**Supplementary Material 1.** Oligonucleotide sequences and conditions used in this study.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Product** | **Secuence (5’-3’)** | **Size (bp)** | **Tm°C** | **Ref** |
| ERIC | ATGTAAGCTCCTGGGGGGATTCAC | Variable | 50 | (Versalovic et al., 1991) |
| AAGTAAGTGACTGGGGGGTGAGCG |
| ybbW | TGATTGGCAAAATCTGGCCG | 670 | 60 | (Carreón, 2019; Walker et al., 2017) |
| ATACTGGCAATCAGTACGCC |
| PAI III536a | F: CGGGCATGCATCAATTATCTTTG | 200 | 55 | (Sabate et al., 2006) |
| R: TGTGTAGATGCAGTCACTCCG |
| PAI IV536a | F: AAGGATTCGCTGTTACCGGAC | 300 |
| R: TCGTCGGGCAGCGTTTCTTCT |
| PAI IICFT073a | F: ATGGATGTTGTATCGCGC | 420 |
| R: ACGAGCATGTGGATCTGC |
| PAI I536a | F: TAATGCCGGAGATTCATTGTC | 1,800 |
| R: AGGATTTGTCTCAGGGCTTT |
| PAI II536a | F: CATGTCCAAAGCTCGAGCC | 1,000 |
| R: CTACGTCAGGCTGGCTTTG |
| PAI IJ96a | F: TCGTGCTCAGGTCCGGAATTT | 400 |
| R: TGGCATCCCACATTATCG |
| PAI IIJ96a | F: GGATCCATGAAAACATGGTTAATGGG | 2,300 |
| R: GATATTTTTGTTGCCATTGGTTACC |
| PAI ICFT073a | F: GGACATCCTGTTACAGCGCGCA | 925 |
| R: TCGCCACCAATCACAGCGAAC |
| *bla*CTX-M-1 y 8b | F: TGTGCAGYACCAGTAARGYKATG | 583 | 55ºC | (Arlet, 1991; Garza-González et al., 2021) |
| R: TARRTSACCAGAAYVAGCGGC |
| *bla*CTX-M-2b | F: CGAGTGGCAGTACCAGTAAGG | 540 |
| R: CGATATCGTTGGTGGTGC |
| *bla*CTX-M-9b | F: ATGGTGACAAAGAGAGTGCAA | 747 |
| R: AATATCATTGGTGGTGCCGTAG |
| *bla*CTX-M-15b | F: GCGGCCATGATAGGTACG | 786 |
| R: AAAGTAAGTCACAATAACCAGCG |
| *bla*TEMb | F: CAACATTTTCGTGTCGCCC | 844 |
| R: GCTTAATCAGTGAGGCACC |
| *bla*SHVb | F: TATTATCTCCCTGTTAGCCA | 783 | 58ºC |
| R: CGCTCTGCTTTGTTATTC |
| *qepA*b | F: GCAGGTCCAGCAGCGGGTAG | 617 | 60ºC | (Skočková et al., 2015; Wang et al., 2008) |
| R: CAACTGCTTGAGCCCGTAG |
| *qnrB*b | F: GATCGTGAAAGCCAGAAAGG | 482 | 53ºC |
| R: ACGATGCCTGGTAGTTGTCC |
| aac(6')-Ib-crb | F: TTGCGATGCTCTATGAGTGGCTA | 469 | 54ºC |
| R: CTCGAATGCCTGGCGTGTTT |
| *daaE*c | F: TGACTGTGACCGAAGAGTGC | 380 | 48°C | (Mansan-Almeida et al., 2013) |
| R: TTAGTTCGTCCAGTAACCCCC |
| *pEAE*c | F: CAGGGTAAAAGAAAGATGATAA | 1,087 | 58°C | (Alikhani et al., 2006) |
| R: TATGGGGACCATGTATTATCA |
| *bfpA*c | F: AATGGTGCTTGCGCTTGCTGC | 326 | 60°C | (Beutin et al., 2003) |
| R: GCCGCTTTATCCAACCTGGTA |
| EAECc | F: CTGGCGAAAGACTGTATCAT | 630 | (Schmidt et al., 1995) |
| R: CAATGTATAGAAATCGCTGTT |
| ST73d | F: TGGTTTTACCATTTTGTCGGA | 490pb | 60ºC | (Doumith et al., 2015) |
| R: GGAAATCGTTGATGTTGGCT |
| ST131d | F: GACTGCATTTCGTCGCCATA | 310pb |
| R: CCGGCGGCATCATAATGAAA |
| ST95d | F: ACTAATCAGGATGGCGAGAC | 200pb |
| R: ATCACGCCCATTAATCCAGT |
| ST69d | F: ATCTGGAGGCAACAAGCATA | 104pb |
| R: AGAGAAAGGGCGTTCAGAAT |

Implementedprimers for: **a:** Pathogenicity islands; **b:** Antibiotic Resistance; **c:** Pathotypes; **d:** Sequence types.

**Supplementary Material 2.** Previously Reported Resistance Profiles of Analyzed Clinical Isolates

|  |  |
| --- | --- |
| **ID** | **Resistant Profile** |
| 8, 9 | - |
| 37 | AMC, AMS |
| 21 | AMK, CFZ, CTX, CRO, AMC, AMS |
| 14 | AMK, CIP, CTX, CRO |
| 19 | AMK, CTX, AMC |
| 4 | AMK, GM |
| 7 | AMK, GM, AMC, MEM |
| 22 | AMK, GM, CFZ, CTX |
| 28 | AMK, GM, CFZ, CTX, CRO, AMC, AMS |
| 39 | AMK, GM, CIP, NOR, CFZ, CTX, CRO, AMC, AMS, IMP |
| 27 | AMK, GM, CIP, NOR, LVX, CX, CFZ, CTX, CRO, ATM, AMC, MEM |
| 32, 34 | AMK, GM, CIP, NOR, LVX, CFZ, CTX, CRO, AMC, AMS |
| 29 | AMK, GM, CIP, NOR, LVX, CFZ, CTX, CRO, ATM, AMC |
| 1 | AMK, GM, CIP, NOR, LVX, CTX, AMC, AMS |
| 35 | AMK, GM, CIP, NOR, LVX, CX, CFZ, CTX, CRO, AMC, IMP |
| 36 | AMK, GM, CIP, NOR, LVX, CX, CFZ, CTX, CRO, ATM, AMC |
| 17 | AMK, GM, CTX |
| 12, 26 | AMK, GM, CFZ, AMC, AMS |
| 23, 25 | AMK, GM, CTX, CRO, AMC |
| 3 | AMK, GM, CTX, CRO, AMC, AMS |
| 20 | AMK, GM, CTX, CRO, ATM, AMC |
| 33 | AMK, GM, CTX, CRO, ATM, AMC, AMS |
| 24 | AMK, GM, CX, CFZ, CTX, CRO, AMC |
| 30 | CFZ, CTX, AMC, AMS |
| 40 | CIP, NOR, LVX, CFZ, CTX, CRO, FEP, ATM, AMC, AMS, IMP |
| 18 | CTX, AMC, AMS |
| 13 | CTX, ATM |
| 5 | CX, CFZ, CTX, CRO, FEP, ATM, AMC, AMS |
| 10 | GM, CFZ, CTX |
| 16 | GM, CFX, CTX, AMC |
| 6 | GM, CIP, NOR, LVX, AMC |
| 11 | GM, CIP, NOR, LVX, CFZ, CTX, AMC |
| 2 | GM, CIP, NOR, LVX, CFZ, CTX, CRO, FEP, ATM, AMC, AMS |
| 38 | GM, LVX, TSX, AMP, CFX, FEP, ATM, AMC, AMS |
| 31 | GM, CIP, NOR, LVX, CX, CFZ, CTX, CRO, AMC |
| 15 | GM, CTX, AMC |

**AMK:** Amikacin; **GM:** Gentamicin; **CIP:** Ciprofloxacin; **NOR:** Norfloxacin; **LVX:** Levofloxacin; **CX:** Cefoxitin; **CFZ:** Ceftazidime; **CTX:** Cefotaxime; **CRO:** Ceftriaxone; **FEP:** Cefepime; **ATM:** Aztreonam; **AMC:** Amoxicillin-Clavulánic Acid; **AMS:** Ampicillin-Sulbactam; **MEM:** Meropenem; **IMP:** Imipenem; **ETP:** Ertapenem.

**Supplementary Material 3 A**. Correlation between antibiotic resistance phenotypes and genotypes.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Variable** | | **AMK** | **GM** | **CIP** | **NOR** | **LVX** | ***qepA*** | ***qnrB*** | ***aac(6')-Ib*** | **ESBLCTX** | **ESBLCFZ** | **ESBLCRO** | **ESBLFEP** | **ESBLATM** |
| 1. AMK | *r* | — |  |  |  |  |  |  |  |  |  |  |  |  |
| *p* | — |  |  |  |  |  |  |  |  |  |  |  |  |
| 2. GM | *r* | 0.9916 | — |  |  |  |  |  |  |  |  |  |  |  |
| *p* | < .001 | — |  |  |  |  |  |  |  |  |  |  |  |
| 3. CIP | *r* | 0.9691 | 0.9757 | — |  |  |  |  |  |  |  |  |  |  |
| *P* | < .001 | < .001 | — |  |  |  |  |  |  |  |  |  |  |
| 4. NOR | *r* | 0.9652 | 0.9753 | 0.9972 | — |  |  |  |  |  |  |  |  |  |
| *p* | < .001 | < .001 | < .001 | — |  |  |  |  |  |  |  |  |  |
| 5. LVX | *r* | 0.9618 | 0.9753 | 0.9916 | 0.994 | — |  |  |  |  |  |  |  |  |
| *p* | < .001 | < .001 | < .001 | < .001 | — |  |  |  |  |  |  |  |  |
| 6. *qepA* | *r* | 0.9491 | 0.9632 | 0.9784 | 0.9807 | 0.9884 | — |  |  |  |  |  |  |  |
| *p* | < .001 | < .001 | < .001 | < .001 | < .001 | — |  |  |  |  |  |  |  |
| 7. *qnrB* | *r* | 0.9557 | 0.9575 | 0.9802 | 0.9744 | 0.9744 | 0.9614 | — |  |  |  |  |  |  |
| *p* | < .001 | < .001 | < .001 | < .001 | < .001 | < .001 | — |  |  |  |  |  |  |
| 8. *aac(6')-Ib* | *r* | 0.9691 | 0.9757 | 1 | 0.9972 | 0.9916 | 0.9784 | 0.9802 | — |  |  |  |  |  |
|  | *p* | < .001 | < .001 | < .001 | < .001 | < .001 | < .001 | < .001 | — |  |  |  |  |  |
| 9. ESBLCTX | *r* | 0.9758 | 0.9809 | 0.9669 | 0.9624 | 0.9582 | 0.9438 | 0.9469 | 0.9669 | — |  |  |  |  |
|  | *p* | < .001 | < .001 | < .001 | < .001 | < .001 | < .001 | < .001 | < .001 | — |  |  |  |  |
| 10. ESBLCFZ | *r* | 0.948 | 0.9461 | 0.9379 | 0.938 | 0.938 | 0.9139 | 0.9252 | 0.9379 | 0.9575 | — |  |  |  |
|  | *p* | < .001 | < .001 | < .001 | < .001 | < .001 | < .001 | < .001 | < .001 | < .001 | — |  |  |  |
| 11. ESBLCRO | *r* | 0.9604 | 0.9575 | 0.9483 | 0.9487 | 0.9401 | 0.9173 | 0.9269 | 0.9483 | 0.9588 | 0.966 | — |  |  |
|  | *p* | < .001 | < .001 | < .001 | < .001 | < .001 | < .001 | < .001 | < .001 | < .001 | < .001 | — |  |  |
| 12. ESBLFEP | *r* | 0.8489 | 0.871 | 0.8681 | 0.8694 | 0.89 | 0.8404 | 0.8391 | 0.8681 | 0.864 | 0.8746 | 0.8779 | — |  |
|  | *p* | < .001 | < .001 | < .001 | < .001 | < .001 | < .001 | < .001 | < .001 | < .001 | < .001 | < .001 | — |  |
| 13. ESBLATM | *r* | 0.919 | 0.9304 | 0.9194 | 0.9195 | 0.9321 | 0.9039 | 0.8847 | 0.9194 | 0.9365 | 0.9008 | 0.9203 | 0.93 | — |
|  | *p* | < .001 | < .001 | < .001 | < .001 | < .001 | < .001 | < .001 | < .001 | < .001 | < .001 | < .001 | < .001 | — |

**R:** Resistance phenotype; **AMK:** Amikacin; **GM:** Gentamicin; **CIP:** Ciprofloxacin; **NOR:** Norfloxacin; **LVX:** Levofloxacin; ***qepA*:** Quinolone efflux pump associated gene; ***qnrB*:** Quinolone resistant associated gene; ***aac(6’)-Ib:*** Acetylase associated gene; **ESBL:** ESBL positive phenotype; **CTX:** Cefotaxime; **CFZ:** Ceftazidime; **CRO:** Ceftriaxone; **FEP:** Cefepime; **ATM:** Aztreonam. The *r* and *p* values were obtained by the Pearson correlation test.

|  |  |  |  |
| --- | --- | --- | --- |
| **Feature** | **Isolates with Plasmids**  **%(n= 23)** | **Isolates without Plasmids**  **%(n= 17)** | ***p* value** |
| Pathogenicity Islands | | | |
| PAI III536 | 17.4 (4) | 41.2 (7) | 0.15 |
| PAI IV536 | 52.2 (12) | 53 (9) | 1 |
| PAI IICFT073 | 22 (5) | 53 (9) | 0.06 |
| PAI II536 | 17.4 (4) | 6 (1) | 0.4 |
| PAI IJ96 | 35 (8) | 35.3 (6) | 1 |
| PAI ICFT073 | 26 (6) | 29.4 (5) | 1 |
| PAI I536 | (0) | 12 (2) | 0.2 |
| PAI IIJ96 | 9 (2) | 12 (2) | 1 |
| ESBL Production Phenotypes | | | |
| ESBLCTX | 48 (11) | 35 (8) | 1 |
| ESBLCFZ | 17.4 (4) | 24 (4) | 0.7 |
| ESBLCRO | 17.4 (4) | 29.4 (5) | 0.45 |
| ESBLFEP | 9 (2) | 6 (1) | 1 |
| ESBLATM | 13 (3) | 18 (3) | 1 |
| Carbapenemase Production Phenotypes | | | |
| CARMEM | 9 (2) | 6 (1) | 1 |
| CARIMP | 9 (2) | (0) | 0.5 |
| ESBL Associated Genes | | | |
| *bla*CTX-M 1 y 8 | 48 (11) | 41.2 (7) | 0.75 |
| *bla*CTX-M-9 | 17.4 (4) | 12 (2) | 1 |
| *bla*TEM | 39.1(9) | 41.2 (7) | 1 |
| *bla*CTX-M-2 | 35 (8) | 53 (9) | 0.33 |
| *bla*CTX-M-15 | 4.3 (1) | 12 (2) | 0.6 |
| Fluoroquinolones and Aminoglycosides Resistance Genes | | | |
| *qepA* | 30.4 (7) | 18 (3) | 0.5 |
| *aac(6')-Ib* | 45 (10) | 24 (4) | 0.31 |
| *qnrB* | 30.4 (7) | 12 (2) | 0.26 |
| Sequence Types | | | |
| ST73 | 4.3 (1) | (0) | 1 |
| ST131 | 70 (16) | 35 (8) | 0.2 |
| ST69 | 9 (2) | 18 (3) | 0.6 |
| Antibiotic Resistance Phenotypes | | | |
| AMK | 61 (14) | 59 (10) | 1 |
| GM | 65.2 (15) | 82.3 (14) | 0.3 |
| CIP | 45 (10) | 24 (4) | 0.31 |
| NOR | 39.1 (9) | 24 (4) | 0.33 |
| LVX | 39.1 (9) | 24 (4) | 0.33 |
| CX | 17.4 (4) | 12 (2) | 1 |
| CFZ | 48 (11) | 41.2 (7) | 0.75 |
| CTX | 83 (19) | 82.3 (14) | 1 |
| CRO | 45 (10) | 59 (10) | 0.52 |
| FEP | 9 (2) | 12 (2) | 1 |
| ATM | 26 (6) | 24 (4) | 1 |
| AMC | 74 (17) | 88.2 (15) | 0.42 |
| AMS | 45 (10) | 41.2 (7) | 1 |
| MEM | 4.3 (1) | 6 (1) | 1 |
| IMP | 13 (3) | (0) | 0.25 |

**Supplementary Material 3 B.** Statistical Analysis for Association Between Plasmids Presence and Virulence or Resistance Evaluated Features

*p* values were obtained by Fisher Exact Test.

**Supplementary Material 3 C.** Statistical Analysis for Correlation Between Plasmid Sizes and Resistance or Virulence Features

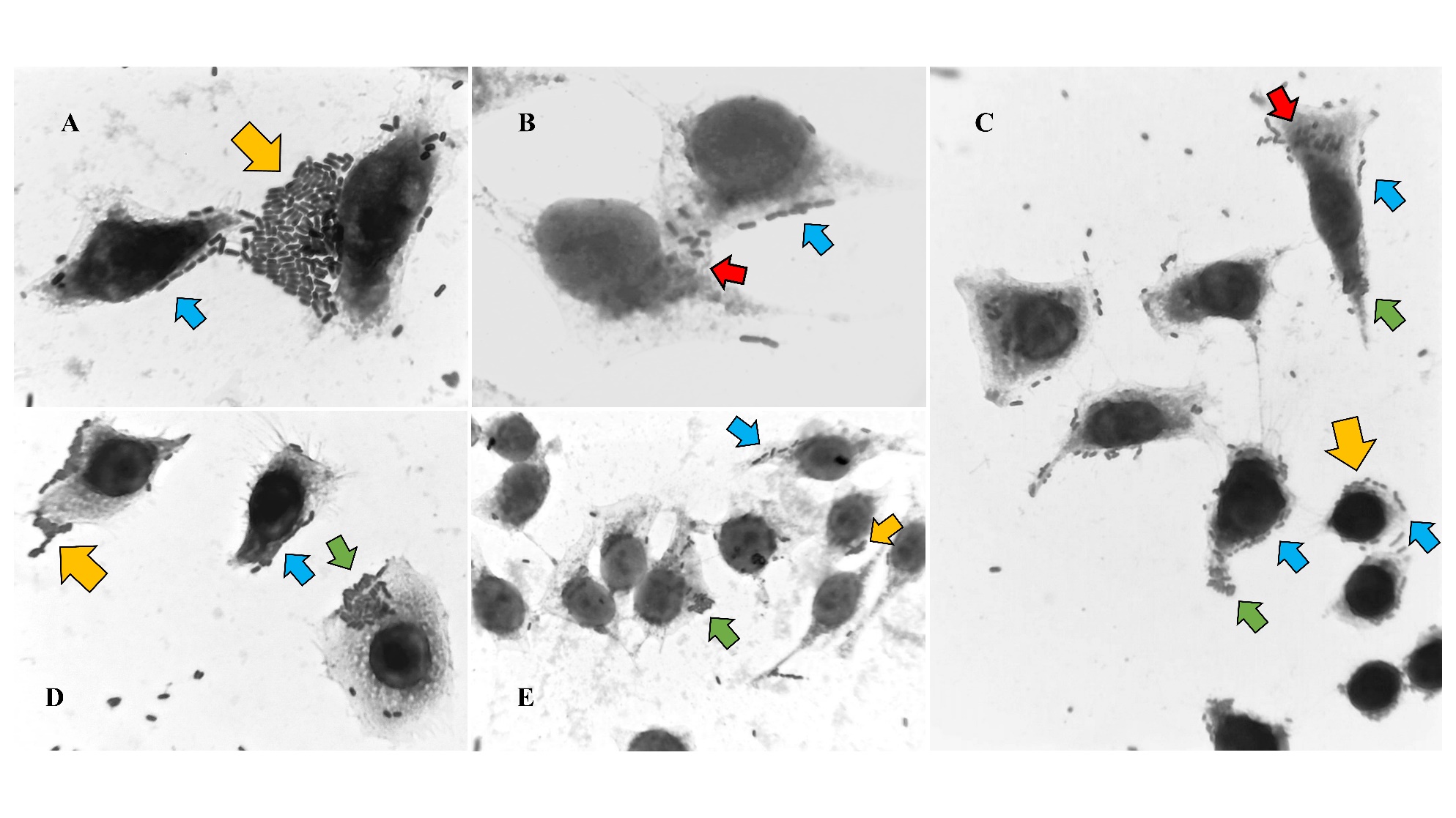
|  |  |  |  |
| --- | --- | --- | --- |
| **Size (kb)** | **Feature** | ***r* value** | ***p* value** |
| 1-5 kb | CIP | 0.3355 | 0.0343 |
| AMC | -0.3851 | 0.0141 |
| *aac(6')-Ib* | 0.3355 | 0.0343 |
| *qnrB* | 0.3236 | 0.0417 |
| 6-10 kb | CIP | 0.368 | 0.0195 |
| *aac(6')-Ib* | 0.368 | 0.0195 |
| *qnrB* | 0.357 | 0.0237 |
| 21-30 kb | CTX | -0.4981 | 0.0011 |
| AMC | -0.4588 | 0.0029 |
| 51-100 kb | FEP | 0.378 | 0.0162 |
| 101-120 kb | LVX | 0.3306 | 0.0372 |
| FEP | 0.6882 | < .001 |
| ATM | 0.3974 | 0.0111 |
| IMP | 0.3702 | 0.0187 |
| ESBLFEP | 0.3691 | 0.0207 |
| ESBLATM | 0.5461 | < .001 |
| *qepA* | 0.3974 | 0.0111 |

The *r* and *p* values were obtained by Pearson Correlation Test. Only significant results are shown.

**Supplementary Material 4.** Virulence genes, PAI profiles, DEC genes and adherence patterns of UPEC clinical isolates.

|  |  |  |  |
| --- | --- | --- | --- |
| ID | Virulence Genes/PAI Profiles | DEC Genes | Adherence Profile |
| 1 | *fimH, papG-II, sat, hlyA, traT, iroN, fyuA,I ha,feoB,*  PAI II536, PAI III536, PAI IV536, PAI ICFT073, PAI IICFT073 | pCVD432, *eaeA, daaE, bfpA* | Lo/Bs |
| 2 | *fimH,fliCD,hlyA,iucD,iutA,feoB,*  PAI II536, PAI III536, PAI IV536, PAI ICFT073, PAI IICFT073 | pCVD432, *bfpA* | Bs/Di |
| 3 | *fimH, papG-II, fliCD,sat,vat,traT,agn43,iroN,iucD,fyuA,iha,feoB* | pCVD432, *bfpA* | Bs/Lo/Ag |
| 4 | *fimH, papG-II, fliCD, sat, vat,traT,agn43,iroN,fyuA,iha,feoB,*  PAI III536, PAI IV536, PAI IJ96 | *pCVD432, bfpA* | Bs/Lo |
| 5 | *fimH,fliCD,sat,kpsM,traT,iucD,feoB,*  PAI III536, PAI IV536, PAI IICFT073 | *daaE, bfpA* | Ag |
| 6 | *fimH, fliCD, sat, vat,traT,agn43,iucD,fyuA,iha,feoB,*  PAI III536, PAI IV536, PAI IICFT073 | *daaE, bfpA* | Lo/Ag/Bs |
| 7 | *fimH,agn43,iutA* | pCVD432, *bfpA* | Bs |
| 8 | *fimH,fliCD,hlyA,kpsM,traT,feoB,*  PAI III536, PAI IIJ96, PAI ICFT073 | *-* | Bs/Lo |
| 9 | *papC,fimH,sfaD/focC,papG-II, fliCD,kpsM,vat,cnf1,iroN,iucD,fyuA,feoB*  PAI IJ96, PAIIJ96, PAI ICFT073 | *daaE, bfpA* | Bs/Ag |
| 10 | *fimH,papG-II,fliCD,vat,traT,iroN,fyuAfeoB,*  PAI IV536, PAI IJ96 | *bfpA* | Bs/Lo |
| 11 | *fimH,sat,hlyA,kpsM,cnf-1,agn43,iucD,feoB,*  PAI IV536 | *daaE, bfpA* | Bs |
| 12 | *papC,fimH,papG-II,sat,cnf-1, traT,agn43,iroN,iucD,fyuA,iha,feoB,*  PAI III536, PAI IV536 | - | Lo |
| 13 | *fimH, papG-II, fliCD, traT, feoB* | *bfpA* | Lo/Ag |
| 14 | *fimH,kpsM,iucD,feoB,*  PAI II536 | *bfpA* | Bs |
| 15 | *fimH, fliCD, cnf-1, traT,agn43,iucD,iha,feoB,*  PAI II536 | - | Bs |
| 16 | *fimH,fliCD,hlyA,iucD,iha,iutA,feoB* | *bfpA* | Bs/Lo |
| 17 | *fimH,papG-II,fliCD,hlyA,iucD,fyuA,iha,feoB* | *bfpA* | Bs |
| 18 | *fimH,papG-II,fliCD,iroN,fyuA,iutA,feoB* | *bfpA* | Bs |
| 19 | *fimH, fliCD, sat, iroN, iucD, fyuA, feoB,*  PAI IJ96, PAI ICFT073 | - | Bs/Lo/Ag |
| 20 | *fimH,papG-II,fliCD,hlyA,traT,feoB,*  PAI III536, PAI IICFT073 | *bfpA* | Bs/Lo/Di/ Ag |

**ID:** Isolate; **PAI:** Pathogenicity islands; **Bs:** Bricks pattern; **Lo:** Localized pattern; **Di:** Diffuse pattern; **Ag:** Aggregative pattern**. *fimH*:** Type 1 pilus Adhesin; ***sfaD/focC*:** S and Dra fimbriae; ***papC*:** Type P pilus chaperone; ***papG-II*:** Type P pilus Adhesin allele 2; ***fliCD*:** Flagellin subunit/flagellar cap; ***hlyA*:** α-hemolysin; ***kpsM*:** Capsular variant; ***sat*:** Autotransporter secreted toxin; ***agn43*:** Antigen 43; vat: Vacuolating autotransporter toxin; ***cnf-1*:** Necrotizing cytotoxic factor; ***traT*:** Complement resistance associated protein; ***fyuA*:** Ferric yersiniabactin uptake receptor; ***iucD*:** Aerobactin; ***iroN*:** Salmocheline receptor; ***iutA*:** Aerobactin receptor; ***feoB*:** Ferrous iron transporter; ***iha*:** IrgA homologue Adhesin/enterobactin receptor.



**Supplementary Material 5**. Mixed adherence pattern in clinical isolates of E. coli. **A)** Ec-9, shown a mixed aggregative and stacked-brick patterns; **B)** Ec-2, shown a mixed diffuse adherence and stacked-brick patterns; **C)** Ec-16, shown a mixed aggregative, diffuse adherence, and stacked-brick patterns; D) Ec-16, shown an aggregative, localized, and steacked-brick patterns; E) Ec-19, shown an aggregative, localized, and sticked-brick patterns. Yellow arrow indicated an aggregative pattern; Blue arrows are for steacked-breack pattern; Green arrows shown the localized pattern; Red arrows, indicated the diffuse adherence pattern.