethics approval and consent to participate

The protocol of this study was approved by the Ethics Committee of Madonna University Elele Nigeria (the committee's reference number is not applicable). The verbal consent obtained was approved by the ethics committee. All sampling procedures were in accordance with guidelines of the National Health Research Ethics Committee, Nigeria (www.nhrec.net), and the patients gave consent for their specimens to be used in the study.

Competing interests

The authors declare no competing interests.

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References

- Alade T, Abdu A, Tattfeng M (2018) Detection of quinolone resistance genes (QnrA, QnrB and QnrS) in *Klebsiella Sp.* isolates from clinical samples in Bayelsa State, Nigeria. *Int J Sci Res* 7(8). ISSN No 2277 - 8179 | IF: 4.758 | IC Value: 93.98
- Andres P, Lucero-Soler-Bistué Guerriero Albornoz Tran Zorreguieta Galas Corso CALETAMA (2013) Differential distribution of plasmid-mediated quinolone resistance genes in clinical enterobacteria with unusual phenotypes of quinolone susceptibility from Argentina. *Antimicrob Agents Chemother* 57:2467–2475
- Cattoir V, Poirel L, Rotimi V, Soussy CJ, Nordmann P (2007) Multiplex PCR for detection of plasmid-mediated quinolone resistance qnr genes in ESBL-producing enterobacterial isolates. *J Antimicrob Chemother* 60(2):394–397
- Cheesbrough M (2000) *District laboratory practice in tropical countries*, Part 2. Cambridge University Press, Cambridge, p 434
- Correia S, Poeta P, Hebraud M, Capelo JL, Igrejas G (2017) Mechanisms of quinolone action and resistance: where do we stand? *J Med Microbiol* 66(5):551–559
- Guessennd N, Bremont S, Gbonon V, Kacou-Ndouba A, Ekaza E, Lambert T (2008) Qnr-type quinolone resistance in extended-spectrum beta-lactamase producing enterobacteria in Abidjan, Ivory Coast. *Pathologie-biologie* 56(7–8):439–446
- labadene H, Messai Y, Ammari H, Ramdani-Bouguessa N, Lounes S, Bakour R et al (2008) Dissemination of ESBL and Qnr determinants in Enterobacter cloacae in Algeria. *J Antimicrob Chemother* 62(1):133–136. Redgrave LS, Sutton SB, Webber MA, Piddock LJV. Fluoroquinolone
- Jacoby GA, Strahilevitz J, Hooper DC (2014) Plasmid-mediated quinolone resistance. *Microbiol Spectr* 2(5)
- Jamali L, Haouzane F, Bouchakour M, Oufrid S, Ghazlane Z, El Mdaghri N (2014) Prévalence des gènes de résistance plasmidique aux quinolones chez des entérobactéries communautaires isolées au Maroc [Prevalence of plasmid mediated quinolone resistance genes among enterobacteria isolates in Moroccan community]. *Int J Innov Sci Res* 11(2):387–399
- Jeong JY, Yoon HJ, Kim ES (2005) Detection of qnr in clinical isolates of *Escherichia coli* from Korea. *Antimicrob Agents Chemother* 2005(49):2522–2524
- Kaper JB, Nataro JP, Mobley HL (2004) Pathogenic *Escherichia coli*. *Nat Rev Microbiol* 2:123–140
- Kuhnert P, Boerlin P, Frey J (2000) Target genes for virulence assessment of *Escherichia coli* isolates from water, food and the environment. *FEMS Microbiol Rev* 24:107–117
- Kurnia RS, Indrawati A, Mayasari NLP, Priadi A (2018) Molecular detection of genes encoding resistance to tetracycline and determination of plasmid-mediated resistance to quinolones in avian pathogenic *Escherichia coli* in Sukabumi, Indonesia. *Veterin World* 11(11):1581–1586
- Lamikanra A, Crowe JL, Lijek RS et al (2011) Rapid evolution of fluoroquinolone-resistant *Escherichia coli* in Nigeria is temporally associated with fluoroquinolone use. *BMC Infect Dis* 11(1):1–10
- Liu BT, Liao XP, Yue L, Chen XY, Li L, Yang SS, Sun J, Zhang S, Liao SD, Liu YH (2013) Prevalence of b-lactamase and 16S rRNA methylase genes among clinical *Escherichia coli* isolates carrying plasmid-mediated quinolone resistance genes from animals. *Microb Drug Resist* 19:237–245
- Minh Vien LT, Baker S, Phuong Thao LT, Phuong Tu LT, Thu Thy C, Thu Nga TT 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(12):1585–1592
- Moghadasi M, Mirzaee M, Mehrabi MR (2016) Frequency of quinolone resistance and qnrB and qnrC genes in clinical isolates of *Klebsiella pneumoniae*. *J Med Bacteriol* 5(5–6):39–45
- Moumouni A, Diagbouga S, Nadembèga C, Metuor Dabire A, Ouattara K, Zohoncon T (2017) Quinolone resistance (qnr) genes in fecal carriage of extended Spectrum beta-lactamases producing Enterobacteria isolated from children in Niger. *Curr Res Microbiol Biotechnol* 5(1):953–957
- Nsofor CA, Iroegbu CU (2013) Antibiotic resistance profile of *Escherichia coli* isolated from five major geopolitical zones of Nigeria. *J Bacteriol Res* 5(3):29–34. <https://doi.org/10.5897/JBR2012.035>
- Poirel L, Cattoir V, Nordmann P (2012) Plasmid-mediated quinolone resistance; interactions between human, animal, and environmental ecologies. *Front Microbiol* 3(24):17
- Redgrave LS, Sutton SB, Webber MA, Piddock LJV (2014) Fluoroquinolone resistance: mechanisms, impact on bacteria, and role in evolutionary success. *Trends Microbiol* 22(8):438–445
- Robicsek A, Jacoby GA, Hooper DC (2006) The worldwide emergence of plasmid-mediated quinolone resistance. *Lancet Infect Dis* 6:629–640
- Salah FD, Diagbouga S, Metuor Dabire A, Sadjji AY, Nadembèga C, Moumouni A (2019) Distribution of quinolone resistance gene (qnr) in ESBL-producing *Escherichia coli* and *Klebsiella spp.* in Lomé, Togo. *Antimicrob Resist Infect Control* 8:104. <https://doi.org/10.1186/s13756-019-0552-0>
- Seo MR, Park YS, Pai H (2010) Characteristics of plasmid-mediated quinolone resistance genes in extended-spectrum cephalosporin resistant isolates of *Klebsiella pneumoniae* and *Escherichia coli* in Korea. *Chemotherapy* 56:46–53
- Shin JH, Jung HJ, Lee JY, Kim HR, Lee JN, Chang CL (2008) High rates of plasmid-mediated quinolone resistance QnrB variants among ciprofloxacin-resistant *Escherichia coli* and *Klebsiella pneumoniae* from urinary tract infections in Korea. *Microb Drug Resist* 14:221–226
- Silva-Sanchez J, Barrios H, Reyna-Flores F, Bello-Diaz M, Sanchez-Perez A, Rojas T et al (2011) Prevalence and characterization of plasmid-mediated quinolone resistance genes in extended-spectrum beta-lactamase-producing Enterobacteriaceae isolates in Mexico. *Microb Drug Resist* 17(4):497–505
- Strahilevitz J, Jacoby GA, Hooper DC, Robicsek A (2009) Plasmid-mediated quinolone resistance: a multifaceted threat. *Clin Microbiol Rev* 22(4):664–689
- The European Committee on Antimicrobial Susceptibility Testing, Breakpoint tables for interpretation of MICs and zone diameters, Version 8.1. <http://www.eucast.org>
- Wang A, Yang Y, Lu Q (2008) Presence of qnr gene in *Escherichia coli* and *Klebsiella pneumoniae* resistant to ciprofloxacin isolated from pediatric patients in China. *BMC Infect Dis* 2008(8):68
- Yang HY, Nam YS, Lee HJ (2014) Prevalence of plasmid-mediated quinolone resistance genes among ciprofloxacin-nonsusceptible *Escherichia coli* and *Klebsiella pneumoniae* isolated from blood cultures in Korea. *Can J Infect Dis Med Microbiol* 25(3):163–169
- Zhang Y, Yang J, Ye L, Luo Y, Wang W, Zhou W, Cui Z, Han L (2012) Characterization of clinical multidrug-resistant *Escherichia coli* and *Klebsiella pneumoniae* isolates, 2007–2009, China. *Microb Drug Resist* 18:465–470
- Zhao L, Zhang J, Zheng B, Wei Z, Shen P, Li S, Li L, Xiao Y (2015) Molecular epidemiology and genetic diversity of fluoroquinolone-resistant *Escherichia coli* isolates from patients with community-onset infections in 30 Chinese county hospitals. *J Clin Microbiol* 53:766–770. <https://doi.org/10.1128/JCM.02594-14>

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