Prevalence of quinolone resistance in *Enterobacteriaceae* from Sierra Leone and the detection of *qnrB* pseudogenes and modified LexA binding sites.

**TABLE S1.** PCR primers and cycling conditions used in this study.

| Primer name | Sequence (5' → 3')[1] | Target | Reference | PCR conditions[2] | | |
| --- | --- | --- | --- | --- | --- | --- |
| | | | | Annealing | Cycles | Extension |
| qnrAm-F | AGAGGATTTCTCACGCCAGG | *qnrA* | (1) | 53 | 30 | 1 |
| qnrAm-R | TGCCAGGCACAGATCTTGAC | | | | | |
| qnrBm-F | GGMATHGAAATTCGCCACTG | *qnrB* | (2) | 53 | 30 | 1 |
| qnrBm-R | TTTGCYGYYCGCCAGTCGAA | | | | | |
| psp2 | AAATTTAAYCAGAAAAAAGC | *qnrB*-full ORF | (3) | 53 | 30 | 1 |
| sc3 | GCTSARGAGAACAGCTATAC | | | | | |
| ds3 | ATGGCTGAAGTTGAGATTAT | | | | | |
| qnrC-F | GGGTTGTACATTTATTGAATCG | *qnrC* | (4) | 53 | 30 | 1 |
| qnrC-R | CACCTACCCATTTATTTTCA | | | | | |
| qnrD-F | CGAGATCAATTTACGGGGAATA | *qnrD* | (5) | 53 | 30 | 1 |
| qnrD-R | AACAAGCTGAAGCGCCTG | | | | | |
| qnrSm-F | GCAAGTTCATTGAACAGGGT | *qnrS* | (1) | 53 | 30 | 1 |
| qnrSm-R | TCTAAACCGTCGAGTTCGGCG | | | | | |
| qnrS_ext_fwd1 | GGGTTGTAATGTGTTGATGTAACAGG | *qnrS*- full ORF | this study | 50 | 40 | 2 |
| qnrS_ext_rev1 | CCCTATGTCTATTATTGCAAGGTTG | | | | | |
| qnrVC-F | AATTTTAAGCGCTCAAACCTCCG | *qnrVC* | (6) | 53 | 30 | 1 |
| qnrVC-F | TCCTGTTGCCACGAGCATATTTT | | | | | |
| aac(6)-Ib | TTGCGATGCTCTATGAGTGGCTA | *aac(6′)-Ib-cr* | (7) | 53 | 30 | 1 |
| aac(6)-Ib-ext-R | ACG TCC CCC TCG ATG GAA G | | this study | | | |
| qepA-F | AACTGCTTGAGCCCGTAGAT | *qepA* | (8) | 50 | 45 | 1 |
| qepA-R | GTCTACGCCATGGACCTCAC | | | | | |
| oqxAB-F | CTCGCAGCGTCTGTTCACG | *oqxA/oqxB* | this study | 50 | 40 | 1 |
| oqxAB-R | GAGACTGCTTCTGGGTGGTGATC | | | | | |
| gyrA-F | GTACTTTACGCCATGAACGT | *gyrA* (QRDR) | (8) | 50 | 40 | 1 |
| gyrA-R | TACCGTCATAGTTATCCACGA | | | | | |
| gyrA-alt-R | ATCACTTCCGTCAGGTTGTGC | | this study | | | |
| parC-F | AATGAGCGATATGGCAGAGC | *parC* (QRDR) | (8) | 50 | 40 | 1 |
| parC-R | TTGGCAGACGGGCAGGTAG | | | | | |
| parC-kleb1-R | GCCACTTCACGCAGGTTGTG | | this study | 53 | 40 | 2 |

[1] M = A or C; H = A or C or T; Y = C or T
[2] For all PCR amplifications the following general cycling program was used: the samples were denatured at 95˚C for 2 min, followed by 30 to 45 cycles of denaturation at 95˚C for 30 s, annealing at 50 to 60˚C for 30 s, and extension at 72˚C for 1 or 2 min. The table provides the actual values for – the annealing temperature in degrees Celsius (annealing), the number of cycles conducted (cycles) and the duration of extension part of the cycle in minutes (extension).

**TABLE S2.**  Quinolone sensitivity phenotypes, PMQR genes and QRDR mutations.

| Isolate[1] | Identification | Quinolone MIC[2] | | | PMQR genes detected[3] | QRDR mutations[4] | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | | | | | GyrA | | ParC | |
| | | ND | CIP | MOX | | Ser83 | Asp87 | Ser80 | Glu84 |
| SL121 | *Escherichia coli* | **≥256** | **≥32** | **≥32** | *qepA1* | Leu | Asn | Ile | |
| SL158 | *Escherichia coli* | **≥256** | **≥32** | **≥32** | *qepA1* | Leu | Asn | Ile | |
| SL176 | *Escherichia coli* | **≥256** | **≥32** | **24** | *qepA1* | Leu | Asn | Ile | Gly |
| SL152 | *Escherichia coli* | **≥256** | 0.75 | 0.75 | | Val | | Arg | |
| SL169 | *Escherichia coli* | **≥256** | 0.38 | 0.5 | | Leu | | | |
| SL171 | *Escherichia coli* | **≥256** | 0.38 | 0.5 | | Leu | | | |
| SL178 | *Escherichia coli* | **≥256** | 0.25 | 0.25 | | Leu | | | |
| SL188 | *Escherichia coli* | **≥256** | 0.25 | 0.38 | | Leu | | | |
| SL115 | *Escherichia coli* | 2 | 0.016 | 0.064 | | | | | |
| SL125 | *Escherichia coli* | 3 | 0.016 | 0.094 | | | | | |
| SL133 | *Escherichia coli* | 2 | 0.016 | 0.047 | | | | | |
| SL137 | *Escherichia coli* | 3 | 0.016 | 0.064 | | | | | |
| SL159 | *Escherichia coli* | 3 | 0.012 | 0.19 | | | | | |
| SL162 | *Klebsiella pneumoniae* | **≥256** | **12** | **≥32** | *oqxAB* | Phe | Ala | Ile | |
| SL108 | *Klebsiella pneumoniae* | **≥256** | **4** | **8** | *oqxAB* | Ile | | Ile | |
| SL116 | *Klebsiella pneumoniae* | **≥256** | **4** | **8** | *oqxAB* | Ile | | Ile | |
| SL163 | *Klebsiella pneumoniae* | **≥256** | 3 | 6 | *oqxAB* | Ile | | Ile | |
| SL164 | *Klebsiella pneumoniae* | **≥256** | 2 | 4 | *oqxAB* | Ile | | Ile | |
| SL165 | *Klebsiella pneumoniae* | **≥256** | 3 | 4 | *oqxAB* | Ile | | Ile | |
| SL185 | *Klebsiella pneumoniae* | **≥256** | **≥32** | **12** | *oqxAB, aac(6')-1b-cr, qnrB1*d | Ile | | Ile | |
| SL186 | *Klebsiella pneumoniae* | **≥256** | **4** | 1.4 | *oqxAB* | Ile | | Ile | |
| SL190 | *Klebsiella pneumoniae* | **≥256** | **≥32** | **16** | *oqxAB, aac(6')-1b-cr* | Tyr | Ala | Ile | |
| SL113 | *Klebsiella pneumoniae* | **24** | **2** | 4 | *oqxAB, aac(6')-1b-cr, qnrB1*d | | | | |
| SL136 | *Klebsiella pneumoniae* | 3 | 0.094 | 0.25 | *oqxAB* | | | | |
| SL141 | *Klebsiella pneumoniae* | 6 | 0.064 | 0.5 | *oqxAB* | | | | |
| SL180 | *Klebsiella pneumoniae* | 8 | 0.75 | 0.75 | *oqxAB, aac(6')-1b-cr, qnrB1*d | | | | |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| SL183 | *Klebsiella pneumoniae* | 3 | 0.032 | 0.094 | *oqxAB* | | |
| SL196 | *Klebsiella pneumoniae* | 12 | **3** | 1 | *oqxAB, aac(6')-1b-cr, qnrB1*d | | |
| SL513 (e) | *Klebsiella pneumoniae* | 3 | 0.032 | 0.064 | *oqxAB* | | |
| SL531 (e) | *Klebsiella pneumoniae* | 3 | 0.032 | 0.094 | *oqxAB* | | |
| SL179 | *Enterobacter cloacae* | 16 | **3** | 1 | *aac(6')-1b-cr, qnrB1*a | | |
| SL182 | *Enterobacter cloacae* | 3 | **1.5** | 0.75 | *aac(6')-1b-cr, qnrB1*a | | |
| SL189 | *Enterobacter cloacae* | 12 | 1 | 0.75 | *aac(6')-1b-cr, qnrB1*a | | |
| SL199 | *Enterobacter cloacae* | 16 | **1.5** | 0.75 | *aac(6')-1b-cr, qnrB1*a | | |
| SL167 | *Enterobacter cloacae* | **24** | 0.75 | **4** | *aac(6')-1b-cr, qnrB1*i | | |
| SL168 | *Enterobacter cloacae* | **24** | 1 | **8** | *aac(6')-1b-cr, qnrB1*i | | |
| SL174 | *Enterobacter cloacae* | 12 | 0.75 | 0.75 | *aac(6')-1b-cr, qnrB1*i | | |
| SL175 | *Enterobacter cloacae* | 12 | 0.75 | 0.75 | *aac(6')-1b-cr, qnrB1*i | | |
| SL181 | *Enterobacter cloacae* | 12 | 0.5 | 0.75 | *aac(6')-1b-cr, qnrB1*i | | |
| SL195 | *Enterobacter cloacae* | 12 | 0.38 | 1 | *aac(6')-1b-cr, qnrB1*i | | |
| SL198 | *Enterobacter cloacae* | 12 | 0.75 | 0.75 | *aac(6')-1b-cr, qnrB1*i | | |
| SL203 | *Enterobacter cloacae* | 12 | 1 | 0.75 | *aac(6')-1b-cr, qnrB1*i | | |
| SL161 | *Enterobacter cloacae* | **24** | **3** | **12** | *oqxAB, aac(6')-1b-cr, qnrB6* | | |
| SL160 | *Enterobacter cloacae* | 6 | 0.125 | 2 | *qnrS1* | Thr | |
| SL192 | *Enterobacter cloacae* | **≥256** | **1.5** | **16** | *qnrS1* | Ile | Ile |
| SL512 (e) | *Enterobacter cloacae* | 6 | 0.19 | 0.5 | *qnrS1* | | |
| SL184 | *Enterobacter* sp./*Leclercia* sp. | **≥256** | **≥32** | **6** | *aac(6')-1b-cr, qnrB1*a | Ile | Ile |
| SL191 | *Enterobacter* sp./*Leclercia* sp. | **≥256** | **≥32** | **6** | *aac(6')-1b-cr, qnrB1*a | Ile | Ile |
| SL201 | *Enterobacter* sp./*Leclercia* sp. | **≥256** | **≥32** | **12** | *aac(6')-1b-cr, qnrB1*a | Ile | Ile |
| SL204 | *Enterobacter* sp./*Leclercia* sp. | **≥256** | **≥32** | **6** | *aac(6')-1b-cr, qnrB1*a | Ile | Ile |
| SL129 | *Citrobacter freundii* | **≥256** | **≥32** | **≥32** | *aac(6')-1b-cr*, qnrA1, $\Delta^1 qnrB^5$ | Ile | Ile |
| SL156 | *Citrobacter freundii* | **≥256** | **≥32** | **≥32** | *aac(6')-1b-cr*, qnrB82, $\Delta^3 qnrB$, qnrS1 | Ile | Ile |
| SL157 | *Citrobacter freundii* | **≥256** | **≥32** | **≥32** | *aac(6')-1b-cr*, qnrB81, $\Delta^3 qnrB$, qnrS1 | Ile | Ile |
| SL187 | *Citrobacter freundii* | **≥256** | **≥32** | **12** | *aac(6')-1b-cr, qnrB1*a, $\Delta^3 qnrB$ | Ile | Ile |
| SL197 | *Citrobacter freundii* | **≥256** | **≥32** | **16** | *aac(6')-1b-cr, qnrB1*a, $\Delta^3 qnrB$ | Ile | Ile |
| SL150 | *Citrobacter freundii* | **≥256** | **≥32** | **≥32** | *aac(6')-1b-cr, qnrB1*d, $\Delta^1 qnrB$ | Ile | Ile |
| SL172 | *Citrobacter freundii* | **≥256** | **≥32** | **≥32** | *aac(6')-1b-cr, qnrB1*d, $\Delta^1 qnrB$ | Ile | Ile |

| SL200 | *Citrobacter freundii* | **≥256** | **≥32** | **≥32** | *aac(6')-1b-cr, qnrB1*d, $\Delta^1$*qnrB* | Ile | | Ile | |
|---|---|---|---|---|---|---|---|---|---|
| SL202 | *Citrobacter freundii* | **≥256** | **≥32** | **≥32** | *aac(6')-1b-cr, qnrB1*d, $\Delta^1$*qnrB* | Ile | | Ile | |
| SL205 | *Citrobacter freundii* | **≥256** | **≥32** | **≥32** | *aac(6')-1b-cr, qnrB1*d, $\Delta^1$*qnrB* | Ile | | Ile | |
| SL154 | *Citrobacter freundii* | **≥256** | **≥32** | **≥32** | *qnrB12* | Ile | Tyr | Ile | |
| SL155 | *Citrobacter freundii* | **≥256** | **≥32** | **≥32** | *qnrB12* | Ile | Tyr | Ile | |
| SL194 | *Citrobacter freundii* | **≥256** | **≥32** | **≥32** | *qnrB12* | Ile | Tyr | Ile | |
| SL124 | *Citrobacter freundii* | **≥256** | **12** | **≥32** | *aac(6')-1b-cr, qnrB6,* $\Delta^2$*qnrB, qnrS1* | Ile | | | |
| SL127 | *Citrobacter freundii* | **≥256** | **12** | **≥32** | *aac(6')-1b-cr, qnrB6,* $\Delta^2$*qnrB, qnrS1* | Ile | | | |
| SL151 | *Citrobacter freundii* | **≥256** | **16** | **≥32** | *aac(6')-1b-cr, qnrB6,* $\Delta^2$*qnrB, qnrS1* | Ile | | | |
| SL153 | *Citrobacter freundii* | **≥256** | **12** | **≥32** | *aac(6')-1b-cr, qnrB6,* $\Delta^2$*qnrB, qnrS1* | Ile | | | |
| SL170 | *Citrobacter freundii* | **≥256** | **12** | **≥32** | *aac(6')-1b-cr, qnrB6,* $\Delta^2$*qnrB, qnrS1* | Ile | | | |
| SL173 | *Citrobacter freundii* | **≥256** | **12** | **12** | *aac(6')-1b-cr, qnrB6,* $\Delta^2$*qnrB, qnrS1* | Ile | | | |
| SL177 | *Citrobacter freundii* | **≥256** | **16** | 6 | *aac(6')-1b-cr, qnrB6,* $\Delta^2$*qnrB, qnrS1* | Ile | | | |
| SL193 | *Citrobacter freundii* | **≥256** | **16** | **12** | *aac(6')-1b-cr, qnrB6,* $\Delta^2$*qnrB, qnrS1* | Ile | | | |
| SL122 | *Citrobacter freundii* | **≥256** | **8** | **16** | *aac(6')-1b-cr,* $\Delta^2$*qnrB, qnrS1* | Ile | | | |
| SL166 | *Escherichia hermannii* | 12 | **3** | 2 | *aac(6')-1b-cr, qnrB1*a, *qnrS1* | | | | |
| SL522 (e) | *Pantoea dispersa* | 2 | 0.016 | 0.047 | | ND | ND | ND | ND |

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