Clonal Clusters, Molecular Resistance Mechanisms and Virulence Factors of Gram-Negative Bacteria Isolated from Chronic Wounds in Ghana

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Abstract: Wound infections are common medical problems in sub-Saharan Africa but data on the molecular epidemiology are rare. Within this study we assessed the clonal lineages, resistance genes and virulence factors of Gram-negative bacteria isolated from Ghanaian patients with chronic wounds. From a previous study, 49 Pseudomonas aeruginosa, 21 Klebsiella pneumoniae complex members and 12 Escherichia coli were subjected to whole genome sequencing. Sequence analysis indicated high clonal diversity with only nine P. aeruginosa clusters comprising two strains each and one E. coli cluster comprising three strains with high phylogenetic relationship suggesting nosocomial transmission. Acquired beta-lactamase genes were observed in some isolates next to a broad spectrum of additional genetic resistance determinants. Phenotypical expression of extended-spectrum beta-lactamase activity in the Enterobacterales was associated with bla\textsubscript{CTX-M-15} genes, which are frequent in Ghana. Frequently recorded virulence genes comprised genes related to invasion and iron-uptake in E. coli, genes related to adherence, iron-uptake, secretion systems and antiphagocytosis in P. aeruginosa and genes related to adherence, biofilm formation, immune evasion, iron-uptake and secretion systems in K. pneumonia complex. In summary, the study provides a piece in the puzzle of the molecular epidemiology of Gram-negative bacteria in chronic wounds in rural Ghana.

Keywords: wounds; Gram-negative bacteria; colonization; infection; clonal lineages; resistance genes; virulence factors

1. Introduction

The microbiology of chronic infected wounds, also on a molecular level, is poorly understood in sub-Saharan Africa (SSA) [1]. However, studies highlight the importance of antibiotic resistant Gram-negative bacteria [2–6].
From other parts in the world, in particular from industrialized countries, information on the microbiology and the role of biofilm-forming microorganisms causing such infections are well established [7–10].

In chronic wounds, *Pseudomonas aeruginosa* is amongst the most frequently isolated Gram-negative bacteria, associated with biofilm formation [11,12]. Tightly adhering biofilms pose a challenge in the diagnosis of *P. aeruginosa* using standard culturing methods [13].

In comparison, the role of Enterobacterales in chronic wounds has been much less characterized [14–17]. Studies have shown that geography seems to play a role in the estimation of their etiological relevance [18]. It was shown that skin colonization with Gram-negative bacteria is frequent in resource-limited (sub)tropical settings [19–21], in contrast to skin colonization of individuals from industrialized countries, where Gram-positive bacteria dominate [19]. Temperature and moisture have been discussed as likely reasons for the difference seen [22].

Isolation of potentially pathogenic bacteria from non-sterile sites like wounds does not necessarily indicate clinical relevance, which poses challenge to clinical interpretation.

In a recent study that focused on the overall bacterial composition of chronic wound infections in Ghana, from which the isolates for the present molecular analysis were taken, Enterobacterales and *Pseudomonas aeruginosa* constituted the majority of isolated bacterial strains [23]. A moderate proportion of ESBL-positive Enterobacterales suggests lower frequencies of antibiotic resistance [23] than what was recorded from other Ghanaian hospitals [5,24].

Within this study, we aim at characterizing clonal lineages, resistance-associated genetic elements and virulence genes of *P. aeruginosa*, the *Klebsiella pneumoniae* complex and *Escherichia coli*, which were recently isolated from chronic wounds of Ghanaian adult patients [23]. The molecular epidemiology of dominating clonal lineages and associated resistance genes will be assessed. Further, analysis of highly abundant virulence factors will be conducted.

2. Results

2.1. Clustering Based on Core Genome Multilocus Sequence Typing (cgMLST) Results

Of the 49 *P. aeruginosa* analyzed, a total of nine clusters comprising isolates without any recorded differences (n = 2) or with one or two alleles difference (n = 7) were found, suggesting closely related phylogeny (Figure 1). In addition to the clusters, 31 singletons with differences ranging from 80 to 3584 alleles were observed. MLST sequence types (ST) are indicated in Figure 1 and Tables A1 and A2. Cluster sequence types included the following: ST244, ST245, ST381, ST554, ST856, ST1485, ST2033, ST3227 and ST3590.

No clusters were identified among the 21 assessed *K. pneumonia* complex members, which were all singletons with differences ranging from 647 to 2244 alleles. *K. pneumoniae* complex sequence types are summarized in Figure 2. From the 12 *E. coli* isolates, three isolates in a cluster of close phylogenetic relationship were found (1 × no allelic differences, 1 × 1 allele difference) (Figure 3). In addition to the cluster observed, nine singletons with differences ranging from 41 to 2365 alleles were recorded. The sequence type of the cluster was ST132 (Pasteur MLST scheme). Sequence types of all *E. coli* isolates are illustrated in Figure 3.
2.2. Identified Molecular Resistance Mechanisms in Correlation to Previous Phenotypic Antibiotic Resistance

Table 1 summarizes acquired antimicrobial resistance determinants for *E. coli* and acquired genes mediating tolerance to disinfectants. Data for *P. aeruginosa* and *K. pneumoniae* are presented in Tables A1 and A2. Tables A3–A8 summarize the phenotypic resistance results as previously recorded [23].
Figure 2. Minimum spanning tree of *K. pneumoniae* complex based on 2358 targets (core genome). Isolate numbers are found within the nodes, and the numbers between the nodes indicate the number of different alleles. Colors demonstrate the MLST sequence type of the isolates.
In the present study, phylogenetically identical or almost identical isolates also carried the same resistomes. All *E. coli* strains harbored acquired beta-lactamase genes with the majority coding for small spectrum beta-lactamases such as *bla*<sub>TEM-1</sub> or *bla*<sub>OXA-1</sub>. Only four strains carried the gene for an ESBL, in all cases *bla*<sub>CTX-M-15</sub>. Among the *K. pneumoniae* complex strains, two belonged to the species *K. variicola*, one to the species *K. quasipneumoniae* and the remaining to the species *K. pneumoniae* sensu stricto as reflected by intrinsic *bla*<sub>LEN</sub>, *bla*<sub>OKP</sub> and *bla*<sub>SHV-1</sub> like, respectively. Genes coding for ESBL (*bla*<sub>CTX-M-15</sub>) were found solely in four out of 18 *K. pneumoniae* sensu stricto strains that also displayed resistance to oxyimino cephalosporins. In addition, several *K. pneumoniae* complex strains harbored *bla*<sub>TEM-1</sub>, single strains also contained *bla*<sub>OXA-1</sub> and *bla*<sub>SCO-1</sub>.

With respect to *P. aeruginosa*, only one strain harbored acquired beta-lactamase genes (*bla*<sub>TEM-1</sub> and *bla*<sub>SCO-1</sub>). Increased minimum inhibitory concentrations (MICs) for carbapenems as observed in some *P. aeruginosa* strains were neither explained by matching acquired carbapenemase genes nor by full sequence analysis of the oprD gene. The associated amino acid sequences are shown in Figure A1. As indicated, the complete oprD gene was found in all 49 *P. aeruginosa* isolates; there was no evidence of protein truncation by premature stop of translation. The 49 isolates could be divided into 7 subgroups according to the protein sequence of the oprD protein, which differ in a total of 30 individual amino acid exchanges and in a single 12aa/10aa-stretch. Therefore, genotypic assessment could not identify the reason for the single carbapenem-resistant *P. aeruginosa* isolate 088 (ST 1682).
Table 1. Analysis of antimicrobial resistance determinants, ordered by strain and MLST type, of the assessed *E. coli* isolates. ST = Sequence type.

| Sample ID | ST-Type | Acquired Resistance Determinants Against | Beta lactams | Sulfonamids | Trimethoprim | Makrolids | Tetracyclins | Fluoroquinolones | Chloramphenicol | Aminoglycosides | Efflux pumps | Amino acid exchanges due to point mutations | Disinfectant resistance genes * |
|-----------|---------|----------------------------------------|-------------|-------------|-------------|-----------|-------------|------------------|----------------|---------------|-------------|---------------------------------|--------------------------------|
| 041       | ST 2    | **bla**<sub>TEM-1B</sub>, **bla**<sub>CTX-M-15</sub>, **bla**<sub>OXA-1</sub>, **bla**<sub>TEM-1B</sub>, **bla**<sub>TEM-1B</sub>, **bla**<sub>TEM-1B</sub>, **sul1**, **dfra17**, **mhp(A)**, **tet(B)**, **acc(6′)-Ib-cr, acc(6′)-Ib-cr** | **sul1**    | **dfra17**  | **mhp(A)**  | **tet(B)** | **acc(6′)-Ib-cr, acc(6′)-Ib-cr** | **catB3, catA1** | **acc(3)-IId, acc(6′)-Ib-cr, aadA5, acc(6′)-Ib-cr** | **mdfr(A)** | **parE p.S458A, gyrA p.S83L, gyrA p.D87N, parC p.S80I** | **sitABCD, qacE** |
| 049       | ST 3    | **bla**<sub>TEM-1B</sub>, **sul2**, **sul1**, **dfra12**, **mhp(A)**, **tet(A)**, **aadA2, aphp(3′)-Ib, aphp(6)-Id** | **tet(A)**  | **mhp(A)**  | **tet(A)**  | **mhp(A)**  | **tet(A)**  | **aadA2, aphp(3′)-Ib, aphp(6)-Id** | **mdfr(A)** | **sitABCD-like, qacE** | **sitABCD-like, qacE** |
| 068       | ST 632  | **bla**<sub>TEM-1B</sub>, **sul3**, **dfra12**, **mhp(A)**, **tet(A)**, **cmrA1** | **tet(A)**  | **cmrA1**   | **tet(A)**  | **cmrA1**   | **tet(A)**  | **cmrA1**   | **aadA1, aadA2** | **mdfr(A)**-like | **parE p.S458A, gyrA p.S83L, gyrA p.D87N, parC p.S80I** | **sitABCD-like, qacE** |
| 117       | ST 4    | **bla**<sub>TEM-1B</sub>, **sul1**, **sul2**, **dfra7**, **tet(A)**, **catA1** | **tet(A)**  | **dfra7**   | **tet(A)**  | **dfra7**   | **tet(A)**  | **dfra7**   | **catA1**   | **mdfr(A)**-like | **sitABCD-like, qacE** |
| 152       | ST 22   | **bla**<sub>CARB-2</sub>, **bla**<sub>TEM-1B</sub>, **sul1**, **dfra1**, **ere(B)**, **tet(B)**, **catA1** | **tet(A)**  | **ere(B)**  | **tet(B)**  | **ere(B)**  | **tet(B)**  | **ere(B)**  | **catA1**   | **mdfr(A)**-like | **gyrA p.S83L, qacE, sitABCD** |
| 176       | ST 132  | **bla**<sub>TEM-1B</sub>, **sul1**, **dfra7**, **tet(A)**, **catA1** | **tet(A)**  | **dfra7**   | **tet(A)**  | **dfra7**   | **tet(A)**  | **dfra7**   | **catA1**   | **mdfr(A)**-like | **qacE, sitABCD** |
| 221       | ST 132  | **bla**<sub>TEM-1B</sub>, **sul1**, **dfra7**, **tet(A)**, **catA1** | **tet(A)**  | **dfra7**   | **tet(A)**  | **dfra7**   | **tet(A)**  | **dfra7**   | **catA1**   | **mdfr(A)**-like | **qacE, sitABCD** |
| 222       | ST 132  | **bla**<sub>TEM-1B</sub>, **sul1**, **sul2**, **dfra7**, **tet(A)**, **catA1** | **tet(A)**  | **dfra7**   | **tet(A)**  | **dfra7**   | **tet(A)**  | **dfra7**   | **catA1**   | **mdfr(A)**-like | **qacE, sitABCD** |
| 225       | ST 506  | **bla**<sub>TEM-1D</sub>, **bla**<sub>CTX-M-15</sub>, **sul1**, **sul2**, **dfra17**, **mhp(A)**, **tet(A)**, **catA1** | **tet(A)**  | **dfra17**  | **mhp(A)**  | **tet(A)**  | **dfra17**  | **mhp(A)**  | **catA1**   | **mdfr(A)**-like | **gyrA p.S83L, parE p.1529L, sitABCD-like, qacE** |
| 245       | ST 2    | **bla**<sub>TEM-1B</sub>, **sul1**, **dfra12**, **mhp(A)**, **tet(B)**, **gyrA4 (neu)**, **catA1** | **tet(B)**  | **dfra12**  | **mhp(A)**  | **tet(B)**  | **dfra12**  | **mhp(A)**  | **catA1**   | **mdfr(A)**-like | **parE p.S458A, gyrA p.S83L, gyrA p.D87N, parC p.S80I, qacE** |
| 270       | ST 2    | **bla**<sub>CTX-M-15</sub>, **tet(B)** | **tet(B)**  | **tet(B)**  | **tet(B)**  | **tet(B)**  | **tet(B)**  | **tet(B)**  | **catA1**   | **mdfr(A)**-like | **gyrA p.S83L, gyrA p.D87N, parE p.5458A, parE p.580I** |
| 299       | ST 1018 | **bla**<sub>TEM-1B</sub>, **sul3**, **dfra14**, **tet(A)**, **qnrS1** | **tet(A)**  | **dfra14**  | **tet(A)**  | **dfra14**  | **tet(A)**  | **dfra14**  | **catA1**   | **mdfr(A)**-like | **qacE** |

* sitABCD = peroxides resistance, qacE = quaternary ammonium compounds resistance.
Other frequently detected resistance genes in *P. aeruginosa* were the fosfomycin resistance gene *fosA*, the chloramphenicol resistance gene *catB7*, the aminoglycoside resistance gene *aph(3′)-IIb* and the fluoroquinolone-resistance gene *crpP*. In the *Klebsiella pneumoniae* complex isolates, single amino acid exchanges and the fosfomycin resistance gene *fosA* were frequent. Various fluoroquinolone resistance genes and disinfectant tolerance mediating genes also quantitatively dominated. Finally, a broad spectrum of acquired genes causing resistance to the assessed classes of antimicrobial drugs and tolerance to disinfectants was observed in the *E. coli* strains.

### 2.3. Identified Molecular Virulence Mechanisms

Table 2 summarizes the analysis of virulence-related genes in *E. coli* (without genes mediating enteropathogenicity). Data for *P. aeruginosa* and *K. pneumoniae* are presented in Tables A9 and A10.

**Table 2.** Analysis of virulence determinants, ordered by strain and MLST type, of the assessed *E. coli* isolates. ST = Sequence type.

| Sample ID | ST-Type | Adherence | Invasion | Pathogenicity Factor Groups | Iron Uptake | Protease |
|-----------|---------|-----------|----------|-----------------------------|-------------|----------|
| 041       | ST 2    | fdeC      | aslA, ompA | entA-like, entB, entC, entE, entF, entS, fepA, fepB, fepC, fepD, fepG, |            |          |
| 049       | ST 3    | aslA, kpsC, kpsD, kpsE, kpsF, kpsM, kpsS-like, ompA | chuS, chuU, chuV, chuW, chuY, entA-like, entB, entC, entE, entF, entS, fepA, fepB, fepC, fepD, fepG |            |          |
| 068       | ST 632  | ompA      |          | entA-like, entB, entC, entE, entF, entS, fepA, fepB, fepC, fepD, fepG |            |          |
| 117       | ST 4    | aslA, kpsC, kpsD, kpsE, kpsF, kpsM, kpsS-like, ompA | hlyB, hlyC, hlyD, tcpC | chuA, chuS, chuT, chuU, chuV, chuW, chuX, chuY, entA-like, entB, entC, entE, entF, entS, fepA, fepB, fepC, fepD, fepG, hlyA, iroN, pic, sat, vat |            |
| 152       | ST 22   | sfaB, sfaC, sfaD, sfaE, sfaG, sfaH, sfaS, sfaX, sfaY | aslA, kpsC, kpsD, kpsE, kpsF, kpsM, kpsS-like, ompA | craf1, hlyA, hlyB, hlyC, hlyD, tcpC | chuA, chuS, chuT, chuU, chuV, chuW, chuX, chuY, entA-like, entB, entC, entE, entF, entS, fepA, fepB, fepC, fepD, fepG, iroN, | vat |
| 176       | ST 132  | aslA, kpsC, kpsD, kpsE, kpsF, kpsM, kpsS-like, ompA |          | entA-like, entB, entC, entE, entF, entS, fepA, fepB, fepC, fepD, fepG, |            | sat |
| 221       | ST 132  | aslA, kpsC, kpsD, kpsE, kpsM, kpsS-like, ompA |          | entA-like, entB, entC, entE, entF, entS, fepA, fepB, fepC, fepD, fepG, |            | sat |
Table 2. Cont.

| Sample ID | ST-Type | Adherence | Invasion | Toxin | Immune Evasion | Iron Uptake | Protease |
|-----------|---------|-----------|----------|-------|----------------|-------------|----------|
| 222 ST 132 | aslA, kpsC, kpsD, kpsE, kpsF, kpsM, kpsU; kpsS-like, ompA | entA-like, entB, entC, entE, entF, entS, fepA, fepB, fepC, fepD, fepG, sat |
| 225 ST 506 | aslA, kpsC, kpsD, kpsE, kpsF, kpsM, kpsU; kpsS-like, ompA | chuA, chuS, chuT, chuU, chuV, chuW, chuX, chuY, entA-like, entB, entC, entE, entF, entS, fepA, fepB, fepC, fepD, fepG, sat |
| 245 ST 2 | aslA, ompA | entA-like, entB, entC, entE, entF, fepA, fepB, fepC, fepD, fepG |
| 270 ST 2 | aslA, ompA | entA-like, entB, entC, entE, entS, fepA, fepB, fepC, fepD, fepG |
| 299 ST 1018 | ompA | entA-like, entB, entC, entE, entF, fepA, fepB, fepD, fepG |

The virulence-associated gene exoU, which has been described in association with the P. aeruginosa high-risk clone ST 135 [25], was recorded three times, associated with ST 135 (sample ID 296), ST 532 (sample ID 310) and ST 2483 (sample ID 22), respectively. Based on a Kleborate assessment, a positive virulence score was calculated for 7 out of 21 K. pneumoniae strains, comprising the known high-risk clones ST 17 (sample IDs 177, 199) and ST 152 (sample ID 100) [26], next to the clones ST 4 (sample ID 146), ST 6 (sample ID 214), ST 36 (sample ID 267) and ST 39 (sample ID 73), respectively. With focus on some important virulence associated genes in Klebsiella spp., ybt genes were detected in the abovementioned 7 samples, iroE was recorded in all 21 strains, while clb or rpmA genes were not detected.

Iron-uptake-related genes were numerous in all analyzed bacterial strains. For P. aeruginosa and K. pneumoniae, various secretion system-associated genes were found. Immune evasion-related genes were highly abundant in K. pneumoniae but not in E. coli isolates. Adherence-related genes were numerous in P. aeruginosa and in K. pneumoniae but not in E. coli.

Numerous invasion-associated genes were detected in E. coli, antiphagocytosis-associated genes were found in P. aeruginosa, and biofilm-associated genes in K. pneumoniae.

Less frequently detected were: toxin genes in E. coli and K. pneumoniae, protease genes in E. coli and P. aeruginosa, regulation genes in P. aeruginosa and K. pneumoniae, biosurfactant and pigment genes in P. aeruginosa and nutrition factor, efflux pumps and serum resistance genes in K. pneumoniae.

3. Discussion
Within this study, we aimed at filling information gaps on the molecular epidemiology of Gram-negative bacteria from chronic infected wounds in rural Ghana. Phylogenetic analyses based on core genome comparison indicated a high clonal diversity of the wound-associated isolates. Clonal clusters were restricted to nine P. aeruginosa clusters and one E. coli cluster, most likely indicating nosocomial transmission, which has most likely occurred in the wound dressing room that patients' visit on a weekly basis.
ST 135 and ST 244, which are among the worldwide top 10 \textit{P. aeruginosa} high-risk clones [25], were found among the \textit{P. aeruginosa} wound isolates. In detail, one ST 135 \textit{Pseudomonas aeruginosa} isolate was detected, carrying the beta-lactamase-encoding genes \textit{bla}_{TEM-1B} and \textit{bla}_{SCO-1} and an \textit{exoU} gene, next to five ST 244 without acquired beta-lactamases. Focusing on known pathogenic \textit{K. pneumoniae} clones [26], two ST 17 strains, a clone reported to be associated with carbapenem-resistance, and one ST 152 strain, a clone known from the Caribbean as common carrier of multiple resistance genes, were detected. Strains carrying the \textit{ybt} and \textit{iro} genes were also identified as high-risk clones by the Kleborate software. From the observed \textit{E. coli} ST types, none have been previously reported as being associated with pathogenic clones so far [27].

In line with the phenotypical antibiotic resistance results previously published [23], numerous acquired resistance determinants were detected in the bacterial strains under investigation. Focusing on the few observed clusters, comparable resistome compositions point towards recent nosocomial transmission. The gene \textit{bla}_{CTX-M-15} was identified as the determinant of the detected extended spectrum beta-lactamase (ESBL) expression in ESBL positive Enterobacterales [23]. This is in line with previous reports from both human and livestock-associated ESBL positive Enterobacterales in Ghana [28–34]. In \textit{P. aeruginosa} and \textit{K. pneumoniae}, \textit{bla}_{SCO-1}, which has initially been described from an \textit{Acinetobacter baumannii} isolate from Argentina [35], was observed. Beta-lactamases with high hydrolytic effects on carbapenems were lacking, the same applies to protein truncation by premature stop of translation of the \textit{oprD} gene in \textit{P. aeruginosa}. Accordingly, the genetic background of carbapenem resistance of a single \textit{P. aeruginosa} strain could not be resolved, although downregulation of \textit{oprD} expression due to mutations outside of the gene or \textit{ampC} (class C betalactamase) overexpression could not be excluded as likely reasons.

Substance-specific genes and genes encoding efflux pumps mediating tolerance to disinfectants were observed in Enterobacterales. Therefore, further monitoring of the spread of disinfectant tolerance-associated genes and the effects of their abundance on disinfectant-based skin and wound decolonization strategies [36] seem advisable.

The importance of highly abundant virulence factors like iron-uptake- and secretion system-related genes in \textit{P. aeruginosa} is comprehensively described in the literature [37,38]. Other genes reported in the literature like regulation-associated virulence genes, recently reported, were less frequently observed in our isolates [39,40]. However, due to lacking information on the individual etiological relevance of each isolate, any association with clinical effects remains speculative.

Further limitations of this study include a rather small sample size and the lack of a comparison strain collection containing isolates from other clinical specimens and environmental strains. Accordingly, the interpretation of the etiological relevance of individual strains remains challenging and is clearly beyond the scope of this work.

In summary, a broad spectrum of Gram-negative clones was isolated from the chronic wounds of the Ghanaian patients. Thereby, known high-risk clones [25–27] played only a minor role. Observed resistance patterns and mechanisms were in line with the spectrum expected from previous reports [23,28–34].

4. Materials and Methods

4.1. Sample Collection, Bacterial Culture and Antibiotic Susceptibility Testing

Single patient strains of \textit{P. aeruginosa}, \textit{E. coli} and \textit{K. pneumoniae} complex were isolated from patients $\geq15$ years with an infected chronic wound at the Outpatient Department (OPD) of the Agogo Presbyterian Hospital, in the Asante Akim North District of rural Ghana. Patients typically visit the wound dressing room of the OPD on a weekly basis. Sampling was performed from January 2016 to November 2016. Sample collection and microbiological investigations were reported previously [23]. Antibiotic susceptibility was tested by the disk diffusion method and interpreted following the European Committee on Antimicrobial Susceptibility Testing (EUCAST) guidelines v.6.0 (http://www.eucast.org)
(accessed on 15 January 2016). Bacterial strains and antibiotic susceptibility were confirmed using the VITEK2 System. Those data have been published before [23].

4.2. DNA Isolation and Whole Genome Sequencing

Bacterial DNA was isolated using the MasterPure Complete DNA and RNA Purification Kit (LGC standards GmbH, Wesel, Germany) and sent for whole genome sequencing (WGS) to BGI Europe, Denmark, Copenhagen. A BGISEQ-500 device was used for sequencing, generating $2 \times 150$ bp paired-end reads with an aimed coverage of $100 \times$. Original raw data were upload for public use to the short-read archive (SRA, NCBI) under the accession number PRJNA699140. Details on the strain-specific SRA accession numbers are provided in Table A11.

4.3. Whole Genome Sequencing and Data Analysis

All raw data passed quality control using FASTQC v.0.11.4 [41] and were used for further analysis. Taxonomic classification and contamination check of raw-reads was performed using KRACKEN2 v.2.0.8-beta [42]. Phylogenetic analysis based on core genome multi locus sequence typing (cgMLST) analysis was performed using the commercial software SeqSphere+ v. 7.2.0 (Ridom GmbH, Münster, Germany) [43]. The software pipeline included assessment of read data and adapter control using FASTQC followed by genome assembly using the internally provided assembler Velvet, applying default settings. The reference genomes NC_000913.3 (E. coli), NC_002516.2 (P. aeruginosa) and NC_01273.1 (K. pneumoniae species complex) were used for cgMLST analyses. Only samples with a ration of “good cgMLST targets” higher than 90% were included in the phylogenetic analysis. Novel cgMLST-based complex types (CT) were automatically assigned by the SeqSphere software. Unknown alleles and profiles of MLST genes were submitted to pubmlst.org or Institute Pasteur to establish novel sequence types (ST). Isolates were defined to be clonally identical with allele differences less than four. Moreover, raw data were assembled with SPAdes v3.13.11 [44] using the careful option. Scaffolds shorter than 500 bp or with a coverage smaller than ten were sorted out, using an in-house script. Abricate v.0.9.9 [45] was used to screen for resistance and virulence genes in SPAdes assembly files, using NCBI AMRFinderPlus [46] and VFDB [47] as reference databases (both updated 6 November 2020), respectively. Additionally, SPAdes assemblies were uploaded to ResFinder4.1 [48] to obtain WGS predicted phenotypes against different antimicrobials by using default settings (%ID > 90, minimum length > 60%) and to Kleborate to predict virulence genes in Klebsiella isolates.

4.4. Ethical Considerations

The Committee on Human Research, Publications and Ethics, School of Medical Science, Kwame Nkrumah University of Science and Technology in Kumasi, Ghana, approved this study (approval number CHRPE/AP/078/16).

5. Conclusions

In conclusion, this study provides a molecular insight into the epidemiology of Gram-negative bacteria isolated from chronic wound infections from patients in rural Ghana. Epidemiological data that focus on the distribution and spread of antimicrobial resistance determinants and associated virulence factors in resource-limited settings are scarce. Although the study is a small cross-sectional assessment, which cannot replace continuous surveillance programs, it might provide a glimpse of prevailing Gram-negative bacteria isolated from wound infections in this area of Ghana. Considering the ongoing need for resistance and virulence surveillance in tropical regions, larger future studies are desirable.
Author Contributions: U.L., D.D. and J.M. designed and coordinated this study. T.T., F.P. and S.T. performed bioinformatic analysis. M.L. supported the management of this study. A.J. managed the data collection. H.F., D.D. and U.L. wrote the first draft of this manuscript. K.O. conducted and supervised fieldwork. C.W.A. and K.T. conducted and supervised lab work. M.K. and S.S. supported the interpretation of the results, writing and editing the manuscript. All authors read and approved the final manuscript.

Funding: This study was funded by institutional funds of the Bernhard Nocht Institute for Tropical Medicine (BNITM).

Institutional Review Board Statement: The study was conducted according to guidelines of the Declaration of Helsinki. The Committee on Human Research, Publications and Ethics, School of Medical Science, Kwame Nkrumah University of Science and Technology in Kumasi, Ghana, approved this study (approval number CHRPE/AP/078/16).

Informed Consent Statement: Informed consent was obtained from all study participants.

Data Availability Statement: All relevant data have been provided in the paper and its Appendix A materials. Raw data are available applying the links as indicated in the methods chapter and can also be provided by the authors on reasonable request.

Acknowledgments: We thank all patients that participated in this study and the staff at the Agogo Presbyterian Hospital. Without their support, this research study would not have been possible. We thank the team of curators pubmlst.org and the Institute Pasteur MLST and whole genome MLST databases for curating the data and making them publicly available at http://bigsdb.pasteur.fr/ (accessed on 22 March 2021).

Conflicts of Interest: The authors declare no conflict of interest.
Appendix A

Red frames: 30 single amino acid differences between the groups were identified (16, 8 and 6 with strong, weak and no similarity, respectively *)

Blue frame: A 12 aa stretch is changed into a differing 10 aa stretch in groups 6 and 7

*) similarities:
** indicates a site belonging to a group exhibiting strong similarity.
* indicates a site belonging to a group exhibiting weak similarity.
The criterion for distinguishing strong from weak similarity is as follows: Strong similarity corresponds to a PAM250 MATRIX score between amino acids of greater than 0.5, while weak similarity corresponds to a score of 0.5 or less.

Figure A1. Clustal omega multiple alignment of oprD proteins—one example for the 7 detected subgroups.
Table A1. Analysis of antimicrobial resistance determinants, ordered by strain and MLST type, of the assessed *P. aeruginosa* isolates. ST = Sequence type.

| Sample ID | ST-Type  | Beta-Lacatams | Sulfonamids | Fosfomycin | Trimethoprim | Makrolides | Tetracyclins | Fluoroquinolones | Chloramphenicol | Rifampicin | Aminoglycosides | Efflux Pumps | Amino Acid Exchanges Due to Point Mutations | Disinfectant Resistance Genes |
|-----------|----------|---------------|-------------|------------|--------------|------------|--------------|----------------|----------------|------------|----------------|-------------|-------------------------------------------|-----------------------------|
| 017       | ST 381   | fosA          |             |            |              |            |              |                |                |            |                |             |                            |                             |
| 022       | ST 2483  | fosA          |             |            |              |            |              |                |                |            |                |             |                            |                             |
| 032       | ST 3587  | sul1, fosA    | dfrA15      | tet(G)     |              |            |              |                |                |            |                |             |                            |                             |
| 069       | ST 360   | fosA          |             |            |              | catB7      |              |                |                |            |                |             |                            |                             |
| 081       | ST 244   | fosA          |             |            |              | catB7      |              |                |                |            |                |             |                            |                             |
| 082       | ST 514   | fosA          |             |            |              | catB7      |              |                |                |            |                |             |                            |                             |
| 088       | ST 1682  | fosA          |             |            |              | catB7      |              |                |                |            |                |             |                            |                             |
| 099       | ST 244   | fosA          |             |            |              | catB7      |              |                |                |            |                |             |                            |                             |
| 106       | ST 1521  | fosA          |             |            |              | catB7      |              |                |                |            |                |             |                            |                             |
| 114       | ST 244   | fosA          |             |            |              | catB7      |              |                |                |            |                |             |                            |                             |
| 137       | ST 3014  | fosA          |             |            |              | catB7      |              |                |                |            |                |             |                            |                             |
| 144       | ST 245   | fosA          |             |            |              | catB7      |              |                |                |            |                |             |                            |                             |
| 147       | ST 245   | fosA          |             |            |              | catB7      |              |                |                |            |                |             |                            |                             |
| 149       | ST 381   | fosA          |             |            |              | catB7      |              |                |                |            |                |             |                            |                             |
| 153       | ST 704   | fosA-like     |             |            |              | catB7-like |              |                |                |            |                |             |                            |                             |
| 154       | ST 244   | fosA          |             |            |              | catB7      |              |                |                |            |                |             |                            |                             |
| 157       | ST 2616  | fosA          |             |            |              | catB7-like |              |                |                |            |                |             |                            |                             |
| 160       | ST 170   | fosA-like     |             |            |              |             |              |                |                |            |                |             |                            |                             |
Table A1. Cont.

| Sample ID | ST-Type | Beta Lacatams | Sulfonamids | Fosfomycin | Trimethoprim | Makrolides | Tetracyclines | Fluoroquinolones | Chloramphenicol | Rifampicin | Amino-glycosides | Efflux Pumps | Amino Acid Exchanges Due to Point Mutations | Disinfectant Resistance Genes |
|-----------|---------|---------------|-------------|------------|--------------|------------|---------------|----------------|-----------------|------------|----------------|-------------|------------------------------------------|-------------------------------|
| 162       | ST 274  | fosA          |             |            |              |            |               |                |                 |            |                |            |                           |                               |
| 180       | ST 856  | fosA          |             |            |              |            |               |                |                 |            |                |            |                           |                               |
| 183       | ST 244  | fosA          |             |            |              |            |               |                |                 |            |                |            |                           |                               |
| 186       | ST 3588 | fosA-like     |             |            |              |            |               |                |                 |            |                |            |                           |                               |
| 190       | ST 871  | fosA          |             |            |              |            |               |                |                 |            |                |            |                           |                               |
| 195       | ST 988  | fosA          |             |            |              |            |               |                |                 |            |                |            |                           |                               |
| 196       | ST 2475 | fosA          |             |            |              |            |               |                |                 |            |                |            |                           |                               |
| 198       | ST 2476 | fosA          |             |            |              |            |               |                |                 |            |                |            |                           |                               |
| 204       | ST 639  | fosA          |             |            |              |            |               |                |                 |            |                |            |                           |                               |
| 208       | ST 132  | fosA          |             |            |              |            |               |                |                 |            |                |            |                           |                               |
| 218       | ST 856  | fosA          |             |            |              |            |               |                |                 |            |                |            |                           |                               |
| 229       | ST 270  | fosA          |             |            |              |            |               |                |                 |            |                |            |                           |                               |
| 233       | ST 3227 | fosA          |             |            |              |            |               |                |                 |            |                |            |                           |                               |
| 236       | ST 266  | fosA          |             |            |              |            |               |                |                 |            |                |            |                           |                               |
| 238       | ST 3589 | fosA-like     |             |            |              |            |               |                |                 |            |                |            |                           |                               |
| 242       | ST 3590 | fosA-like     |             |            |              |            |               |                |                 |            |                |            |                           |                               |
| 243       | ST 3590 | fosA-like     |             |            |              |            |               |                |                 |            |                |            |                           |                               |
Table A1. Cont.

| Sample ID | ST-Type | Acquired Resistance Determinants Against |
|-----------|---------|------------------------------------------|
|           |         | Beta Lacatams | Sulfonamids | Fosfomycin | Trimethoprim | Makrolides | Tetracyclins | Fluoroquinolones | Chloramphenicol | Rifampicin | Aminoglycosides | Efflux Pumps | Amino Acid Exchanges Due to Point Mutations | Disinfectant Resistance Genes |
| 272       | ST 2033 | fosA          | catB7-like |               |             |            |              |                |                |            |               |             |                         |                         |
| 274       | ST 2033 | fosA          | catB7-like |               |             |            |              |                |                |            |               |             |                         |                         |
| 278       | ST 988  | fosA          | crpP-like  | catB7-like   |             |            |              |                |                |            |               |             |                         |                         |
| 282       | ST 554  | fosA          | crpP-like  | catB7        |             |            |              |                |                |            |               |             |                         |                         |
| 285       | ST 554  | fosA          | crpP-like  | catB7        |             |            |              |                |                |            |               |             |                         |                         |
| 289       | ST 1485 | fosA          | catB7      |             |             |            |              |                |                |            |               |             |                         |                         |
| 290       | ST 1485 | fosA          | catB7      |             |             |            |              |                |                |            |               |             |                         |                         |
| 296       | ST 235  | fosA          | tet(G)     | catB7-like   |             |            |              |                |                |            |               |             |                         |                         |
| 298       | ST 3227 | fosA          | catB7      |             |             |            |              |                |                |            |               |             |                         |                         |
| 301       | ST 3593 | fosA-like     | catB7-like |             |             |            |              |                |                |            |               |             |                         |                         |
| 302       | ST 1755 | fosA          | catB7      |             |             |            |              |                |                |            |               |             |                         |                         |
| 309       | ST 3592 | fosA-like     | crpP-like  | catB7-like   |             |            |              |                |                |            |               |             |                         |                         |
| 310       | ST 532  | sulI          |           |             |             |            |              |                |                |            |               |             |                         |                         |
| 312       | ST 381  | fosA          |           |             |             |            |              |                |                |            |               |             |                         |                         |

Acquired resistance genes for macrolides, rifampicin, resistance-associated point mutations, genes for efflux pumps or genes mediating tolerance against disinfectants were not detected.
Table A2. Analysis of antimicrobial resistance determinants, ordered by strain and MLST type, of the assessed *K. pneumoniae* isolates. ST = Sequence type.

| Sample ID | ST-Type | Beta-Lactamases | Sulfonamides | Fosfomycin | Trimethoprim | Macrolides | Tetracyclines | Fluoroquinolones | Chloramphenicol | Rifampicin | Aminoglycosides | Efflux Pumps | Amino Acid Exchanges Due to Point Mutations | Disinfectant Resistance Genes * |
|-----------|---------|-----------------|--------------|------------|--------------|------------|---------------|-----------------|----------------|------------|----------------|-------------|-----------------------------------------|-----------------------------|
| 044       | ST 327  |                |              |            |              |            |               |                 |                |            |                |            | ompK37 p.I70M, ompK37 p.I128M, ompK37 p.I128M, ompK36 p.L59V, ompK36 p.L191S, ompK36 p.F207W, ompK36 p.A217S, ompK36 p.N218H, ompK36 p.D224E, ompK36 p.L228V, ompK36 p.E232R, ompK36 p.T254S, acrR p.P161R, acrR p.G164A, acrR p.F172S, acrR p.R173G, acrR p.L195V, acrR p.F197I, acrR p.K201M | oqxB, oqxA |
| 060       | ST 5379 | blTEM-1C        | sul1, sul2   | fosA       | dfrA12       | mph(A)     |               |                 |                |            |                |            | acrR p.P161R, acrR p.G164A, acrR p.F172S, acrR p.R173G, acrR p.L195V, acrR p.F197I, acrR p.K201M | oqxA, oqxB, oqxE, oqxB |
| Sample ID | ST-Type | Beta Lacatams | Sulfonamids | Fosfomycin | Trimethoprim | Macrolides | Tetracyclines | Fluoroquinolones | Chloramphenicol | Rifampicin | Amino-glycosides | Efflux Pumps | Amino Acid Exchanges Due to Point Mutations | Disinfectant Resistance Genes * |
|-----------|---------|---------------|-------------|-------------|--------------|------------|---------------|----------------|----------------|------------|------------------|-------------|------------------------------------------------|----------------------------------|
| 073       | ST 39   | blaTEM-1B, blaCTX-M-15 | sulI, fosA  | dfrA27 | erm(B), mphp(A) | tet(D) | oqxB, qpxA, aac(6’)-Ib-cr, qnrB2, aac(6’)-Ib-cr | catA2-like | ARR-3 | aac(6’)-Ib-cr, aadA16, aac(3)-Ia, aac(6’)-Ib-cr, aph(3’)-Ib-cr, aac(6’)-Ib-cr, aph(3’)-Ib-cr, aac(3)-Ib-cr, aac(6’)-Ib-cr, aph(3’)-Ib-cr, aac(6’)-Ib-cr, aph(3’)-Ib-cr | oqxB, oqxA, qacE |
| 100       | ST 152  | blaCTX-M-15, blaoxa-1, blaTEM-1B | sul2, sulI | fosA  | dfrA1, dfrA27 | mphp(A) | tet(D) | aac(6’)-Ib-cr, qnrB6, oqxA, aac(6’)-Ib-cr, qnrB2, aac(6’)-Ib-cr | catB3, catA1, catB3 | ARR-3 | aac(3)-Ia, aadA1, aadA16, aph(3’)-Ia, aac(6’)-Ib-cr, aph(3’)-Ib-cr, aac(6’)-Ib-cr, aph(3’)-Ib-cr, aac(6’)-Ib-cr, aph(3’)-Ib-cr, aac(6’)-Ib-cr, aph(3’)-Ib-cr | ompK36 p.N495, ompK36 p.L59V, ompK36 p.G189T, ompK36 p.F198Y, ompK36 p.F207Y, ompK36 p.A217S, ompK36 p.D222L, ompK36 p.E232R, ompK36 p.N304E, acrR p.L195V, acrR p.F197I, acrR p.K201M, ompk36 p.L70M, ompk36 p.L1228M, ompk36 p.N230G |
Table A2. Cont.

| Sample ID | ST-Type | Acquired Resistance Determinants Against | Efflux Pumps | Disinfectant Resistance Genes * |
|-----------|---------|------------------------------------------|--------------|--------------------------------|
|           |         | Beta-Lactams                              |              |                               |
|           |         | Sulfonylamids                             |              |                               |
|           |         | Fosfomycin                                |              |                               |
|           |         | Trimethoprim                              |              |                               |
|           |         | Macrolides                                |              |                               |
|           |         | Tetracyclines                             |              |                               |
|           |         | Fluoroquinolones                          |              |                               |
|           |         | Chloramphenicol                           |              |                               |
|           |         | Rifampicin                                |              |                               |
|           |         | Aminoglycosides                           |              |                               |
|           |         | Efflux Pumps                              |              |                               |

| 102       | ST 514  | fosA                                      | tet(C)       | oqxAB, oqxA, catA1           | ompK36 p.N49S, ompK36 p.L59V, ompK36 p.L191S, ompK36 p.F207W, ompK36 p.A217S, ompK36 p.N218H, ompK36 p.D224E, ompK36 p.L228V, ompK36 p.E232R, ompK37 p.T254S, ompK37 p.I70M, ompK37 p.I128M, ompK37 p.N230G, acrR p.P161R, acrR p.G164A, acrR p.F172S, acrR p.R173G, acrR p.L195V, acrR p.F197I, acrR p.K201M |

| 124       | ST 399  | fosA                                      | oqxA, oqxB   | catA1                        | ompK36 p.N49S, ompK36 p.L59V, ompK36 p.G189T, ompK36 p.F207Y, ompK36 p.A217S, ompK36 p.T222I, ompK36 p.D223G, ompK36 p.E232R, acrR p.P161R, acrR p.G164A, acrR p.F172S, acrR p.R173G, acrR p.F197I, acrR p.K201M |

| 146       | ST 4    | sul2                                      | tet(D)       | oqxA, oqxB, catA2-like       | oqxA, oqxB |
| Sample ID | ST-Type | Acquired Resistance Determinants Against | Efflux Pumps | Amino Acid Exchanges Due to Point Mutations | Disinfectant Resistance Genes * |
|-----------|---------|----------------------------------------|-------------|------------------------------------------|-------------------------------|
| 177       | ST 17   | sul1, sul2, fosA, dfrA15, tet(A), oqxA, oqxB-like, catA1, aadA1, aph(3’)-Ib, aph(6)-Id |             | ompK37 p.I70M, ompK37 p.I128M, acrR p.F161R, acrR p.G164A, acrR p.F172S, acrR p.R173G, acrR p.L195V, acrR p.F197I, acrR p.K201M, ompK36 p.N495, ompK36 p.L59V,ompK36 p.L191S, ompK36 p.F207W, ompK36 p.A217S, ompK36 p.N218H, ompK36 p.D224E, ompK36 p.L228V, ompK36 p.E232RompK36 p.T254S | qacE, oqxB-like, oqxA |
| 181       | ST 5380 | fosA, oqxA, oqxB                        |             | ompK36 p.N495, ompK36 p.L59V, ompK36 p.L191S, ompK36 p.F207W, ompK36 p.A217S, ompK36 p.N218H, ompK36 p.D224E, ompK36 p.L228V, ompK36 p.E232RompK36 p.T254SompK37 p.I70M, ompK37 p.I128M, acrR p.F161R, acrR p.G164A, acrR p.F172S, acrR p.R173G, acrR p.L195V, acrR p.F197I, acrR p.K201M | qacA, oqxB |
Table A2. Cont.

| Sample ID | ST-Type | Acquired Resistance Determinants Against | Amino Acid Exchanges Due to Point Mutations | Disinfectant Resistance Genes |
|-----------|---------|-----------------------------------------|--------------------------------------------|-----------------------------|
| 184       | ST 5381 | fosA, oqxA-like, oqxB-like             | ompK37 p.L70M, ompK37 p.I128M, ompK36 p.N38S, ompK36 p.L59V, ompK36 p.L191Q, ompK36 p.F198Y, ompK36 p.A217S, ompK36 p.N218H, ompK36 p.Q227N, ompK36 p.L229V, ompK36 p.N304E, acrR p.P161R, acrR p.G164A, acrR p.F172S, acrR p.R173G, acrR p.L195V, acrR p.F197I, acrR p.K201M | oqxA-like, oqxB-like |
| 199       | ST 17   | sul2, fosA-like, dfrA16                 | acrR p.P161R, acrR p.G164A, acrR p.F172S, acrR p.R173G, acrR p.L195V, acrR p.F197I, acrR p.K201M, ompK37 p.L70M, ompK37 p.I128M, ompK36 p.N49S, ompK36 p.L59V, ompK36 p.L191Q, ompK36 p.F198Y, ompK36 p.A217S, ompK36 p.N218H, ompK36 p.Q227N, ompK36 p.L229V, ompK36 p.N304E, acrR p.P161R, acrR p.G164A, acrR p.F172S, acrR p.R173G, acrR p.L195V, acrR p.F197I, acrR p.K201M | oqxA, oqxB, qacE |
Table A2. Cont.

| Sample ID | ST-Type | Acquired Resistance Determinants Against | Amino Acid Exchanges Due to Point Mutations | Disinfectant Resistance Genes * |
|-----------|---------|----------------------------------------|---------------------------------------------|-------------------------------|
| 214       | ST 6    | sulI, fosA-like, dfrA14, oqxB-like, oqxA | *ompK37 p.I70M, ompK37 p.I128M, ompK37 p.N49S, ompK36 p.L59V, ompK36 p.G189T, ompK36 p.F198Y, ompK36 p.F207Y, ompK36 p.T222L, ompK36 p.D223G, ompK36 p.E232R, acrR p.P161R, acrR p.G164A, acrR p.F172S, acrR p.R173G, acrR p.L195V, acrR p.F197I, acrR p.K201M | oqxB-like, oqxA |
| 217       | ST 3154 | sulI, sulII, fosA, dfrA12, dfrA14, tet(A) | *ompK37 p.I70M, ompK37 p.I128M, ompK37 p.N49S, ompK36 p.L59V, ompK36 p.G189T, ompK36 p.F198Y, ompK36 p.F207Y, ompK36 p.T222L, ompK36 p.D223G, ompK36 p.E232R, acrR p.P161R, acrR p.G164A, acrR p.F172S, acrR p.R173G, acrR p.L195V, acrR p.F197I, acrR p.K201M | acrR p.P161R, acrR p.G164A, acrR p.F172S, acrR p.R173G, acrR p.L195V, acrR p.F197I, acrR p.K201M |

Sample ID: 214 and 217
ST-Type: ST 6 and ST 3154
Acquired Resistance Determinants Against: Beta-Lactams, Sulfonamids, Fosfomycin, Trimethoprim, Macrolides, Tetracyclines, Fluoroquinolones, Chloramphenicol, Rifampicin, Aminoglycosides, Efflux Pumps
Efflux Pumps: Efflux Pumps
Amino Acid Exchanges Due to Point Mutations: *ompK37 p.I70M, ompK37 p.I128M, ompK37 p.N49S, ompK36 p.L59V, ompK36 p.G189T, ompK36 p.F198Y, ompK36 p.F207Y, ompK36 p.T222L, ompK36 p.D223G, ompK36 p.E232R, acrR p.P161R, acrR p.G164A, acrR p.F172S, acrR p.R173G, acrR p.L195V, acrR p.F197I, acrR p.K201M
Disinfectant Resistance Genes *: oqxB-like, oqxA

*a: AcrA, aceE, oqxB-like
Table A2. Cont.

| Sample ID | ST-Type | Acquired Resistance Determinants Against | Amino Acid Exchanges Due to Point Mutations | Efflux Pumps | Disinfectant Resistance Genes * |
|-----------|---------|------------------------------------------|---------------------------------------------|--------------|-------------------------------|
|           |         | Beta Laclatams | Sulfoxanmids | Fosfomycin | Trimethoprim | Macrolides | Tetracyclines | Fluoroquinolones | Chloramphenicol | Rifampicin | Aminoglycosides | Efflux Pumps |                                      |
| 220       | ST 5382 |          |            | fosA-like |            |            |            |                |                |            |              |                |              | ompK37 p.I70M, ompK36 p.L191S, ompK36 p.L228V, ompK36 p.F207W, acrR p.F197I, acrR p.K201M |
| 234       | ST 109  |          |            | fosA      |            |            |            |                |                |            |              |                |              | ompK37 p.I70M, ompK36 p.L191S, ompK36 p.L228V, ompK36 p.F207W, acrR p.F197I, acrR p.K201M |

*For sample 220 ST 5382, the resistance genes include fosA-like, oqxA-like, and catA1. For sample 234 ST 109, the resistance genes include oqxA, oqxB-like.
| Sample ID | ST-Type | Acquired Resistance Determinants Against |
|-----------|---------|-------------------------------------|
|           |         | Beta Lacatams Sulfoxanamids Fosfomycin Trimethoprim Macrolides Tetacyclines Fluoroquinolones Chloramphenicol Rifampicin Aminoglycosides Efflux Pumps | Disinfectant Resistance Genes |
| 240       | ST 5383 | fosA-like | tet(D) | oqxA, oqxB-like | ompK36 p.N49S, ompK36 p.L59V, ompK36 p.L191S, ompK36 p.F207W, ompK36 p.A217S, ompK36 p.N218H, ompK36 p.D224E, ompK36 p.L228V, ompK36 p.E232R, ompK37 p.I70M, ompK37 p.I128M, acrR p.I161R, acrR p.G164A, acrR p.F172S, acrR p.R173G, acrR p.L195V, acrR p.F197L, acrR p.K201M |
| 248       | ST 5384 | fosA-like | tet(A) | oqxB-like, oqxA-like, catA1 | ompK36 p.N49S, ompK36 p.L59V, ompK36 p.L191S, ompK36 p.F198Y, ompK36 p.F207W, ompK36 p.A217S, ompK36 p.N218H, ompK36 p.D224E, ompK36 p.L228V, ompK36 p.E232R, ompK37 p.I70M, ompK37 p.I128M, acrR p.I161R, acrR p.G164A, acrR p.F172S, acrR p.R173G, acrR p.L195V, acrR p.F197L, acrR p.K201M |
**Table A2. Cont.**

| Sample ID | ST-Type | Beta-Lactams | Sulphonamids | Fosfomycin | Trimethoprim | Macrolides | Tetracyclines | Fluoroquinolones | Chloramphenicol | Rifampicin | Aminoglycosides | Efflux Pumps | Amino Acid Exchanges Due to Point Mutations | Disinfectant Resistance Genes * |
|-----------|---------|--------------|--------------|------------|--------------|------------|--------------|-----------------|----------------|------------|----------------|-------------|-------------------------------------------------|-----------------------------|
| 252 ST 607 | blαTEM-1B, sul2, sul1 fosA-like dfrA7 | tet(A) oqxB-like, oqxA catA1 | aph(3”)-Ib, aph(6)-Id | ompK37 p.I70M, ompK37 p.I128M, ompK37 p.N230G, ompK36 p.N495S, ompK36 p.L29V, ompK36 p.L191S, ompK36 p.F207W, ompK36 p.A217S, ompK36 p.N218H, ompK36 p.D224E, ompK36 p.L228V, ompK36 p.E232R, ompK36 p.T254S, acrR p.P161R, acrR p.G164A, acrR p.F172S, acrR p.R173G, acrR p.L195V, acrR p.F197I, acrR p.K190M | oqxB-like, oprA, qacE |
| 267 ST 36 blαCTX-M-15, blαTEM-1B | sul2, sul1 fosA dfrA27 | tet(D) aac(6’)-Ib-cr, oqxA, oqxB catA2-like ARR-3 | aph(6)-Id, aph(3”)-Ib, aac(6’)-Ib-cr, aadA16, aac(3)-Ib-cr, aac(6)-Ib-cr, catA1 | ompK36 p.N495S, ompK36 p.L59V, ompK36 p.T184P, ompK37 p.I70M, ompK37 p.I128M, ompK37 p.N230G, acrR p.P161R, acrR p.G164A, acrR p.F172S, acrR p.R173G, acrR p.L195V, acrR p.F197I, acrR p.K190M | oprA, qacE, oqxB |
Table A2. Cont.

| Sample ID | ST-Type | Beta Lacatams | Sulphonamids | Fosfomycin | Trimethoprim | Macrolides | Tetracyclines | Fluoroquinolones | Chloramphenicol | Rifampicin | Aminoglycosides | Efflux Pumps | Amino Acid Exchanges Due to Point Mutations | Disinfectant Resistance Genes * |
|-----------|---------|--------------|--------------|-----------|-------------|-----------|--------------|----------------|---------------|------------|----------------|-------------|------------------------------------------|-------------------------------|
| 277       | ST 530  | blaTEM-35    | sul2         | fesA-like | dfrA14      | tet(D)    | oqxA, oqxB-like |                |               |            |                |             | acrR p.P161R, acrR p.G164A, acrR p.F172S, acrR p.L195V, acrR p.L1915, oqxA, oqxB p.N495, ompK36 p.L59V, ompK36 p.F207W, ompK36 p.A217S, ompK36 p.N218H, ompK36 p.D224E, ompK36 p.E232R, ompK36 p.T2545, ompK36 p.L70M, ompK37 p.I128M | acrA, oqxB-like |
| 279       | ST 5385 | fesA         |              |           |             |           | oqxA, oqxB     |                |               |            |                |             | acrR p.P161R, acrR p.G164A, acrR p.F172S, acrR p.L195V, acrR p.F1971, acrR p.K201M, ompK36 p.N495, ompK36 p.L59V, ompK36 p.F207W, ompK36 p.A217S, ompK36 p.N218H, ompK36 p.D224E, ompK36 p.E232R, ompK36 p.T2545, ompK36 p.L70M, ompK37 p.I128M | oqxA, oqxB |

* qacE = quaternary ammonium compounds resistance and oqxB and oqxA = efflux pumps mediating resistance against disinfectants.
Table A3. Phenotypic resistance the *P. aeruginosa* strains. Data are missing for strains 198, 218 and 312, due to loss during subcultivation. MIC = minimum inhibitory concentration. N.a. = value missing due to loss of strain or failed reaction.

| Sample ID | Piperacillin MIC | Interpretation | Piperacillin/Tazobactam MIC | Interpretation | Ceftrazidime MIC | Interpretation | Cefepime MIC | Interpretation | Imipenem MIC | Interpretation | Meropenem MIC | Interpretation | Gentamicin MIC | Interpretation |
|-----------|------------------|----------------|-----------------------------|----------------|----------------|---------------|--------------|---------------|--------------|---------------|--------------|---------------|--------------|--------------|
| 17        | ≤ 4              | S              | ≤ 4                         | S              | ≤ 1            | S             | ≤ 1          | S             | ≤ 0.25       | S             | ≤ 0.25       | S             | ≤ 1          | S             |
| 22        | ≤ 4              | S              | ≤ 4                         | S              | ≤ 1            | S             | ≤ 0.25       | S             | ≤ 0.25       | S             | ≤ 1          | S             |
| 32        | ≤ 4              | S              | 8                           | S              | 2              | S             | 2            | 1             | S             | ≤ 0.25       | S             | ≤ 1          | S             |
| 69        | ≤ 4              | S              | ≤ 4                         | S              | 4              | S             | 2            | 1             | S             | ≤ 0.25       | S             | ≤ 1          | S             |
| 81        | ≤ 4              | S              | 8                           | S              | 2              | S             | ≤ 1          | S             | 1             | S             | 1            | S             | ≤ 1          | S             |
| 82        | 16               | S              | 8                           | S              | 4              | S             | 2            | 2             | S             | ≤ 0.25       | S             | ≤ 1          | S             |
| 88        | ≥ 128            | R              | ≥ 128                        | R              | ≥ 64           | R             | 32           | R             | ≥ 16         | R             | 4            | I             | ≤ 1          | S             |
| 99        | 8                | S              | 8                           | S              | 4              | S             | 2            | 2             | S             | 1            | S             | ≤ 1          | S             |
| 106       | ≤ 4              | S              | 8                           | S              | 2              | S             | 2            | 2             | S             | 1            | S             | ≤ 1          | S             |
| 114       | ≤ 4              | S              | 8                           | S              | 2              | S             | ≤ 1          | 2             | S             | 1            | S             | ≤ 1          | S             |
| 137       | 16               | S              | 8                           | S              | 4              | S             | 2            | 2             | 2            | S             | ≤ 1          | S             |
| 144       | 16               | S              | 8                           | S              | 4              | S             | 2            | 2             | 1            | S             | ≤ 1          | S             |
| 147       | 8                | S              | ≤ 4                         | S              | 4              | S             | 8            | S             | 2             | 0.5          | S             | 4            | S             |
| 149       | 8                | S              | 8                           | S              | 4              | S             | 2            | S             | ≤ 0.25       | S             | ≤ 0.25       | S             | ≤ 1          | S             |
| 153       | ≤ 4              | S              | 8                           | S              | 2              | S             | ≤ 1          | S             | 1            | S             | ≤ 0.25       | S             | ≤ 1          | S             |
| 154       | 64               | R              | ≤ 4                         | S              | ≤ 1            | S             | ≤ 1          | S             | 2            | S             | 0.5          | S             | ≤ 1          | S             |
| 157       | 16               | S              | 8                           | S              | 4              | S             | 4            | 2             | S             | ≤ 0.25       | S             | 2            | S             |
| 160       | ≥ 128            | R              | 32                          | R              | 16             | R             | 32           | R             | 8            | 1            | 8            | 1            | 8            | R             |
| 162       | 64               | R              | 32                          | R              | 8              | S             | 8            | S             | 2            | S             | 1            | S             | 2            | S             |
| 180       | 16               | S              | 8                           | S              | 4              | S             | 2            | 2             | S             | 0.5          | S             | ≤ 1          | S             |
| 183       | 8                | S              | 8                           | S              | 4              | S             | 2            | 2             | S             | 0.5          | S             | ≤ 1          | S             |
| 186       | 16               | n.a.           | n.a.                        | S              | 4              | S             | 2            | 2             | S             | ≤ 0.25       | S             | ≤ 1          | S             |
| 190       | 16               | S              | 8                           | S              | 4              | S             | 2            | 2             | S             | 0.5          | S             | ≤ 1          | S             |
| 195       | 8                | S              | 8                           | S              | 4              | S             | ≤ 1          | 2             | S             | ≤ 0.25       | S             | ≤ 1          | S             |
| 196       | ≤ 4              | S              | ≤ 4                         | S              | 2              | S             | ≤ 1          | S             | 2             | S             | 0.5          | S             | ≤ 1          | S             |
| 198       | n.a.             | n.a.           | n.a.                        | n.a.           | n.a.          | n.a.          | n.a.         | n.a.          | n.a.         | n.a.         | n.a.         | n.a.         | n.a.         | n.a.         |

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**Table continued...**
| Sample ID | Piperacillin MIC | Interpretation | Piperacillin/Tazobactam MIC | Interpretation | Ceftrazidime MIC | Interpretation | Cefepime MIC | Interpretation | Imipenem MIC | Interpretation | Meropenem MIC | Interpretation | Gentamicin MIC | Interpretation |
|-----------|-----------------|----------------|-----------------------------|----------------|----------------|----------------|--------------|----------------|--------------|----------------|----------------|----------------|----------------|----------------|
| 204       | 8               | S              | 8                           | S              | ≤1             | S              | 2            | ≤0.25          | S             | ≤1             | S              |                 |                 |                 |
| 208       | 8               | S              | 8                           | S              | 2              | S              | 2            | ≤0.25          | S             | ≤1             | S              |                 |                 |                 |
| 218       | n.a.            | n.a.           | n.a.                        | n.a.           | n.a.           | n.a.           | n.a.         | n.a.           | n.a.         | n.a.           | n.a.           |                 |                 |                 |
| 229       | 8               | S              | 8                           | S              | 2              | S              | 1            | ≤0.25          | S             | ≤1             | S              |                 |                 |                 |
| 233       | ≥128            | R              | ≥128                        | R              | 32             | R              | 8            | 1              | 4             | 1              | ≤1             | S              |                 |                 |
| 236       | 16              | S              | 16                          | S              | 4              | S              | 2            | 2              | S             | 0.5            | S              | 2              | S              |                 |
| 238       | 8               | S              | 16                          | S              | 4              | S              | 2            | S              | ≤0.25         | S              | ≤1             | S              |                 |                 |
| 242       | 8               | S              | 8                           | S              | 4              | S              | 2            | 1              | S              | ≤0.25          | S              | ≤1             | S              |                 |
| 243       | 16              | S              | 8                           | S              | 4              | S              | 2            | 1              | S              | ≤0.25          | S              | ≤1             | S              |                 |
| 272       | 64              | R              | 64                          | R              | 8              | S              | 4            | 2              | S             | 1              | S              | ≤1             | S              |                 |
| 274       | 16              | S              | 8                           | S              | 4              | S              | 2            | S              | 0.5           | S              | ≤1             | S              |                 |                 |
| 278       | ≤4              | S              | ≤4                          | S              | 2              | S              | ≤1           | S              | 2              | ≤0.25          | S              | ≤1             | S              |                 |
| 282       | ≤4              | S              | ≤4                          | S              | ≤1            | S              | ≤1          | S              | 2              | S              | 1              | S              | ≤1             | S              |
| 285       | ≤4              | S              | ≤1                          | S              | ≤1            | S              | 2              | 1              | S              | ≤1             | S              |                 |                 |                 |
| 289       | ≤4              | S              | ≤1                          | S              | ≤1            | S              | 2              | 1              | S              | ≤1             | S              |                 |                 |                 |
| 290       | 8               | S              | 8                           | S              | ≤1            | S              | ≤1          | S              | 1              | S              | ≤1             | S              |                 |                 |
| 296       | ≥128            | R              | ≥128                        | R              | 64             | R              | 4            | 8              | 1              | S              | ≥16            | R              |                 |                 |
| 298       | ≥128            | R              | ≥64                         | R              | 8              | S              | 8            | 4              | 1              | 4              | ≤1             | S              |                 |                 |
| 301       | 16              | S              | 8                           | S              | 4              | S              | 2            | S              | 0.5           | S              | ≤1             | S              |                 |                 |
| 302       | 8               | S              | 8                           | S              | 4              | S              | ≤1           | S              | 2              | S              | 0.5            | S              | ≤1             | S              |
| 309       | 16              | S              | 8                           | S              | 4              | S              | 2            | S              | 1              | S              | ≤1             | S              |                 |                 |
| 310       | 32              | R              | 16                          | S              | 4              | S              | 4            | S              | 2              | S              | 1              | S              | ≤1             | S              |
| 312       | n.a.            | n.a.           | n.a.                        | n.a.           | n.a.           | n.a.           | n.a.         | n.a.           | n.a.         | n.a.           | n.a.           |                 |                 |                 |
Table A4. Phenotypic resistance of *P. aeruginosa* strains. Data are missing for strains 198, 218 and 312 due to loss during subcultivation. MIC = minimum inhibitory concentration. N.a. = value missing due to loss of strain or failed reaction.

| Sample ID | Ciprofloxacin | Moxifloxacin | Aztreonam | Amikacin | Tobramycin | Fosfomycin | Colistin |
|-----------|---------------|--------------|-----------|----------|------------|------------|----------|
|           | MIC Interpretation | MIC Interpretation | MIC Interpretation | MIC Interpretation | MIC Interpretation | MIC Interpretation | MIC Interpretation |
| 17        | ≤0.25 S         | 1 R          | 4 I       | ≤2 S     | ≤1 S       | 128 R      | ≤0.5 S   |
| 22        | ≤0.25 S         | 1 R          | 2 I       | ≤2 S     | ≤1 S       | 128 R      | 1 S      |
| 32        | ≤0.25 S         | 2 R          | 4 I       | ≤2 S     | ≤1 S       | 128 R      | ≤0.5 S   |
| 69        | ≤0.25 S         | 0.5 R        | 4 I       | ≤2 S     | ≤1 S       | 128 R      | ≤0.5 S   |
| 81        | ≤0.25 S         | 0.5 R        | 4 I       | ≤2 S     | ≤1 S       | ≥256 R     | ≤0.5 S   |
| 82        | ≤0.25 S         | 1 R          | 16 I      | ≤2 S     | ≤1 S       | 128 R      | ≤0.5 S   |
| 88        | 2 R             | ≥8 R         | 32 R      | ≤2 S     | ≤1 S       | 128 R      | ≤0.5 S   |
| 99        | ≤0.25 S         | 2 R          | 16 I      | ≤2 S     | ≤1 S       | 128 R      | ≤0.5 S   |
| 106       | 2 R             | 1 R          | 8 I       | ≤2 S     | ≤1 S       | ≥256 R     | ≤0.5 S   |
| 114       | ≤0.25 S         | 0.5 R        | 4 I       | ≤2 S     | ≤1 S       | 128 R      | ≤0.5 S   |
| 137       | ≤0.25 S         | 1 R          | 16 I      | ≤2 S     | ≤1 S       | ≥256 R     | ≤0.5 S   |
| 144       | ≤0.25 S         | 2 R          | 4 I       | ≤2 S     | ≤1 S       | ≥256 R     | ≤0.5 S   |
| 147       | ≤0.25 S         | 2 R          | 4 I       | 8 S      | ≤1 S       | ≥256 R     | ≤0.5 S   |
| 149       | ≤0.25 S         | 1 R          | 16 I      | ≤2 S     | ≤1 S       | ≥256 R     | ≤0.5 S   |
| 153       | ≤0.25 S         | 2 R          | 4 I       | ≤2 S     | ≤1 S       | ≤16 R      | ≤0.5 S   |
| 154       | ≤0.25 S         | 0.5 R        | 4 I       | ≤2 S     | ≤1 S       | ≥256 R     | ≤0.5 S   |
| 157       | ≤0.25 S         | 1 R          | 16 I      | ≤2 S     | ≤1 S       | ≥256 R     | ≤0.5 S   |
| 160       | 1 R             | ≥8 R         | ≥64 R     | 16 I     | ≤1 S       | 64 R       | ≤0.5 S   |
| 162       | 0.5 S           | 2 R          | 32 R      | 4 S      | ≤1 S       | 128 R      | ≤0.5 S   |
| 180       | ≤0.25 S         | 1 R          | 16 I      | ≤2 S     | ≤1 S       | ≥256 R     | ≤0.5 S   |
| 183       | ≤0.25 S         | 0.5 R        | 4 I       | ≤2 S     | ≤1 S       | ≥256 R     | ≤0.5 S   |
| 186       | ≤0.25 S         | 1 R          | 16 I      | ≤2 S     | ≤1 S       | 32 R       | ≤0.5 S   |
| 190       | ≤0.25 S         | 1 R          | 16 I      | 4 S      | ≤1 S       | 32 R       | ≤0.5 S   |
| 195       | ≤0.25 S         | 0.5 R        | 4 I       | ≤2 S     | ≤1 S       | 64 R       | ≤0.5 S   |
| 196       | ≤0.25 S         | 0.5 R        | 4 I       | ≤2 S     | ≤1 S       | 64 R       | ≤0.5 S   |
| 198       | n.a.            | n.a.         | n.a.      | n.a.     | n.a.       | n.a.       | n.a.     |
| Sample ID | Ciprofloxacin | Moxifloxacin | Aztreonam | Amikacin | Tobramycin | Fosfomycin | Colistin |
|-----------|---------------|--------------|-----------|----------|------------|------------|---------|
|           | MIC Interpretation | MIC Interpretation | MIC Interpretation | MIC Interpretation | MIC Interpretation | MIC Interpretation | MIC Interpretation |
| 204       | ≤0.25 S | 1 R | 2 I | ≤2 S | ≤1 S | 32 R | 2 S |
| 208       | ≤0.25 S | 1 R | 8 I | ≤2 S | ≤1 S | 128 R | ≤0.5 S |
| 218       | n.a. n.a. n.a. n.a. n.a. n.a. n.a. n.a. n.a. n.a. n.a. n.a. n.a. n.a. n.a. n.a. |
| 229       | ≤0.25 S | 1 R | 4 I | ≤2 S | ≤1 S | 128 R | ≤0.5 S |
| 233       | ≤0.25 S | 2 R | 16 I | ≤2 S | ≤1 S | 64 R | ≤0.5 S |
| 236       | ≤0.25 S | 1 R | 16 I | 8 S | ≤1 S | 64 R | ≤0.5 S |
| 238       | ≤0.25 S | 2 R | 8 I | ≤2 S | ≤1 S | 128 R | ≤0.5 S |
| 242       | ≤0.25 S | 1 R | 8 I | ≤2 S | ≤1 S | 128 R | ≤0.5 S |
| 243       | ≤0.25 S | 2 R | 16 I | ≤2 S | ≤1 S | 64 R | ≤0.5 S |
| 272       | ≤0.25 S | 2 R | 32 R | ≤2 S | ≤1 S | 128 R | ≤0.5 S |
| 274       | ≤0.25 S | 2 R | 16 I | ≤2 S | ≤1 S | 256 R | ≤0.5 S |
| 278       | ≤0.25 S | 0.5 R | 4 I | ≤2 S | ≤1 S | 128 R | ≤0.5 S |
| 282       | ≤0.25 S | 1 R | 2 I | ≤2 S | ≤1 S | 128 R | ≤0.5 S |
| 285       | ≤0.25 S | 1 R | 2 I | ≤2 S | ≤1 S | 128 R | ≤0.5 S |
| 289       | ≤0.25 S | 0.5 R | 4 I | ≤2 S | ≤1 S | 128 R | ≤0.5 S |
| 290       | ≤0.25 S | 0.5 R | 4 I | ≤2 S | ≤1 S | 128 R | ≤0.5 S |
| 296       | ≥4 R | ≥8 R | 32 R | ≤2 S | ≥16 S | 64 R | ≤0.5 S |
| 298       | ≤0.25 S | 2 R | 16 I | ≤2 S | ≤1 S | 16 R | ≤0.5 S |
| 301       | ≤0.25 S | 2 R | 16 I | ≤2 S | ≤1 S | 16 R | ≤0.5 S |
| 302       | ≤0.25 S | 1 R | 4 I | ≤2 S | ≤1 S | 128 R | ≤0.5 S |
| 309       | ≤0.25 S | 1 R | 4 I | ≤2 S | ≤1 S | 16 R | ≤0.5 S |
| 310       | ≤0.25 S | 2 R | 16 I | ≤2 S | ≤1 S | 128 R | ≤0.5 S |
| 312       | n.a. n.a. n.a. n.a. n.a. n.a. n.a. n.a. n.a. n.a. n.a. n.a. n.a. n.a. n.a. n.a. |
Table A5. Phenotypic resistance of the *Klebsiella* strains. MIC = minimum inhibitory concentration. ESBL = signal in phenotypic testing for extended-spectrum beta-lactamases.

| Sample ID | ESBL | Ampicillin | Ampicillin/Sulbactam | Piperacillin/Tazobactam | Cefuroxime | Cefuroxime Axetil | Cefpodoxime | Cefotaxime | Ceftrazidime |
|-----------|------|------------|----------------------|-------------------------|------------|-------------------|-------------|------------|-------------|
|           |      | MIC        |                      | Interpreta             | MIC        | Interpreta        | MIC         | Interpreta | MIC         |
| 44        | negative | ≥32        | R                    |                         | ≤4         | S                 | 4           | I          | ≤0.25       |
| 60        | negative | ≥32        | R                    |                         | ≤4         | S                 | ≤1          | I          | ≤1          |
| 73        | positive | ≥32        | R                    |                         | ≥128       | R                 | ≥64         | R          | ≥8          |
| 100       | positive | ≥32        | R                    |                         | ≥128       | R                 | ≥64         | R          | ≥8          |
| 102       | negative | ≥32        | R                    | ≤2                      | 8          | S                 | 8           | I          | ≤0.25       |
| 124       | negative | ≥32        | R                    | ≤2                      | 8          | S                 | 2           | I          | ≤0.25       |
| 146       | negative | ≥32        | R                    | ≤2                      | 8          | S                 | 2           | I          | ≤0.25       |
| 177       | positive | ≥32        | R                    | ≥32                     | ≥128       | R                 | ≥64         | R          | ≥8          |
| 181       | negative | ≥32        | R                    | ≤2                      | 8          | S                 | 2           | I          | ≤0.25       |
| 184       | negative | ≥32        | R                    | ≤2                      | 8          | S                 | 2           | I          | ≤0.25       |
| 199       | positive | ≥32        | R                    | ≥32                     | 8          | R                 | ≥64         | R          | ≥8          |
| 214       | negative | ≥32        | R                    | ≤2                      | 8          | S                 | 2           | I          | ≤0.25       |
| 217       | negative | ≥32        | R                    | ≥32                     | ≥128       | R                 | ≥64         | R          | ≥8          |
| 220       | negative | ≥32        | R                    | ≤2                      | 8          | S                 | 4           | I          | ≤0.25       |
| 234       | negative | ≥32        | R                    | ≤2                      | 8          | S                 | 2           | I          | ≤0.25       |
| 240       | negative | ≥32        | R                    | ≤2                      | 8          | S                 | 2           | I          | ≤0.25       |
| 248       | negative | ≥32        | R                    | ≤2                      | 8          | S                 | 2           | I          | ≤0.25       |
| 252       | negative | ≥32        | R                    | 16                      | 8          | S                 | 2           | I          | ≤0.25       |
| 267       | positive | ≥32        | R                    | ≥32                     | 8          | R                 | ≥64         | R          | ≥8          |
| 277       | negative | ≥32        | R                    | ≥32                     | 8          | R                 | 2           | I          | ≤0.25       |
| 279       | negative | ≥32        | R                    | ≤2                      | 8          | S                 | 2           | I          | ≤0.25       |
Table A6. Phenotypic resistance of the *Klebsiella* strains. MIC = minimum inhibitory concentration. ESBL = signal in phenotypic testing for extended-spectrum beta-lactamases.

| Sample ID | ESBL | Eradapenem | Imipenem | Meropenem | Gentamicin | Ciprofloxacin | Moxifloxacin | Tigecycline | Trimethoprim/Sulfamethoxazole |
|-----------|------|------------|----------|-----------|------------|---------------|---------------|-------------|--------------------------------|
|           | MIC  | Interpretation | MIC  | Interpretation | MIC  | Interpretation | MIC  | Interpretation | MIC  | Interpretation | MIC  | Interpretation |
| 44        | negative | ≤0.5 | S | ≤0.25 | S | ≤0.25 | S | ≤0.25 | S | ≤0.25 | S | ≤0.25 | S | ≤0.25 | S | ≤0.5 | S | ≤20 | S |
| 60        | negative | ≤0.5 | S | ≤0.25 | S | ≤0.25 | S | ≥16 | R | 1 | R | 2 | R | ≤0.5 | S | ≥320 | R |
| 73        | positive | ≤0.5 | S | ≤0.25 | S | ≤0.25 | S | ≥16 | R | 1 | R | 2 | R | ≤0.5 | S | ≥320 | R |
| 100       | positive | ≤0.5 | S | ≤0.25 | S | ≤0.25 | S | ≥4 | R | ≥8 | R | ≤0.5 | S | ≥320 | R |
| 102       | negative | ≤0.5 | S | ≤0.25 | S | ≤0.25 | S | ≤0.25 | S | 0.5 | R | 4 | R | ≤20 | S |
| 124       | negative | ≤0.5 | S | ≤0.25 | S | ≤0.25 | S | ≤0.25 | S | ≥16 | R | ≥4 | R | ≤20 | S |
| 146       | negative | ≤0.5 | S | ≤0.25 | S | ≤0.25 | S | ≤0.25 | S | ≤0.25 | S | 1 | S | ≤20 | S |
| 177       | negative | ≤0.5 | S | ≤0.25 | S | ≤0.25 | S | ≤0.25 | S | ≤0.25 | S | 2 | 1 | ≥320 | R |
| 181       | negative | ≤0.5 | S | ≤0.25 | S | ≤0.25 | S | ≤0.25 | S | ≤0.25 | S | ≤0.5 | S | ≤20 | S |
| 184       | negative | ≤0.5 | S | ≤0.25 | S | ≤0.25 | S | ≤0.25 | S | ≤0.25 | S | ≤0.5 | S | ≤20 | S |
| 199       | positive | ≤0.5 | S | ≤0.25 | S | ≤0.25 | S | ≥16 | R | ≤0.25 | S | ≤0.25 | S | ≤0.5 | S | ≥320 | R |
| 214       | negative | ≤0.5 | S | ≤0.25 | S | ≤0.25 | S | ≤0.25 | S | ≤0.25 | S | ≤0.5 | S | ≥320 | R |
| 217       | negative | ≤0.5 | S | ≤0.25 | S | ≤0.25 | S | ≥16 | R | ≤0.25 | S | ≤0.25 | S | 2 | 1 | ≥320 | R |
| 220       | negative | ≤0.5 | S | ≤0.25 | S | ≤0.25 | S | ≤0.25 | S | 0.5 | R | 1 | S | ≤20 | S |
| 234       | negative | ≤0.5 | S | ≤0.25 | S | ≤0.25 | S | ≤0.25 | S | 0.5 | R | 1 | S | ≤20 | S |
| 240       | negative | ≤0.5 | S | ≤0.25 | S | ≤0.25 | S | ≤0.25 | S | ≤0.25 | S | ≤0.5 | S | ≤20 | S |
| 248       | negative | ≤0.5 | S | ≤0.25 | S | ≤0.25 | S | ≤0.25 | S | ≤0.25 | S | 2 | 1 | ≤20 | S |
| 252       | negative | ≤0.5 | S | ≤0.25 | S | ≤0.25 | S | ≤0.25 | S | ≤0.25 | S | 1 | 1 | ≥320 | R |
| 267       | positive | ≤0.5 | S | ≤0.25 | S | ≤0.25 | S | ≥16 | R | ≤0.25 | S | ≤0.25 | S | ≤0.5 | S | ≥320 | R |
| 277       | negative | ≤0.5 | S | ≤0.25 | S | ≤0.25 | S | ≤0.25 | S | 0.5 | R | 4 | R | ≤20 | S |
| 279       | negative | ≤0.5 | S | ≤0.25 | S | ≤0.25 | S | ≤0.25 | S | ≤0.25 | S | ≤0.5 | S | ≤20 | S |
Table A7. Phenotypic resistance of *Escherichia coli* strains. MIC = minimum inhibitory concentration. ESBL = signal in phenotypic testing for extended-spectrum beta-lactamases.

| Sample ID | ESBL | Ampicillin | Ampicillin/Sulbactam | Piperacillin/Tazobactam | Cefuroxime | Cefuroxime Axetil | Cefpodoxime | Cefotaxime | Ceftrazidime | MIC Interpretation | MIC Interpretation | MIC Interpretation | MIC Interpretation | MIC Interpretation | MIC Interpretation | MIC Interpretation |
|-----------|------|------------|----------------------|-------------------------|------------|-------------------|-------------|-------------|-------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|
| 41        | positive | ≥32 | R | ≥32 | R | 64 | R | ≥64 | R | ≥64 | R | ≥8 | R | ≥64 | R | 16 | R |
| 49        | negative | ≥32 | R | 16 | R | ≤4 | S | 4 | I | 4 | S | ≤0.25 | S | ≤1 | S | ≤1 | S |
| 68        | negative | ≥32 | R | 16 | R | ≤4 | S | ≤1 | I | ≤1 | S | ≤0.25 | S | ≤1 | S | ≤1 | S |
| 117       | negative | ≥32 | R | ≥32 | R | 64 | R | 4 | I | 4 | S | ≤0.25 | S | ≤1 | S | ≤1 | S |
| 152       | negative | ≥32 | R | ≥32 | R | ≥128 | R | 4 | I | 4 | S | 0.5 | S | ≤1 | S | ≤1 | S |
| 176       | negative | ≥32 | R | ≥32 | R | ≤4 | I | 2 | I | 2 | S | ≤0.25 | S | ≤1 | S | ≤1 | S |
| 221       | negative | ≥32 | R | ≥32 | R | ≤4 | I | 2 | I | 2 | S | ≤0.25 | S | ≤1 | S | ≤1 | S |
| 222       | negative | ≥32 | R | ≥32 | R | ≤4 | I | 4 | I | 4 | S | ≤0.25 | S | ≤1 | S | ≤1 | S |
| 225       | positive | ≥32 | R | ≥32 | R | ≤4 | R | ≥64 | R | ≥64 | R | ≥8 | R | ≥64 | R | 16 | R |
| 245       | positive | ≥32 | R | ≥32 | R | 16 | I | 16 | R | 16 | R | 1 | S | 2 | I | ≤1 | S |
| 270       | positive | ≥32 | R | 16 | R | ≤4 | R | ≥64 | R | ≥64 | R | ≥8 | R | ≥64 | R | ≥64 | R |
| 299       | negative | ≥32 | R | ≤2 | I | ≤4 | S | 4 | I | 4 | S | ≤0.25 | S | ≤1 | S | ≤1 | S |
Table A8. Phenotypic resistance of *Escherichia coli* strains. MIC = minimum inhibitory concentration. ESBL = signal in phenotypic testing for extended-spectrum beta-lactamases.

| Sample ID | ESBL | Ertapenem | Imipenem | Meropenem | Gentamicin | Ciprofloxacin | Moxifloxacin | Tigecycline | Trimethoprim/ Sulfamethoxazole |
|-----------|------|-----------|----------|-----------|------------|---------------|--------------|-------------|---------------------------------|
|           |      | MIC       | Interpretation | MIC   | Interpretation | MIC   | Interpretation | MIC   | Interpretation | MIC   | Interpretation | MIC   | Interpretation | |
| 41        | positive | ≤0.5 | S | ≤0.25 | S | ≤0.25 | S | ≥16 | R | ≥4 | R | ≥8 | R | <0.5 | S | ≥320 | R |
| 49        | negative | ≤0.5 | S | ≤0.25 | S | ≤0.25 | S | ≤1 | S | ≤0.25 | S | ≤0.25 | S | <0.5 | S | ≥320 | R |
| 68        | negative | ≤0.5 | S | ≤0.25 | S | ≤0.25 | S | ≤1 | S | ≥4 | R | ≥8 | R | <0.5 | S | ≥320 | R |
| 117       | negative | ≤0.5 | S | ≤0.25 | S | ≤0.25 | S | ≤1 | S | ≤0.25 | S | ≤0.25 | S | <0.5 | S | ≥320 | R |
| 152       | negative | ≤0.5 | S | ≤0.25 | S | ≤0.25 | S | 2 | S | 1 | R | 2 | R | <0.5 | S | ≥320 | R |
| 176       | negative | ≤0.5 | S | ≤0.25 | S | ≤0.25 | S | ≤1 | S | ≤0.25 | S | ≤0.25 | S | <0.5 | S | ≥320 | R |
| 221       | negative | ≤0.5 | S | ≤0.25 | S | ≤0.25 | S | ≤1 | S | ≤0.25 | S | ≤0.25 | S | <0.5 | S | ≥320 | R |
| 222       | negative | ≤0.5 | S | ≤0.25 | S | ≤0.25 | S | ≤1 | S | ≤0.25 | S | ≤0.25 | S | <0.5 | S | ≥320 | R |
| 225       | positive | ≤0.5 | S | ≤0.25 | S | ≤0.25 | S | ≤1 | S | 0.5 | I | 1 | R | <0.5 | S | ≥320 | R |
| 245       | positive | ≤0.5 | S | 0.5 | S | ≤0.25 | S | ≥16 | R | ≥4 | R | ≥8 | R | <0.5 | S | ≥320 | R |
| 270       | positive | ≤0.5 | S | ≤0.25 | S | ≤0.25 | S | ≤1 | S | ≥4 | R | ≥8 | R | <0.5 | S | ≤20 | S |
| 299       | negative | ≤0.5 | S | ≤0.25 | S | ≤0.25 | S | ≤1 | S | 0.5 | I | 2 | R | <0.5 | S | ≥320 | R |
Table A9. Analysis of virulence determinants, ordered by strain and MLST type, of the assessed *P. aeruginosa* isolates. ST = Sequence type.

| Sample ID | ST-Type | Adherence | Anti-Phagocytosis | Biosurfactant | Iron Uptake | Pigment | Protease | Toxin | Regulation | Secretion |
|-----------|---------|-----------|-------------------|---------------|-------------|---------|----------|-------|------------|-----------|
| 017       | ST 381  | waaA, waaC, waaF, waaG, waaP, wzy, wzz, chpA, chpB, chpC, chpD, chpE, fimV, pilB, pilD, pilE, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX, pilY1, pilY2, pilC, xcpA/pilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algP/algR3 algI, algJ, algK, algL, algQ, algR, algU, algW, algX, algZ, mucA, mucB, mucC | rhlA, rhlB | fptA, fptA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, pchR, pvdA, pvdD, pvdE | phzM, phzS | aprA, lasA | toxA, plcH | lasI, rhlI |
| 022       | ST 2483 | waaA, waaC, waaF, waaG, waaP, chpA, chpC, chpD, chpE, fimT, fimU, fimV, pilB, pilD, pilE, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX, pilY1, pilY2, pilC, xcpA/pilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algI, algJ, algK, algL, algQ, algR, algU, algW, algX, algZ, mucA, mucB, mucC | rhlA, rhlB | fptA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, pchR, pvdA | phzM, phzS | aprA, lasA | toxA, plcH | lasI, rhlI | xcpP, xcpQ, xcpR, xcpS, xcpT, xcpU, xcpV, xcpW, xcpX, xcpY, xcpZ |
Table A9. Cont.

| Sample ID | ST-Type | Adherence | Anti-Phagocytosis | Biosurfactant | Iron Uptake | Pigment | Protease | Toxin | Regulation | Secretion System |
|-----------|---------|-----------|-------------------|---------------|-------------|----------|----------|-------|------------|------------------|
| 032       | ST 3587 | waaA, waaC, waaF, waaG, waaP, chpA, chpB, chpC, chpD, chpE, fimT, fimU, fimV, pilB, pilD, pilE, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX pilY1, pilY2, pilC like, xcpA/pilD | alg44, alg8, algA, algB, algC, algD, algE, algG, algJ, algK, algL, algQ, algR, algU, algW, algX, algZ, mucA, mucB, mucC | rhlA, rhlB | fptA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, pchJ, pvdA | phzM, phzS | aprA, lasA | toxA, plcH | lasI, rhlI | xcpP, xcpQ, xcpR, xcpS, xcpT, xcpU, xcpV, xcpW, xcpX, xcpY, xcpZ |
| 069       | ST 360  | waaA, waaC, waaF, waaG, waaP, wzy, wzz, chpA, chpB, chpC, chpD, chpE, fimT, fimU, fimV, pilB, pilD, pilE, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX pilY1, pilY2, pilC like, xcpA/pilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algJ, algK, algL, algQ, algR, algU, algW, algX, algZ, mucA, mucB, mucC | rhlA, rhlB | fptA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, pchJ, pvdA | phzM, phzS | aprA, lasA | toxA, plcH | lasI, rhlI | xcpP, xcpQ, xcpR, xcpS, xcpT, xcpU, xcpV, xcpW, xcpX, xcpY, xcpZ |
| Sample ID | ST-Type | Pathogenicity Factor Groups |
|-----------|---------|----------------------------|
|           |         | Adherence Anti-Phagocytosis | Biosurfactant | Iron Uptake | Pigment | Protease | Toxin | Regulation | Secretion System |
| 081       | ST 244  | waaA, waaC, waaF, waaG, waaP, wzy, wzz, chpA, chpB, chpC, chpD, chpE, fimT, fimU, fimV, pilA like, pilB, pilD, pilE, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX pilY1, pilY2, pilC, xcpA/pilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algI, algJ, algK, algL, algQ, algR, algU, algW, algX, algZ, mucA, mucB, mucC | rhlA, rhlB | fptA, fptV, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, pchR, pvdA, pvdE | phzM, phzS | aprA, lasA | toxA, plcH | lasI, rhlI |
| 082       | ST 514  | waaA, waaC, waaF, waaG, waaP, chpA, chpB, chpC, chpD, chpE, fimV, pilB, pilD, pilE, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX, pilY1, pilY2, xcpA/pilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algI, algJ, algK, algL, algQ, algR, algU, algW, algX, algZ, mucA, mucB, mucC | rhlA, rhlB | fptA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, pchR, pvdA | phzM, phzS | aprA, lasA | toxA, plcH | lasI, rhlI |
| 088       | ST 1682 | waaA, waaC, waaF, waaG, waaP, wzy, wzz, chpA, chpB, chpC, chpD, chpE, fimT, fimU, fimV, pilB, pilD, pilE, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX, pilY1, pilY2, xcpA/pilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algI, algJ, algK, algL, algQ, algR, algU, algW, algX, algZ, mucA, mucB, mucC | rhlA, rhlB | fptA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, pchR, pvdA | phzM, phzS | aprA, lasA | toxA, plcH | lasI, rhlI |
| Sample ID | ST-Type | Adherence | Anti-Phagocytosis | Biosurfactant | Iron Uptake | Pigment | Protease | Toxin | Regulation | Secretion System |
|-----------|---------|-----------|------------------|--------------|-------------|---------|---------|-------|------------|------------------|
| 099       | ST 244  | waaA, waaC, waaF, waaG, waaP, wzy, wzz, chpA, chpB, chpC, chpD, chpE, fimT, fimU, fimV, pilA, pilB, pilD, pilE, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX pilY1, pilY2, pilC, xcpA/pilD | algA, algB, algC, algD, algE, algF, algG, algH, algI, algK, algL, algM, algN, algO, algP, algR3, algQ, algR, algU, algW, algX, algZ, mucA, mucB, mucC | rhlA, rhlB | fptA, fptB, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, pchR, phzM, phzS, aprA, lasA, plcH, lasI, rhlI | xcpP, xcpQ, xcpR, xcpS, xcpT, xcpU, xcpV, xcpW, xcpX, xcpY, xcpZ |
| 106       | ST 1521 | waaA, waaC, waaF, waaG, waaP, wzy, wzz, chpA, chpB, chpC, chpD, chpE, fimT, fimU, fimV, pilA, pilB, pilD, pilE, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX pilY1, pilY2, pilC, xcpA/pilD | algA, algB, algC, algD, algE, algF, algG, algH, algI, algK, algL, algM, algN, algO, algP, algR3, algQ, algR, algU, algW, algX, algZ, mucA, mucB, mucC | rhlA, rhlB | fptA, fptB, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, pchR, phzM, phzS, aprA, lasA, plcH, lasI, rhlI | xcpP, xcpQ, xcpR, xcpS, xcpT, xcpU, xcpV, xcpW, xcpX, xcpY, xcpZ |
Table A9. Cont.

| Sample ID | ST-Type | Adherence | Anti-Phagocytosis | Biosurfactant | Iron Uptake | Pigment | Protease | Toxin | Regulation | Secretion System |
|-----------|---------|-----------|-------------------|---------------|-------------|---------|----------|-------|------------|------------------|
| 114       | ST 244  | waaA, waaC, waaF, waaG, waaP, wzy, wzz, chpA, chpB, chpC, chpD, chpE, fimT, fimU, fimV, pilA like, pilB, pilD, pilE, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX pilY1, pilY2, pilC, xcpA/pilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algI, algJ, algK, algL, algQ, algR, algU, algW, algX, algZ, mucA, mucB, mucC | rhlA, rhlB | fptA, fptA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, pchR, prdA, prdE | phzM, phzS | aprA, lasA | toxA, plcH | lasI, rhlI |
| 137       | ST 3014 | waaA, waaC, waaF, waaG, waaP, wzy, wzz, chpA, chpB, chpC, chpD, chpE, fimT, fimU, fimV, pilA like, pilB, pilD, pilE, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX pilY1, pilY2, pilC, xcpA/pilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algI, algJ, algK, algL, algP/alr3, algQ, algR, algU, algW, algX, algZ, mucA, mucB, mucC | rhlA, rhlB | fptA, fptA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, pchR, prdA, prdE | phzM, phzS | aprA, lasA | toxA, plcH | lasI, rhlI |
Table A9. Cont.

| Sample ID | ST-Type | Adherence | Anti-Phagocytosis | Biosurfactant | Iron Uptake | Pigment | Protease | Toxin | Regulation | Secretion System |
|-----------|---------|-----------|-------------------|---------------|-------------|---------|----------|-------|------------|------------------|
| 144       | ST 245  | waaA, waaC, waaF, waaG, waaP, wzy, wzz, chpA, chpB, chpC, chpD, chpE, fimT, fimU, fimV, pilA, pilB, pilD, pilE, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX pilY1, pilY2, pilC like, xcpA/pilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algI, algJ, algK, algL, algQ, algR, algU, algW, algX, algZ, mucA, mucB, mucC | rhlA, rhlB | fptA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchl, pchlR, pvdA | phzM, phzS | aprA, lasA | toxA, plcH | lasI, rhlI | xcpP, xcpQ, xcpR, xcpS, xcpT, xcpU, xcpV, xcpW, xcpX, xcpY, xcpZ |
| 147       | ST 245  | waaA, waaC, waaF, waaG, waaP, wzy, wzz, chpA, chpB, chpC, chpD, chpE, fimT, fimU, fimV, pilA, pilB, pilD, pilE, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX pilY1, pilY2, pilC like, xcpA/pilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algI, algJ, algK, algL, algQ, algR, algU, algW, algX, algZ, mucA, mucB, mucC | rhlA, rhlB | fptA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchl, pchlR, pvdA | phzM, phzS | aprA, lasA | toxA, plcH | lasI, rhlI | xcpP, xcpQ, xcpR, xcpS, xcpT, xcpU, xcpV, xcpW, xcpX, xcpY, xcpZ |
| Sample ID | ST-Type | Adherence | Anti-Phagocytosis | Biosurfactant | Iron Uptake | Pigment | Protease | Toxin | Regulation | Secretion System |
|-----------|---------|-----------|------------------|--------------|-------------|---------|----------|-------|------------|------------------|
| 149       | ST 381  | waaA, waaC, waaF, waaG, waaP, wzy, wzz, chpA, chpB, chpC, chpD, chpE, fimV, pilA, pilB, pilD, pilE, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX pilY1, pilY2, pilC like, xcpA/pilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algI, algJ, algK, algL, algP/algR3, algQ, algR, algU, algW, algX, algZ, mucA, mucB, mucC | rhlA, rhlB | fptA, fprA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, pchR, pvdA, pvdE | phzM, phzS, aprA, lasA, toxA, plcH, lasI, rhlI | xcpP, xcpQ, xcpR, xcpS, xcpT, xcpU, xcpV, xcpW, xcpX, xcpY, xcpZ |
| 153       | ST 704  | waaA, waaC, waaF, waaG, waaP, wzy, wzz, chpA, chpB, chpC, chpD, chpE, fimT, fimU, fimV, pilA, pilB, pilD, pilE, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX pilY1, pilY2, pilC like, xcpA/pilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algI, algJ, algK, algL, algQ, algR, algU, algW, algX, algZ, mucA, mucB, mucC | rhlA, rhlB | fptA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, pchR, pvdA | phzM, phzS, aprA, lasA, plcH | last | xcpP, xcpQ, xcpR, xcpS, xcpT, xcpU, xcpV, xcpW, xcpX, xcpY, xcpZ |
| 154       | ST 244  | waaA, waaC, waaF, waaG, waaP, wzy, wzz, chpA, chpB, chpC, chpD, chpE, fimT, fimU, fimV, pilA like, pilB, pilD, pilE, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX pilY1, pilY2, pilC, xcpA/pilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algI, algJ, algK, algL, algP/algR3, algQ, algR, algU, algW, algX, algZ, mucA, mucB, mucC | rhlA, rhlB | fptA, fprA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, pchR, pvdA | phzM, phzS, aprA, lasA, toxA, plcH | last, rhlI | xcpP, xcpQ, xcpR, xcpS, xcpT, xcpU, xcpV, xcpW like, xcpX, xcpY, xcpZ |
| Sample ID | ST-Type | Adherence | Anti-Phagocytosis | Biosurfactant | Iron Uptake | Pigment | Protease | Toxin | Regulation | Secretion System |
|-----------|---------|-----------|-------------------|---------------|-------------|---------|---------|------|------------|------------------|
| 157       | ST 2616 | waaA, waaC, waaE, waaG, waaP, chpA, chpB, chpC, chpD, chpE, fimV, pilA, pilB, pilD, pilE, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilC like, xcpA/pilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algI, algJ, algK, algL, algM, algQ, algR, algU, algW, algX, algZ, mucA, mucB, mucC | rhlA, rhlB | fptA, fprA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, pchR, prdA, prdE | phzM, phzS | aprA, lasA | toxA, plcH | lasI, rhlI | xcpP, xcpQ, xcpR, xcpS, xcpT, xcpU, xcpV, xcpW, xcpX, xcpY, xcpZ |
| 160       | ST 170  | waaA, waaC, waaE, waaG, waaP, chpA, chpB, chpC, chpD, chpE, fimV, pilA, pilB, pilD, pilE, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilC like, xcpA/pilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algI, algJ, algK, algL, algM, algP/algR3, algQ, algR, algU, algW, algX, algZ, mucA, mucB, mucC | rhlA, rhlB | fptA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, pchR, pvdA, pvdE | phzM, phzS | aprA, lasA | toxA, plcH | lasI, rhlI | xcpP, xcpQ, xcpR, xcpS, xcpT, xcpU, xcpV, xcpW, xcpX, xcpY, xcpZ |
| 162       | ST 274  | waaA, waaC, waaE, waaG, waaP, chpA, chpB, chpC, chpD, chpE, fimV, pilA, pilB, pilD, pilE, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilC like, xcpA/pilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algI, algJ, algK, algL, algM, algP/algR3, algQ, algR, algU, algW, algX, algZ, mucA, mucB, mucC | rhlA, rhlB | fptA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, pchR, pvdA, pvdE | phzM, phzS | aprA, lasA | toxA, plcH | lasI, rhlI | xcpP, xcpQ, xcpR, xcpS, xcpT, xcpU, xcpV, xcpW, xcpX, xcpY, xcpZ |
Table A9. Cont.

| Sample ID | ST-Type | Adherence | Anti-Phagocytosis | Biosurfactant | Iron Uptake | Pigment | Protease | Toxin | Regulation | Secretion System |
|-----------|---------|-----------|-------------------|---------------|-------------|----------|----------|-------|------------|------------------|
| 180       | ST 856  | waaA, waaC, waaF, waaG, waaP, chpA, chpC, chpD, chpE, fimT, fimU, fimV, pilA, pilB, pilD, pilE, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX pilY1, pilY2, pilC like, xcpA/pilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algI, algJ, algK, algL, algP/algR3, algQ, algR, algU, algW, algX, algZ, mucA, mucB, mucC | rhlA, rhlB | fptA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, pchR, pvdA | phzM, phzS | aprA, lasA | toxA, plcH | lasI, rhlI | xcpP, xcpQ, xcpR, xcpS, xcpT, xcpU, xcpV, xcpW, xcpX, xcpY, xcpZ |
| 183       | ST 244  | waaA, waaC, waaF, waaG, waaP, wzy, wzz, chpA, chpB, chpC, chpD, chpE, fimT, fimU, fimV, pilA like, pilB, pilD, pilE, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX pilY1, pilY2, pilC, xcpA/pilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algI, algJ, algK, algL, algQ, algR, algU, algW, algX, algZ, mucA, mucB, mucC | rhlA, rhlB | fptA, fprA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, pchR, pvdA, pvdE | phzM, phzS | aprA, lasA | toxA, plcH | lasI, rhlI | xcpP, xcpQ, xcpR, xcpS, xcpT, xcpU, xcpV, xcpW like, xcpX, xcpY, xcpZ |
Table A9. Cont.

| Sample ID | ST-Type | Adherence | Anti-Phagocytosis | Biosurfactant | Iron Uptake | Pigment | Protease | Toxin | Regulation | Secretion System |
|-----------|---------|-----------|-------------------|---------------|-------------|---------|----------|-------|------------|------------------|
| 186       | ST 3588 | waaA, waaC, waaF, waaG, waaP, chpA, chpB, chpC, chpD, chpE, fimT, fimU, fimV, pilA like, pilB, pilD, pilE, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX pilY1, pilY2, pilC like, xcpA/pilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algI, algJ, algK, algL, algM, algN, algO, algP, algQ, algR, algS, algT, algU, algV, algW, algX, algY, algZ, mucA, mucB, mucC | rhlA, rhlB | fptA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, plcH, pchR, pchT, pchU, pchV, pchW, pchX, pchY, pchZ | phzM, phzS aprA, lasA lasI, rhlI |
| 190       | ST 871  | waaA, waaC, waaF, waaG, waaP, chpA, chpB, chpC, chpD, chpE, fimT, fimU, fimV, pilA, pilB, pilD, pilE, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX pilY1, pilY2, pilC like, xcpA/pilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algI, algJ, algK, algL, algM, algN, algO, algP/algR3, algQ, algR, algS, algT, algU, algV, algW, algX, algY, algZ, mucA, mucB, mucC | rhlA, rhlB | fptA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, plcH, pchR, pchT, pchU, pchV, pchW, pchX, pchY, pchZ | phzM, phzS aprA, lasA toxA, plcH lasI, rhlI |
| 195       | ST 988  | waaA, waaC, waaF, waaG, waaP, chpA, chpB, chpC, chpD, chpE, fimT, fimU, fimV, pilA, pilB, pilD, pilE, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX pilY1, pilY2, pilC like, xcpA/pilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algI, algJ, algK, algL, algM, algN, algO, algP/algR3, algQ, algR, algS, algT, algU, algV, algW, algX, algY, algZ, mucA, mucB, mucC | rhlA, rhlB | fptA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, plcH, pchR, pchT, pchU, pchV, pchW, pchX, pchY, pchZ | phzM, phzS aprA, lasA toxA, plcH lasI, rhlI |
Table A9. Cont.

| Sample ID | ST-Type | Adherence | Anti-Phagocytosis | Biosurfactant | Iron Uptake | Pigment | Protease | Toxin | Regulation | Secretion System |
|-----------|---------|-----------|-------------------|---------------|-------------|----------|----------|-------|------------|------------------|
| 196       | ST 2475 | **waaA, waaC, waaF, waaG, waaP, wzy, wzz, chpA, chpB, chpC, chpD, chpE, fimT, fimU, fimV, pilA, pilB, pilD, pilE, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX, pilY1, pilY2, pilC, xcpA/pilD** | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algI, algJ, algK, algL, algP/algR3, algQ, algR, algU, algW, algX, algZ, mucA, mucB, mucC | **rhlA, rhlB** | fptA, fptV, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, pchR, pvdA, pvdE | phzM, phzS | aprA, lasA | toxA, plcH | lasI, rhlI | xcpP, xcpQ, xcpR, xcpS, xcpT, xcpU, xcpV, xcpW, xcpX, xcpY, xcpZ |
| 198       | ST 2476 | **waaA, waaC, waaF, waaG, waaP, chpA, chpB, chpC, chpD, chpE, fimT, fimU, fimV, pilA, pilB, pilD, pilE, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX, pilY1, pilY2, pilC like, xcpA/pilD** | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algI, algJ, algK, algL, algP/algR3, algQ, algR, algU, algW, algX, algZ, mucA, mucB, mucC | **rhlA, rhlB** | fptA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, pchR, pvdA | phzM, phzS | aprA, lasA | toxA, plcH | lasI, rhlI | xcpP, xcpQ, xcpR, xcpS, xcpT, xcpU, xcpV, xcpW, xcpX, xcpY, xcpZ |
| 204       | ST 639  | **waaA, waaC, waaF, waaG, waaP, chpA, chpB, chpC, chpD, chpE, fimT, fimU, fimV, pilA, pilB, pilD, pilE, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX, pilY1, pilY2, pilC like, xcpA/pilD** | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algI, algJ, algK, algL, algQ, algR, algU, algW, algX, algZ, mucA, mucB, mucC | **rhlA, rhlB** | fptA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, pchR, pvdA | phzM, phzS | aprA, lasA | toxA, plcH | rhlIl | xcpP, xcpQ, xcpR, xcpS, xcpT, xcpU, xcpV, xcpW, xcpX, xcpY, xcpZ |
| Sample ID | ST-Type | Adherence | Pathogenicity Factor Groups |
|-----------|---------|-----------|-----------------------------|
| 208       | ST 132  | waaA, waaC, waaF, waaG, waaP, chpA, chpB, chpC, chpD, chpE, fimT, fimU, fimV, pilA like, pilB, pilD, pilE, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX, pilY1, pilY2, pilC, xcpA/pilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algI, algJ, algK, algL, algM, algQ, algR, algI, algW, algX, algZ, mucA, mucB, mucC, rhlA, rhlB, phzM, phzS, aprA, lasA, toxA, plcH, lasI, rhlI, xcpP, xcpQ, xcpR, xcpS, xcpT, xcpU, xcpV, xcpW, xcpX, xcpY, xcpZ |
| 218       | ST 856  | waaA, waaC, waaF, waaG, waaP, chpA, chpB, chpC, chpD, chpE, fimT, fimU, fimV, pilB, pilD, pilE, pilF, pilG, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX, pilY1, pilY2, pilC like, xcpA/pilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algI, algJ, algK, algL, algM, algQ, algR, algI, algW, algX, algZ, mucA, mucB, mucC, rhlA, rhlB, phzM, phzS, aprA, lasA, toxA, plcH, lasI, rhlI, xcpP, xcpQ, xcpR, xcpS, xcpT, xcpU, xcpV, xcpW, xcpX, xcpY, xcpZ |
| 229       | ST 270  | waaA, waaC, waaF, waaG, waaP, uex, uex, chpA, chpB, chpC, chpD, chpE, fimT, fimU, fimV, pilB, pilD, pilE, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX, pilY1, pilY2, pilC like, xcpA/pilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algI, algJ, algK, algL, algM, algQ, algR, algI, algW, algX, algZ, mucA, mucB, mucC, rhlA, rhlB, phzM, phzS, aprA, lasA, toxA, plcH, lasI, rhlI, xcpP, xcpQ, xcpR, xcpS, xcpT, xcpU, xcpV, xcpW, xcpX, xcpY, xcpZ |
Table A9. Cont.

| Sample ID | ST-Type | Adherence | Anti-Phagocytosis | Biosurfactant | Iron Uptake | Pigment | Protease | Toxin | Regulation | Secretion System |
|-----------|---------|-----------|-------------------|---------------|-------------|---------|----------|-------|------------|-----------------|
| 233       | ST 3227 | waaA, waaC, waaF, waaG, waaP, chapA, chapB, chapC, chapD, chapE, fimV, pilB, pilD, pilE, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilC like, xcpA/pilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algI, algJ, algK, algL, algP/algR3, algQ, algR, algU, algW, algX, algZ, mucA, mucB, mucC | rhlA, rhlB | fptA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, pchR, pvdA | phzM, phzS | aprA, lasA | toxA, plcH | lasI, rhlI |
| 236       | ST 266  | waaA, waaC, waaF, waaG, waaP, chapA, chapB, chapC, chapD, chapE, fimT, fimU, fimV, pilB, pilD, pilE, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX pilY1, pilY2, pilC like, xcpA/pilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algI, algJ, algK, algL, algQ, algR, algU, algV, algW, algX, algZ, mucA, mucB, mucC | rhlA, rhlB | fptA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, pchR, pvdA | phzM, phzS | aprA, lasA | toxA, plcH | lasI, rhlI |
| 238       | ST 3589 | waaA, waaC, waaF, waaG, waaP, chapA, chapB, chapC, chapD, chapE, fimT, fimU, fimV, pilA, pilB, pilD, pilE, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX pilY1, pilY2, pilC like, xcpA/pilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algI, algJ, algK, algL, algQ, algR, algU, algW, algX, algZ, mucA, mucB, mucC | rhlA, rhlB | fptA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, pchR, pvdA | phzM, phzS | aprA, lasA | plcH | lasI, rhlI |


| Sample ID | ST-Type | Adherence | Anti-Phagocytosis | Biosurfactant | Iron Uptake | Pigment | Protease | Toxin | Regulation | Secretion System |
|-----------|---------|-----------|-------------------|---------------|-------------|----------|----------|-------|------------|------------------|
| 242       | ST 3590 | waaA, waaC, waaF, waaG, waaP, chpA, chpB, chpC, chpD, chpE, fimT, fimU, fimV, pilB, pilD, pilE, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX pilY1, pilY2, pilC like, xcpA/pilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algI, algJ, algK, algL, algP, algR3 like, algQ, algR, algU, algW, algX, algZ, mucA, mucB, mucC | rhlA, rhlB | fptA, fprA | pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, pchR, pvdA, pvdE | phzM, phzS | aprA, lasA | toxA, plcH | lasI, rhlI | xcpP, xcpQ, xcpS, xcpT, xcpU, xcpV, xcpW, xcpX, xcpY, xcpZ |
| 243       | ST 3590 | waaA, waaC, waaF, waaG, waaP, chpA, chpB, chpC, chpD, chpE, fimT, fimU, fimV, pilB, pilD, pilE, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX pilY1, pilY2, pilC like, xcpA/pilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algI, algJ, algK, algL, algP, algR3 like, algQ, algR, algU, algW, algX, algZ, mucA, mucB, mucC | rhlA, rhlB | fptA, fprA | pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, pchR, pvdA, pvdE | phzM, phzS | aprA, lasA | toxA, plcH | lasI, rhlI | xcpP, xcpQ, xcpS, xcpT, xcpU, xcpV, xcpW, xcpX, xcpY, xcpZ |
| 272       | ST 2033 | waaA, waaC, waaF, waaG, waaP, chpA, chpB, chpC, chpD, chpE, fimT, fimU, fimV, pilA, pilB, pilD, pilE, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX pilY1, pilY2, pilC, xcpA/pilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algI, algJ, algK, algL, algQ, algR, algU, algW, algX, algZ, mucA, mucB, mucC | rhlA, rhlB | fptA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, pchR, pvdA, pvdE | phzM, phzS | aprA, lasA | toxA, plcH | lasI, rhlI | xcpP, xcpQ, xcpR, xcpS, xcpT, xcpU, xcpV, xcpW, xcpX, xcpY, xcpZ |
Table A9. Cont.

| Sample ID | ST-Type | Adherence | Anti-Phagocytosis | Biosurfactant | Iron Uptake | Pigment | Protease | Toxin | Regulation | Secretion System |
|-----------|---------|-----------|-------------------|---------------|-------------|---------|---------|-------|------------|------------------|
| 274       | ST 2033 | waaA, waaC, waaF, waaG, waaP, chpA, chpB, chpC, chpD, chpE, fimT, fimU, fimV, pilA, pilB, pilD, pilE, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX pilY1, pilY2, pilC, xcpA/pilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algJ, algL, algQ, algR, algU, algW, algX, algZ, mucA, mucB, mucC | rhlA, rhlB | ftpA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, pchL, pchR, pvdA | phzM, phzS | aprA, lasA | toxA, plcH | lasI, rhlI | xcpP, xcpQ, xcpR, xcpS, xcpT, xcpU, xcpV, xcpW, xcpX, xcpY, xcpZ |
| 278       | ST 988  | waaA, waaC, waaF, waaG, waaP, chpA, chpB, chpC, chpD, chpE, fimT, fimU, fimV, pilB, pilD, pilE, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX pilY1, pilY2, pilC like, xcpA/pilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algJ, algL, algQ, algR, algU, algW, algX, algZ, mucA, mucB, mucC | rhlA, rhlB | ftpA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, pchL, pchR, pvdA | phzM, phzS | aprA, lasA | toxA, plcH | lasI, rhlI | xcpP, xcpQ, xcpR, xcpS, xcpT, xcpU, xcpV, xcpW, xcpX, xcpY, xcpZ |
Table A9. Cont.

| Sample ID | ST-Type | Adherence | Anti-Phagocytosis | Biosurfactant | Iron Uptake | Pigment | Protease | Toxin | Regulation | Pathogenicity Factor Groups | Secretion System |
|-----------|---------|-----------|-------------------|---------------|-------------|---------|----------|-------|------------|-----------------------------|-----------------|
| 282       | ST 554  | waaA, waaC, waaF, waaG, waaP, wzy, wzz, chpA, chpB, chpC, chpD, chpE, fimT, fimU, fimV, pilA like, pilB, pilD, pilE, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX pilY1, pilY2, pilC, xcpA/pilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algI, algJ, algK, algL, algQ, algR, algU, algW, algX, algZ, mucA, mucB, mucC | rhlA, rhlB | fptA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, pchJ, pchK, pchL, pchM, pchN, pchO, pchP, pchQ, pchR, pchS, pchT, pchU, pchV, pchW, pchX, pchY, pchZ | phzM, phzS | aprA, lasA | toxA, plcH | lasI, rhII | xcpP, xcpQ, xcpR, xcpS, xcpT, xcpU, xcpV, xcpW, xcpX, xcpY, xcpZ |
| 285       | ST 554  | waaA, waaC, waaF, waaG, waaP, wzy, wzz, chpA, chpB, chpC, chpD, chpE, fimT, fimU, fimV, pilA like, pilB, pilD, pilE, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX pilY1, pilY2, pilC, xcpA/pilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algI, algJ, algK, algL, algQ, algR, algU, algW, algX, algZ, mucA, mucB, mucC | rhlA, rhlB | fptA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, pchJ, pchK, pchL, pchM, pchN, pchO, pchP, pchQ, pchR, pchS, pchT, pchU, pchV, pchW, pchX, pchY, pchZ | phzM, phzS | aprA, lasA | toxA, plcH | lasI, rhII | xcpP, xcpQ, xcpR, xcpS, xcpT, xcpU, xcpV, xcpW, xcpX, xcpY, xcpZ |
| Sample ID | ST-Type | Pathogenicity Factor Groups |
|-----------|---------|----------------------------|
| 289       | ST 1485 | waaA, waaC, waaF, waaG, waaP, chpA, chpB, chpC, chpD, chpE, fimT, fimU, fimV, pilB, pilD, pilE, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX pilY1, pilY2, pilC like, xcpA/pilD |
|           |         | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algH, algI, algJ, algK, algL, algM, algN, algO, algP, algQ, algR, algS, algT, algU, algV, algW, algX, algY, algZ, mucA, mucB, mucC |
|           |         | fptA, fprA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, pchR, pchS, pchT, pchU, pchV, pchW, pchX, pchY, pchZ |
| 290       | ST 1485 | waaA, waaC, waaF, waaG, waaP, chpA, chpB, chpC, chpD, chpE, fimT, fimU, fimV, pilB, pilD, pilE, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX pilY1, pilY2, pilC like, xcpA/pilD |
|           |         | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algH, algI, algJ, algK, algL, algM, algN, algO, algP, algQ, algR, algS, algT, algU, algV, algW, algX, algY, algZ, mucA, mucB, mucC |
|           |         | fptA, fprA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, pchR, pchS, pchT, pchU, pchV, pchW, pchX, pchY, pchZ |
| 296       | ST 235  | waaA, waaC, waaF, waaG, waaP, chpA, chpB, chpC, chpD, chpE, fimT, fimU, fimV, pilB, pilD, pilE, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX pilY1, pilY2, pilC, xcpA/pilD |
|           |         | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algH, algI, algJ, algK, algL, algM, algN, algO, algP, algQ, algR, algS, algT, algU, algV, algW, algX, algY, algZ, mucA, mucB, mucC |
|           |         | fptA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, pchR, pchS, pchT, pchU, pchV, pchW, pchX, pchY, pchZ |
Table A9. Cont.

| Sample ID | ST-Type | Adherence | Anti-Phagocytosis | Biosurfactant | Iron Uptake | Pigment | Protease | Toxin | Regulation | Secretion System |
|-----------|---------|-----------|-------------------|---------------|-------------|---------|----------|-------|------------|------------------|
| 298       | ST 3227 | waaA, waaC, waaF, waaG, waaP, chpA, chpB, chpC, chpD, chpE, fimV, pilB, pilD, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilT, pilU, pilV, pilC, xcpA/pilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algI, algJ, algK, algL, algQ, algR, algL1, algW, algX, algZ, mucA, mucB, mucC | rhlA, rhlB | fptA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, pchR, plcH, plcM, plcS, aprA, lasA, toxA, lasI, rhlI | xcpP, xcpQ, xcpR, xcpS, xcpT, xcpU, xcpV, xcpW, xcpX, xcpY, xcpZ |
| 301       | ST 3593 | waaA, waaC, waaF, waaG, waaP, wzy, wzz, chpA, chpB, chpC, chpD, chpE, fimT, fimU, fimV, pilB, pilD, pilE, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilT, pilU, pilV, pilW, pilX pilY1, pilY2, pilC, xcpA/pilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algI, algJ, algK, algL, algQ(algR3), algQ', algR, algU, algW, algX, algZ, mucA, mucB, mucC | rhlA, rhlB | fptA, fptA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchI, pchR, plcH, plcM, plcS, aprA, lasA, toxA, lasI, rhlI | xcpP, xcpQ, xcpR, xcpS, xcpT, xcpU, xcpV, xcpW, xcpX, xcpY, xcpZ |
| 302       | ST 1755 | waaA, waaC, waaF, waaG, waaP, wzy, wzz, chpA, chpB, chpC, chpD, chpE, fimT, fimU, fimV, pilB, pilD, pilE, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilV, pilW, pilX pilY1, pilY2, pilC like, xcpA/pilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algI, algJ, algK, algL, algQ, algR, algL1, algW, algX, algZ, mucA, mucB, mucC | rhlA, rhlB | fptA, fptA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchI, pchR, plcH, plcM, plcS, aprA, lasA, toxA, lasI, rhlI | xcpP, xcpQ, xcpR, xcpS, xcpT, xcpU, xcpV, xcpW, xcpX, xcpY, xcpZ |
| Sample ID | ST-Type | Adherence | Antiphagocytosis | Biosurfactant | Iron Uptake | Pigment | Protease | Toxin | Regulation | Secretion System |
|-----------|---------|-----------|------------------|---------------|------------|---------|----------|------|------------|------------------|
| 309       | ST 3592 | waaA, waaC, waaF, waaG, waaP, wzy, wzz, chpA, chpB, chpC, chpD, chpE, fimT, fimU, fimV, pilB, pilD, pilE, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilW, pilX pilY1, pilY2, pilC, xcpApilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algI, algJ, algK, algL, algQ, algR, algU, algW, algX, algZ, mucA, mucB, mucC | rhlA, rhlB | fptA, fprA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchl, pchr, pvdA, pvdE | phzM, phzS | aprA, lasA | plcH | lasI, rhlI | xcpP, xcpQ, xcpS, xcpT, xcpU, xcpV, xcpW, xcpX, xcpY, xcpZ |
| 310       | ST 532  | waaA, waaC, waaF, waaG, waaP, chpA, chpB, chpC, chpD, chpE, fimV, pilB, pilD, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilC like, xcpApilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algI, algJ, algK, algL, algQ, algR, algU, algW, algX, algZ, mucA, mucB, mucC | rhlA, rhlB | fptA, fprA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchl, pchr, pvdA, pvdE | phzM, phzS | aprA lasA | toxA, plcH | lasI, rhlI | xcpP, xcpQ, xcpR, xcpS, xcpT, xcpU, xcpV, xcpW, xcpX, xcpY, xcpZ |
| 312       | ST 381  | waaA, waaC, waaF, waaG, waaP, wzy, wzz, chpA, chpB, chpC, chpD, chpE, fimV, pilB, pilD, pilF, pilG, pilH, pilI, pilK, pilM, pilN, pilO, pilP, pilQ, pilR, pilS, pilT, pilU, pilC like, xcpApilD | alg44, alg8, algA, algB, algC, algD, algE, algF, algG, algI, algJ, algK, algL, algP/algR3, algQ, algR3, algU, algW, algX, algZ, mucA, mucB, mucC | rhlA, rhlB | fptA, pchA, pchB, pchC, pchD, pchE, pchF, pchG, pchH, pchl, pchr, pvdA, pvdE | phzM, phzS | aprA, lasA | toxA, plcH | lasI, rhlI | xcpP, xcpQ, xcpR, xcpS, xcpT, xcpU, xcpV, xcpW, xcpX, xcpY, xcpZ |
Table A10. Analysis of virulence determinants, ordered by strain and MLST type, of the assessed *K. pneumoniae* isolates. ST = Sequence type.

| Sample ID | ST-Type | Adherence | Biofilm Formation | Efflux Pump | Immune Evasion | Iron Uptake | Nutritional Factor | Regulation | Secretion System | Serum Resistance | Toxin |
|-----------|---------|-----------|------------------|-------------|----------------|-------------|-------------------|------------|------------------|------------------|-------|
| 044       | ST 327  | fimA, fimB, fimC, fimD, fimE, fimF, fimG, fimH, fimI, fimK | mrkA, mrkB, mrkC, mrkD, mrkF, mrkH, mrkI, mrkJ | acrA, acrB | cpsACP, galF, gnd, ugd, wza like, wzi | entA, entB, entC, entD, entE, entF, fepA, fepB, fepC, fepD, fepG, fes, ybdA, iroE like | rcsA, rcsB | impA/tssA like, sciN/tssJ, tssF, tssG, vasE/tssK, vgrG/tssl, vipA/tssB, vioB/tssC | glf, wbbM, wbbN, wbbO, wzm, wzt |
| 060       | ST 5379 | fimA, fimB, fimC, fimD, fimE, fimF, fimG, fimH, fimI, fimK | mrkA, mrkB, mrkC, mrkD, mrkF, mrkH, mrkI, mrkJ | acrA, acrB | cpsACP, galF, gnd, ugd, wza like, wzi | entA, entB, entC, entE, entF, fepA, fepB, fepC, fepD, fepG, fes, ybdA, iroE like | rcsA, rcsB | impA/tssA, sciN/tssJ, tssF, tssG, vasE/tssK, vgrG/tssl, vipA/tssB, vioB/tssC | |
| 073       | ST 39   | fimA, fimB, fimC, fimD, fimE, fimF, fimG, fimH, fimI, fimK | mrkA, mrkB, mrkC, mrkD, mrkF, mrkH, mrkI, mrkJ | acrA, acrB | cpsACP, galF, gnd, ugd, wza like, wzi | entA, entB, entC, entD, entE, entF, fepA, fepB, fepC, fepD, fepG, fes, ybdA, iroE, irp1, irp2, ybtA, ybtE, ybtP, ybtQ, ybtS, ybtT, ybtU, ybtX | rcsA, rcsB | impA/tssA, sciN/tssJ, tle1, tle2, tle3, tssF, tssG, vasE/tssK, vgrG/tssl, vipA/tssB, vioB/tssC | glf, wbbM, wbbN, wbbO, wzm, wzt |
| 100       | ST 152  | fimA, fimB, fimC, fimD, fimE, fimF, fimG, fimH, fimI, fimK | mrkA, mrkB, mrkC, mrkD, mrkF, mrkH, mrkI, mrkJ | acrA, acrB | cpsACP, galF, gnd, ugd, wza like, wzi | entA, entB, entC, entD, entE, entF, fepA, fepB, fepC, fepD, fepG, fes, ybdA, iroE, irp1, irp2, ybtA, ybtE, ybtP, ybtQ, ybtS, ybtT, ybtU, ybtX | rcsA, rcsB | impA/tssA like, sciN/tssJ, tssF, tssG | |
Table A10. Cont.

| Sample ID | ST-Type | Adherence Factor Groups | Pathogenicity Factor Groups |
|-----------|---------|-------------------------|-----------------------------|
|           |         | **Biofilm Formation**   | **Efflux Pump**             | **Immune Evasion** | **Iron Uptake** | **Nutritional Factor** | **Regulation** | **Secretion System** | **Serum Resistance** | **Toxin** |
| 102       | ST 514  | fimA, fimB, fimC, fimD, fimE, fimF, fimG, fimH, fimI, fimK | mrkA, mrkB, mrkC, mrkD, mrkF, mrkI, mrkJ | acrA, acrB | cpsACP, galF, gnd, manB, manC, wza, wzi | entA, entB, entC, entE, entF, fepA, fepB, fepC, fepD, fepG, fes, ybdA, iroE | rcsA, rcsB | impA/tssA like, sciN/tssJ, tssE, tssG, vasE/tssK, vgrG/tssI, vipA/tssB, vipB/tssC | glf, wbbM, wbbN, wbbO, wzm, wzt |
| 124       | ST 399  | fimA, fimB, fimC, fimD, fimE, fimF, fimG, fimH, fimI, fimK | mrkF, mrkH, mrkJ | acrA, acrB | cpsACP, galF, gnd, wza like, wzi | entA, entB, entC, entE, entF, fepA, fepB, fepC, fepD, fepG, fes, ybdA, iroE | rcsA, rcsB | impA/tssA like, sciN/tssJ, tssE, tssG, vasE/tssK, vgrG/tssI, vipA/tssB, vipB/tssC | glf, wbbM, wbbN, wbbO, wzm, wzt |
| 146       | ST 4    | fimA, fimC, fimD, fimE, fimF, fimG, fimH, fimI, fimK | mrkA, mrkB, mrkC, mrkD, mrkF, mrkH, mrkI, mrkJ | acrA, acrB | cpsACP, galF, gnd, manB, manC, wza, wzi | entA, entB, entC, entD, entE, entF, fepA, fepB, fepC, fepD, fepG, fes, ybdA, iroE, irp1, irp2, ybtA, ybtE, ybtP, ybtQ, ybtS, ybtT, ybtU, ybtX | rcsA, rcsB | impA/tssA like, sciN/tssJ, tssE, tssG, vasE/tssK, vgrG/tssI, vipA/tssB, vipB/tssC | glf, wbbM, wbbN, wbbO, wzm, wzt |
| 177       | ST 17   | fimA, fimB, fimC, fimD, fimE, fimF, fimG, fimH, fimI, fimK | mrkA, mrkB, mrkD, mrkF, mrkH, mrkJ | acrA, acrB | cpsACP, galF, gnd, manB, manC, wza like, wzi | entA, entB, entC, entD, entE, entF, fepA, fepB, fepC, fepD, fepG, fes, ybdA, iroE, ybtA, ybtE, ybtP, ybtQ, ybtS, ybtT, ybtU, ybtX | rcsA, rcsB | impA/tssA like, sciN/tssJ, tssE, tssG, vasE/tssK, vgrG/tssI, vipA/tssB, vipB/tssC | glf, wbbM, wbbN, wbbO, wzm, wzt |
| Sample ID | ST-Type | Adherence | Biofilm Formation | Efflux Pump | Immune Evasion | Iron Uptake | Nutritional Factor | Regulation | Secretion System | Serum Resistance | Toxin |
|-----------|---------|-----------|------------------|-------------|---------------|-------------|-------------------|------------|------------------|----------------|-------|
| 181       | ST 5380 | fimA, fimB, fimC, fimD, fimE, fimF, fimG, fimH, fimI, fimK | mrkA, mrkB, mrkC, mrkD, mrkF, mrkH, mrkl, mrkJ | acrA, acrB | cpsACP, galF, gmd like, gnd, manB, manC, ugd, wza like, wzi | entA, entB, entC, entE, entF, fepA, fepB, fepC, fepD, fepG, fes, ybdA, iroE | rcsA, rcsB | impA/tssA, sciN/tssF, tle1, tle2, tssE, tssG, tssK, vraE/tssI, vipA/tssB, vipB/tssC | glf, wbbM, wbbN, wbbO, wzm, wzt |
| 184       | ST 5381 | fimA, fimB, fimC, fimD, fimE, fimF, fimG, fimH, fimI, fimK | mrkA, mrkB, mrkC, mrkD, mrkF, mrkH, mrkl, mrkJ | acrA, acrB | cpsACP, galF, gmd like, gnd, wza like, wzi | entA, entB, entC, entD like, entE, entF, fepA, fepB, fepC, fepD, fepG, fes, ybdA, iroE like | rcsA, rcsB | impA/tssA, sciN/tssF, tssG, vraE/tssK, vraG/tssL, vipA/tssB, vipB/tssC | |
| 199       | ST 17   | fimA, fimB, fimC, fimD, fimE, fimF, fimG, fimH, fimI, fimK | mrkA, mrkB, mrkC, mrkD, mrkF, mrkH, mrkl, mrkJ | acrA, acrB | cpsACP, galF, gmd like, manB, manC, ugd, wza, wzi | entA, entB, entC, entE, entF, fepA, fepB, fepC, fepD, fepG, fes, ybdA, iroE, irp1, irp2, ybtA, ybtE, ybtP, ybtQ, ybtS, ybtT, ybtU, ybtX | rcsA, rcsB | impA/tssA, sciN/tssF, tssG, vraE/tssK, vraG/tssL, vipA/tssB, vipB/tssC | |
| 214       | ST 6    | fimA, fimB, fimC, fimD, fimE, fimF, fimG, fimH, fimI, fimK | mrkB, mrkC, mrkD, mrkF, mrkH, mrkl, mrkJ | acrA, acrB | cpsACP, galF, gmd like, manB, manC, ugd, wza like, wzi | entA, entB, entC, entE, entF, fepA, fepB, fepC, fepD, fepG, fes, ybdA, iroE, irp1, irp2, ybtA, ybtE, ybtP, ybtQ, ybtS, ybtT, ybtU, ybtX | rcsA, rcsB | impA/tssA like, sciN/tssF, tssG, vraE/tssK, vraG/tssL, vipA/tssB, vipB/tssC | glf, wbbM, wbbN, wbbO, wzm, wzt |
| Sample ID | ST-Type | Adherence | Biofilm Formation | Efflux Pump | Immune Evasion | Iron Uptake | Nutritional Factor | Regulation | Secretion System | Serum Resistance | Toxin |
|-----------|---------|-----------|------------------|-------------|---------------|------------|-------------------|------------|-----------------|----------------|-------|
| 217 ST 3154 | fimA, fimB, fimC, fimD, fimE, fimF, fimG, fimH, fimI, fimK | mrkA, mrkB, mrkC, mrkD, mrkF, mrkH, mrkI, mrkJ | mrkA, mrkB, mrkC, mrkD, mrkF, mrkH, mrkI, mrkJ | acrA, acrB | cpsACP, galF, gnd, manB, manC, ugd, wza like, wzi | entA, entB, entC, entE, entF, fepA, fepB, fepC, fepD, fepG, fes, ybdA, iroE | rcsA, rcsB | impA/tssA like, sciN/tssJ, tssF, tssG, tssE/tssK, tgrG/tssl, vipA/tssB, vipB/tssC | glf, wbbM, wbbN, wbbO, wzm, wzt |
| 220 ST 5382 | fimA, fimB, fimC, fimD, fimE, fimF, fimG, fimH, fimI, fimK | mrkA, mrkB, mrkC, mrkD, mrkF, mrkH, mrkI, mrkJ | mrkA, mrkB, mrkC, mrkD, mrkF, mrkH, mrkI, mrkJ | acrA, acrB | cpsACP, galF, gnd, manB, manC, ugd, wza like, wzi | entA, entB, entC, entE, entF, fepA, fepB, fepC, fepD, fepG, fes, ybdA, iroE | allA, allB, allC, allD, allR, allS | rcsA, rcsB | |
| 234 ST 109 | fimA, fimB, fimC, fimD, fimE, fimF, fimG, fimH, fimI, fimK | mrkA, mrkB, mrkC, mrkD, mrkF, mrkH, mrkI, mrkJ | mrkA, mrkB, mrkC, mrkD, mrkF, mrkH, mrkI, mrkJ | acrA, acrB | cpsACP, galF, gnd, manB, manC, ugd, wza like, wzi | entA, entB, entC, entE, entF, fepA, fepB, fepC, fepD, fepG, fes, ybdA, iroE | rcsA, rcsB, impA/tssA, sciN/tssJ, tssF, tssG, tssE/tssK, tgrG/tssl, vipA/tssB, vipB/tssC | glf, wbbM, wbbN, wbbO, wzm, wzt |
| 240 ST 5383 | fimC, fimD, fimE, fimF, fimG, fimI, fimK | mrkF, mrkH, mrkI, mrkJ | mrkF, mrkH, mrkI, mrkJ | acrA, acrB | cpsACP, galF, gnd, ugd, wza like, wzi | entA, entB, entC, entE, entF, fepA, fepB, fepC, fepD, fepG, fes, ybdA, iroE | rcsA, rcsB | tssE/tssK, tgrG/tssl, vipA/tssB, vipB/tssC | glf, wbbM, wbbN, wbbO, wzm, wzt |
| 248 ST 5384 | fimC, fimD, fimE, fimF, fimG, fimI, fimK | mrkC, mrkD, mrkF, mrkH, mrkJ | mrkC, mrkD, mrkF, mrkH, mrkJ | acrA, acrB | cpsACP, galF, gnd, manB, manC, ugd, wza like, wzi | entA, entB, entC, entE, entF, fepA, fepB, fepC, fepD, fepG, fes, ybdA, iroE | rcsA, rcsB | tssE/tssK, tgrG/tssl, vipA/tssB, vipB/tssC | glf, wbbM, wbbN, wbbO, wzm, wzt |
| 252 ST 607 | fimA, fimB, fimC, fimD, fimE, fimF, fimG, fimH, fimI, fimK | mrkA, mrkB, mrkC, mrkD, mrkF, mrkH, mrkJ | mrkA, mrkB, mrkC, mrkD, mrkF, mrkH, mrkJ | acrA, acrB | cpsACP, galF, gnd, wza like, wzi | entA, entB, entC, entE, entF, fepA, fepB, fepC, fepD, fepG, fes, ybdA, iroE | rcsA, rcsB | sciN/tssJ, tssF, tssG, tssE/tssK, tgrG/tssl, vipA/tssB, vipB/tssC | glf, wbbM, wbbN, wbbO, wzm, wzt |
| Sample ID | ST-Type | Adherence | Biofilm Formation | Eflux Pump | Immune Evasion | Iron Uptake | Nutritional Factor | Regulation | Secretion System | Serum Resistance | Toxin |
|-----------|---------|-----------|------------------|------------|---------------|-------------|------------------|------------|------------------|----------------|-------|
| 267       | ST 36   | fimA, fimB, fimC, fimD, fimE, fimF, fimG, fimH, fimI, fimK | mrkA, mrkB, mrkC, mrkD, mrkE, mrkF, mrkH, mrkI, mrkJ | acrA, acrB | cpsACP, galF, gnd, manB, manC, ugd, wza, wzi | entA, entB, entC, entE, entF, fepA, fepB, fepC, fepD, fepG, fes, ybdA, iroE, irp1, irp2, ybtA, ybtB, ybtP, ybtQ, ybtS, ybtT, ybtU, ybtX | rcsA, rcsB | impA/tssA, sciN/tssJ, tle1, tli1, tssE, tssG, vgrG/tssK, vipA/tssB, vipB/tssC | glf, wbbM, wbbN, wbbO, wzm, wzt |
| 277       | ST 530  | fimA, fimB, fimC, fimD, fimE, fimF, fimG, fimH, fimI, fimK | mrkA, mrkB, mrkC, mrkD, mrkE, mrkF, mrkH, mrkJ | acrA, acrB | cpsACP, galF, gnd, manB, manC, ugd, wza, wzi | entA, entB, entC, entE, entF, fepA, fepB, fepC, fepD, fepG, fes, ybdA, iroE | rcsA, rcsB | impA/tssA like, sciN/tssJ, tssF, tssG, vusE/tssK, vgrG/tssK, vipA/tssB, vipB/tssC | glf, wbbM, wbbN, wbbO, wzm, wzt |
| 279       | ST 5385 | fimA, fimB, fimC, fimD, fimE, fimF, fimG, fimH, fimI, fimK | mrkA, mrkB, mrkC, mrkD, mrkE, mrkF, mrkH, mrkJ | acrA, acrB | cpsACP, galF, gnd, ugd, wza, wzi | entA, entB, entC, entE, entF, fepA, fepB, fepC, fepD, fepG, fes, ybdA, iroE | rcsA, rcsB, impA/tssA, sciN/tssJ, tle1, tli1, tssE, tssG, vusE/tssK, vgrG/tssK, vipA/tssB, vipB/tssC | wzm, wzt |
Table A11. Details on the strain-specific short-read archive (SRA) accession numbers.

| Sample ID  | Percentage of Good Targets (SeqSphere+) | Average Coverage (Assembled) (SeqSphere+) | Approximated Genome Size (Megabases) (SeqSphere+) | Species (Kraken2) | Sequence Type | Complex Type (SeqSphere+) | SRA Accession  |
|------------|-----------------------------------------|-------------------------------------------|-------------------------------------------------|------------------|---------------|--------------------------|----------------|
| Iso00017   | 99.4                                    | 105                                       | 6.7                                             | *Pseudomonas aeruginosa* | 381           | 1791                     | SRR13617317    |
| Iso00022   | 99.4                                    | 102                                       | 6.9                                             | *Pseudomonas aeruginosa* | 2483          | 1792                     | SRR13617316    |
| Iso00032   | 99.2                                    | 106                                       | 6.6                                             | *Pseudomonas aeruginosa* | 3587          | 1793                     | SRR13617305    |
| Iso00041   | 99.4                                    | 97                                        | 5.0                                             | *Escherichia coli*     | 2 (Pasteur)  | 11349                    | SRR13617294    |
| Iso00044   | 99.7                                    | 116                                       | 5.1                                             | *Klebsiella pneumoniae* | 327           | 5462                     | SRR13617283    |
| Iso00049   | 98.7                                    | 94                                        | 5.2                                             | *Escherichia coli*     | 3 (Pasteur)  | 11350                    | SRR13617272    |
| Iso00060   | 99.6                                    | 112                                       | 5.3                                             | *Klebsiella pneumoniae* | 5379          | 5463                     | SRR13617261    |
| Iso00068   | 99.6                                    | 109                                       | 4.9                                             | *Escherichia coli*     | 632 (Pasteur) | 11351                    | SRR13617250    |
| Iso00069   | 99.6                                    | 104                                       | 6.8                                             | *Pseudomonas aeruginosa* | 360           | 1794                     | SRR13617239    |
| Iso00073   | 99.4                                    | 104                                       | 5.8                                             | *Klebsiella pneumoniae* | 39            | 5464                     | SRR13617236    |
| Iso00081   | 98.7                                    | 108                                       | 6.6                                             | *Pseudomonas aeruginosa* | 244           | 1795                     | SRR13617315    |
| Iso00082   | 99.4                                    | 112                                       | 6.3                                             | *Pseudomonas aeruginosa* | 514           | 1796                     | SRR13617314    |
| Iso00088   | 97.8                                    | 105                                       | 6.8                                             | *Pseudomonas aeruginosa* | 1682          | 1797                     | SRR13617313    |
| Iso00099   | 99.4                                    | 106                                       | 6.6                                             | *Pseudomonas aeruginosa* | 244           | 1798                     | SRR13617312    |
| Iso00100   | 99.2                                    | 108                                       | 5.5                                             | *Klebsiella pneumoniae* | 152           | 5465                     | SRR13617311    |
| Iso00102   | 99.2                                    | 111                                       | 5.4                                             | *Klebsiella pneumoniae* | 514           | 5466                     | SRR13617310    |
| Iso00106   | 99.5                                    | 110                                       | 6.4                                             | *Pseudomonas aeruginosa* | 1521          | 1799                     | SRR13617309    |
| Iso00114   | 99.4                                    | 105                                       | 6.7                                             | *Pseudomonas aeruginosa* | 244           | 1800                     | SRR13617308    |
| Iso00117   | 99.2                                    | 95                                        | 5.3                                             | *Escherichia coli*     | 4 (Pasteur)  | 11352                    | SRR13617307    |
| Iso00124   | 99.4                                    | 112                                       | 5.3                                             | *Klebsiella pneumoniae* | 399           | 5467                     | SRR13617306    |
| Iso00137   | 99.4                                    | 110                                       | 6.4                                             | *Pseudomonas aeruginosa* | 3014          | 1801                     | SRR13617304    |
| Iso00144   | 99.6                                    | 109                                       | 6.5                                             | *Pseudomonas aeruginosa* | 245           | 1802                     | SRR13617303    |
| Iso00146   | 99.4                                    | 110                                       | 5.5                                             | *Klebsiella pneumoniae* | 4             | 5468                     | SRR13617302    |
| Iso00147   | 99.5                                    | 108                                       | 6.6                                             | *Pseudomonas aeruginosa* | 245           | 1802                     | SRR13617301    |
Table A11. Cont.

| Sample ID | Percentage of Good Targets (SeqSphere+) | Average Coverage (Assembled) (SeqSphere+) | Approximated Genome Size (Megabases) (SeqSphere+) | Species (Kraken2) | Sequence Type | Complex Type (SeqSphere+) | SRA Accession |
|-----------|----------------------------------------|------------------------------------------|--------------------------------------------------|-------------------|----------------|--------------------------|---------------|
| Iso00149  | 99.6                                   | 104                                      | 6.9                                              | *Pseudomonas aeruginosa* | 381            | 1803                     | SRR13617300   |
| Iso00152  | 99.4                                   | 98                                       | 5.2                                              | *Escherichia coli*    | 22 (Pasteur)   | 11353                    | SRR13617299   |
| Iso00153  | 98.5                                   | 111                                      | 6.4                                              | *Pseudomonas aeruginosa* | 704            | ?                        | SRR13617298   |
| Iso00154  | 99.4                                   | 102                                      | 7.0                                              | *Pseudomonas aeruginosa* | 244            | 1805                     | SRR13617297   |
| Iso00157  | 99.6                                   | 114                                      | 6.3                                              | *Pseudomonas aeruginosa* | 2616           | 1806                     | SRR13617296   |
| Iso00160  | 99.2                                   | 115                                      | 6.2                                              | *Pseudomonas aeruginosa* | 170            | 1807                     | SRR13617295   |
| Iso00162  | 99.1                                   | 111                                      | 6.5                                              | *Pseudomonas aeruginosa* | 274            | 1808                     | SRR13617293   |
| Iso00176  | 99.0                                   | 98                                       | 5.1                                              | *Escherichia coli*    | 132 (Pasteur)  | 11354                    | SRR13617292   |
| Iso00177  | 99.6                                   | 108                                      | 5.5                                              | *Klebsiella pneumoniae* | 17             | 5469                     | SRR13617291   |
| Iso00180  | 99.8                                   | 110                                      | 6.5                                              | *Pseudomonas aeruginosa* | 856            | 1809                     | SRR13617290   |
| Iso00181  | 99.9                                   | 107                                      | 5.6                                              | *Klebsiella pneumoniae* | 5380           | 5470                     | SRR13617289   |
| Iso00183  | 99.5                                   | 107                                      | 6.7                                              | *Pseudomonas aeruginosa* | 244            | 1795                     | SRR13617288   |
| Iso00184  | 98.3                                   | 104                                      | 5.6                                              | *Klebsiella variicola subsp. variicola* | 5381           | 5471                     | SRR13617287   |
| Iso00186  | 98.7                                   | 113                                      | 6.3                                              | *Pseudomonas aeruginosa* | 3588           | 1810                     | SRR13617286   |
| Iso00190  | 99.7                                   | 114                                      | 6.3                                              | *Pseudomonas aeruginosa* | 871            | 1811                     | SRR13617285   |
| Iso00195  | 99.5                                   | 111                                      | 6.5                                              | *Pseudomonas aeruginosa* | 988            | 1812                     | SRR13617284   |
| Iso00196  | 99.5                                   | 101                                      | 7.1                                              | *Pseudomonas aeruginosa* | 2475           | 1813                     | SRR13617282   |
| Iso00198  | 99.6                                   | 112                                      | 6.4                                              | *Pseudomonas aeruginosa* | 2476           | 1814                     | SRR13617281   |
| Iso00199  | 99.4                                   | 108                                      | 5.6                                              | *Klebsiella pneumoniae* | 17             | 5472                     | SRR13617280   |
| Iso00204  | 99.5                                   | 104                                      | 6.9                                              | *Pseudomonas aeruginosa* | 639            | 1815                     | SRR13617279   |
| Iso00208  | 99.7                                   | 109                                      | 6.5                                              | *Pseudomonas aeruginosa* | 132            | 1816                     | SRR13617278   |
| Iso00214  | 99.7                                   | 108                                      | 5.5                                              | *Klebsiella pneumoniae* | 6              | 5473                     | SRR13617277   |
| Iso00217  | 99.8                                   | 104                                      | 5.7                                              | *Klebsiella pneumoniae* | 3154           | 5474                     | SRR13617276   |
| Iso00218  | 99.7                                   | 109                                      | 6.5                                              | *Pseudomonas aeruginosa* | 856            | 1809                     | SRR13617275   |
Table A11. Cont.

| Sample ID   | Percentage of Good Targets (SeqSphere+) | Average Coverage (Assembled) (SeqSphere+) | Approximated Genome Size (Megabases) (SeqSphere+) | Species (Kraken2) | Sequence Type | Complex Type (SeqSphere+) | SRA Accession |
|-------------|----------------------------------------|------------------------------------------|-------------------------------------------------|-------------------|---------------|--------------------------|----------------|
| Iso00220    | 97.8                                   | 110                                      | 5.4                                             | *Klebsiella quasipneumoniae* subsp. *similipneumoniae* | 5382           | 5475                     | SRR13617274    |
| Iso00221    | 99.0                                   | 94                                       | 5.1                                             | *Escherichia coli*                                        | 132 (Pasteur)  | 11354                    | SRR13617273    |
| Iso00222    | 99.0                                   | 96                                       | 5.1                                             | *Escherichia coli*                                        | 132 (Pasteur)  | 11354                    | SRR13617271    |
| Iso00225    | 99.1                                   | 99                                       | 5.2                                             | *Escherichia coli*                                        | 506 (Pasteur)  | 11355                    | SRR13617270    |
| Iso00229    | 99.6                                   | 109                                      | 6.5                                             | *Pseudomonas aeruginosa*                                  | 270            | 1817                     | SRR13617269    |
| Iso00233    | 97.8                                   | 114                                      | 6.1                                             | *Pseudomonas aeruginosa*                                  | 3227           | 1818                     | SRR13617268    |
| Iso00234    | 99.7                                   | 111                                      | 5.5                                             | *Klebsiella pneumoniae*                                   | 109            | 5476                     | SRR13617267    |
| Iso00236    | 99.7                                   | 112                                      | 6.4                                             | *Pseudomonas aeruginosa*                                  | 266            | 1819                     | SRR13617266    |
| Iso00238    | 98.7                                   | 108                                      | 6.6                                             | *Pseudomonas aeruginosa*                                  | 3589           | 1820                     | SRR13617265    |
| Iso00240    | 98.9                                   | 112                                      | 5.4                                             | *Klebsiella pneumoniae*                                   | 5383           | 5477                     | SRR13617264    |
| Iso00242    | 98.9                                   | 111                                      | 6.4                                             | *Pseudomonas aeruginosa*                                  | 3590           | 1821                     | SRR13617263    |
| Iso00243    | 98.9                                   | 111                                      | 6.4                                             | *Pseudomonas aeruginosa*                                  | 3590           | 1821                     | SRR13617262    |
| Iso00245    | 99.3                                   | 107                                      | 4.8                                             | *Escherichia coli*                                         | 2 (Pasteur)    | 11356                    | SRR13617260    |
| Iso00248    | 97.2                                   | 108                                      | 5.5                                             | *Klebsiella quasivariicola*                               | 5384           | 5478                     | SRR13617259    |
| Iso00252    | 99.6                                   | 112                                      | 5.3                                             | *Klebsiella pneumoniae*                                   | 607            | 5479                     | SRR13617258    |
| Iso00267    | 99.6                                   | 103                                      | 5.7                                             | *Klebsiella pneumoniae*                                   | 36             | 5480                     | SRR13617257    |
| Iso00270    | 99.2                                   | 100                                      | 4.9                                             | *Escherichia coli*                                         | 2 (Pasteur)    | 11358                    | SRR13617256    |
| Iso00272    | 99.5                                   | 109                                      | 6.5                                             | *Pseudomonas aeruginosa*                                  | 2033           | 1822                     | SRR13617255    |
| Iso00274    | 99.4                                   | 109                                      | 6.5                                             | *Pseudomonas aeruginosa*                                  | 2033           | 1822                     | SRR13617254    |
| Iso00277    | 99.4                                   | 109                                      | 6.5                                             | *Klebsiella pneumoniae*                                   | 530            | 5481                     | SRR13617253    |
| Iso00278    | 99.6                                   | 110                                      | 6.5                                             | *Pseudomonas aeruginosa*                                  | 988            | 1823                     | SRR13617252    |
| Iso00279    | 99.7                                   | 111                                      | 5.5                                             | *Klebsiella pneumoniae*                                   | 5385           | 5482                     | SRR13617251    |
| Iso00282    | 99.3                                   | 108                                      | 6.6                                             | *Pseudomonas aeruginosa*                                  | 554            | 1824                     | SRR13617249    |
| Iso00285    | 99.3                                   | 109                                      | 6.5                                             | *Pseudomonas aeruginosa*                                  | 554            | 1824                     | SRR13617248    |
Table A11. Cont.

| Sample ID  | Percentage of Good Targets (SeqSphere+) | Average Coverage (Assembled) (SeqSphere+) | Approximated Genome Size (Megabases) (SeqSphere+) | Species (Kraken2) | Sequence Type | Complex Type (SeqSphere+) | SRA Accession |
|------------|----------------------------------------|-------------------------------------------|---------------------------------------------------|------------------|---------------|---------------------------|---------------|
| Iso00289   | 99.6                                   | 112                                       | 6.3                                               | *Pseudomonas aeruginosa* | 1485          | 1825                      | SRR13617247   |
| Iso00290   | 99.7                                   | 113                                       | 6.3                                               | *Pseudomonas aeruginosa* | 1485          | 1825                      | SRR13617246   |
| Iso00296   | 99.7                                   | 106                                       | 6.7                                               | *Pseudomonas aeruginosa* | 235           | 1826                      | SRR13617245   |
| Iso00298   | 97.8                                   | 116                                       | 6.1                                               | *Pseudomonas aeruginosa* | 3227          | 1818                      | SRR13617244   |
| Iso00299   | 99.3                                   | 108                                       | 4.6                                               | *Escherichia coli*     | 1018 (Pasteur)| 11357                     | SRR13617243   |
| Iso00301   | 98.6                                   | 112                                       | 6.3                                               | *Pseudomonas aeruginosa* | 3593          | 1827                      | SRR13617242   |
| Iso00302   | 99.6                                   | 113                                       | 6.3                                               | *Pseudomonas aeruginosa* | 1755          | 1828                      | SRR13617241   |
| Iso00309   | 98.6                                   | 109                                       | 6.5                                               | *Pseudomonas aeruginosa* | 3592          | 1829                      | SRR13617240   |
| Iso00310   | 99.3                                   | 105                                       | 6.8                                               | *Pseudomonas aeruginosa* | 532           | 1830                      | SRR13617238   |
| Iso00312   | 99.4                                   | 106                                       | 6.7                                               | *Pseudomonas aeruginosa* | 381           | 1791                      | SRR13617237   |
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