

Table S1. The Oligonucleotide primers used in this study

| PCR method | Primer name | Primer sequences(5'→3') | Reference | |
|-----------------------------|-------------|--------------------------|------------------------|-----|
| ERIC-PCR | ERIC1R | ATGTAAGCTCCTGGGGATTAC | (1) | |
| | ERIC2 | AAGTAAGTGACTGGGGTGAGCG | (1) | |
| detection of ESBL genes | CTX-M-1-F | GCTGTTGTTAGGAAGTGTGC | (2) | |
| | CTX-M-1-R | CCATTGCCCCGAGGTGAAG | (2) | |
| | CTX-M-9-F | GCAGATAATACGCAGGTG | (2) | |
| | CTX-M-9-R | CGGCGTGGTGGTGTCTCT | (2) | |
| phylogenetic classification | chuA.1b | ATGGTACCGGACGAACCAAC | (3) | |
| | chuA.2 | TGCCGCCAGTACCAAAGACA | (4) | |
| | yjaA.1b | CAAACGTGAAGTGTGTCAGGAG | (3) | |
| | yjaA.2b | AATGCGTTCCTCAACCTGTG | (3) | |
| | TspE4C2.1b | CACTATTCGTAAGGTCATCC | (3) | |
| | TspE4C2.2b | AGTTTATCGCTGCGGGTCGC | (3) | |
| | AceK.f | AACGCTATTCGCCAGCTTGC | (3) | |
| | ArpA1.r | TCTCCCCATACCGTACGCTA | (5) | |
| | ArpAgpE.f | GATTCCATCTTGTCAAAATATGCC | (6) | |
| | ArpAgpE.r | GAAAAGAAAAAGAATTCCCAAGAG | (6) | |
| | trpAgpC.1 | AGTTTTATGCCCAGTGCGAG | (6) | |
| | trpAgpC.2 | TCTGCGCCGGTCACGCCC | (6) | |
| | trpBA.f | CGGCGATAAAGACATCTTCAC | (7) | |
| | trpBA.r | GCAACGCGGCCTGGCGGAAG | (7) | |
| | MLST-PCR | ST73_for | TGGTTTTACCATTTTGTGCGGA | (8) |
| | | ST73_rev | GGAAATCGTTGATGTTGGCT | (8) |
| | | ST131_for | GACTGCATTTTCGTCGCCATA | (8) |
| | | ST131_rev | CCGGCGGCATCATAATGAAA | (8) |
| | | ST95_for | ACTAATCAGGATGGCGAGAC | (8) |
| ST95_rev | | ATCACGCCCATTAATCCAGT | (8) | |
| ST69_for | | ATCTGGAGGCAACAAGCATA | (8) | |
| ST69_rev | | AGAGAAAGGGCGTTCAGAAT | (8) | |
| adk_F | | ATTCTGCTTGGCGCTCCGGG | (9) | |
| adk_R | | CCGTCAACTTTCGCGTATTT | (9) | |
| fumC_F | | TCACAGGTCGCCAGCGCTTC | (9) | |
| fumC_R | | GTACGCAGCGAAAAAGATTC | (9) | |
| gyrB_F | | TCGGCGACACGGATGACGGC | (9) | |

| | | | |
|------------------|---------|-------------------------------|------|
| | gyrB_R | ATCAGGCCTTCACGCGCATC | (9) |
| | icd_F | ATGGAAAGTAAAGTAGTTGTTCCGGCACA | (9) |
| | icd_R | GGACGCAGCAGGATCTGTT | (9) |
| | mdh_F1 | AGCGCGTTCTGTTCAAATGC | (9) |
| | mdh_R1 | CAGGTTCAGAACTCTCTCTGT | (9) |
| | purA_F1 | TCGGTAACGGTGTGTGCTG | (9) |
| | purA_R | CATACGGTAAGCCACGCAGA | (9) |
| | recA_F | CGCATTGCTTTACCCTGACC | (9) |
| | recA_R | TCGTCGAAATCTACGGACCGGA | (9) |
| VF determination | afa1 | GCTGGGCAGCAAACCTGATAATCTC | (10) |
| | afa2 | CATCAAGCTGTTTGTTCGTCCGCCG | (10) |
| | fimH_F | TGCAGAACGGATAAGCCGTGG | (11) |
| | fimH_R | GCAGTCACCTGCCCTCCGGTA | (11) |
| | sfa1 | CTCCGGAGAACTGGGTGCATCTTAC | (10) |
| | sfa2 | CGGAGGAGTAATTACAAACCTGGCA | (10) |
| | pap1 | GACGGCTGTACTGCAGGGTGTGGCG | (10) |
| | pap2 | ATATCCTTTCTGCAGGGATGCAATA | (10) |
| | papG2_F | GGGATGAGCGGGCCTTTGAT | (12) |
| | papG2_R | CGGGCCCCCAAGTAACTCG | (12) |
| | iha_F | CTGGCGGAGGCTCTGAGATCA | (13) |
| | iha_R | TCCTTAAGCTCCCGCGGCTGA | (13) |
| | Aer1 | TACCGGATTGTCATATGCAGACCGT | (14) |
| | Aer2 | AATATCTTCCCTCCAGTCCGGAGAAG | (14) |
| | AerJ_F | GGCTGGACATCATGGGAACTGG | (15) |
| | AerJ_R | CGTCGGGAACGGGTAGAATCG | (15) |
| | fyuA_F | TGATTAACCCCGCGACGGGAA | (11) |
| | fyuA_R | CGCAGTAGGCACGATGTTGTA | (16) |
| | iroN_F | AAGTCAAAGCAGGGGTTGCCCG | (17) |
| | iroN_R | GACGCCGACATTAAGACGCAG | (17) |
| | cnf1 | AAGATGGAGTTICCTA'IGCAGGAG | (14) |
| | cnf2 | CATTCAGAGTCCCTGCCCTCATTATT | (14) |
| | sat_F | GTTGTCTCTGGCTGTTGC | (18) |
| | sat_R | AATGATGTTCCCTCCAGAGC | (18) |
| | hly_F | AACAAGGATAAGCACTGTTCTGGCT | (14) |
| | hly_R | ACCATATAAGCGGTCATTCCCGTCA | (14) |

| | | |
|-----------|------------------------------|------|
| kpsMTII_F | GCGCATTTGCTGATACTGTTG | (11) |
| kpsMTII_R | CATCCAGACGATAAGCATGAGCA | (11) |
| usp_N6 | ATGCTACTGTTTTCCGGGTAGTGTGT | (19) |
| usp_N7 | CATCATGTAGTCGGGGCGTAACAAT | (19) |
| ibe10_F | AGGCAGGTGTGCGCCGCGTAC | (20) |
| ibe10_R | TGGTGCTCCGGCAAACCATGC | (11) |
| TraT_F | GGTGTGGTGCATGAGCACAG | (11) |
| TraT_R | CACGGTTCAGCCATCCCTGAG | (11) |
| CoIV-C_F | CACACACAAACGGGAGCTGTT | (11) |
| CoIV-C_R | CTTCCCGCAGCATAGTTCCAT | (11) |
| ompT_F | TCATCCCGGAAGCCTCCCTCACTACTAT | (21) |
| ompT_R | TAGCGTTTGCTGCACTGGCTTCTGATAC | (21) |
| TcpC_F | GGCAACAATATGTATAATATCCT | (22) |
| TcpC_R | GCCCAGTCTATTTCTGCTAAAGA | (22) |

ERIC-PCR: enterobacterial repetitive intergenic consensus polymerase chain reaction, ESBL: extended-spectrum β -lactamase, VF: virulence factor, MLST: multilocus sequence typing

Table S2: Distribution of STs, phylogenetic group, biofilm formation ability, and possession of ESBL gene of each genetically identical *E. coli* strain

| Isolate Number | ST | phylogenetic group | biofilm formation(LB) | biofilm formation(BHI) | possession of ESBL gene |
|----------------|--------|--------------------|-----------------------|------------------------|-------------------------|
| 1 | ST457 | F | - | - | - |
| 2 | ST569 | B2 | - | - | - |
| 3 | ST362 | E | - | - | - |
| 4 | ST1193 | B2 | + | - | - |
| 5 | ST73 | B2 | + | - | - |
| 6 | ST131 | B2 | - | + | CTX M-9 |
| 7 | ST95 | B2 | + | - | - |
| 8 | ST83 | B2 | - | - | - |
| 9 | ST95 | B2 | - | - | - |
| 10 | ST131 | B2 | + | - | CTX M-1 |
| 11 | ST73 | B2 | + | - | - |
| 12 | ST357 | B2 | - | - | - |
| 13 | ST95 | B2 | + | - | - |
| 14 | ST95 | B2 | + | - | - |
| 15 | ST131 | B2 | + | + | - |
| 16 | ST95 | B2 | - | - | - |
| 17 | ST73 | B2 | - | - | - |
| 18 | ST1193 | B2 | - | - | CTX M-9 |
| 19 | ST73 | B2 | - | - | - |
| 20 | ST131 | B2 | - | - | - |
| 21 | ST131 | B2 | - | - | - |
| 22 | ST73 | B2 | + | - | - |
| 23 | ST131 | B2 | - | + | - |
| 24 | ST6769 | E | - | - | - |
| 25 | ST95 | B2 | + | + | - |
| 26 | ST131 | B2 | - | - | - |
| 27 | new ST | B2 | + | - | - |
| 28 | ST1193 | B2 | - | - | - |
| 29 | ST131 | B2 | - | - | - |
| 30 | ST131 | B2 | + | + | - |
| 31 | ST95 | B2 | + | - | - |
| 32 | ST131 | B2 | - | - | CTX M-1 |
| 33 | ST95 | B2 | + | - | - |
| 34 | ST70 | B2 | - | + | - |
| 35 | ST131 | B2 | + | + | CTX M-9 |
| 36 | ST131 | B2 | - | + | CTX M-9 |
| 37 | ST131 | B2 | - | - | - |
| 38 | ST131 | B2 | + | + | CTX M-9 |

| | | | | | |
|----|-------|----|---|---|---------|
| 39 | ST405 | E | - | + | CTX M-1 |
| 40 | ST95 | B2 | + | + | - |
| 41 | ST131 | B2 | + | + | CTX M-9 |
| 42 | ST131 | B2 | + | + | CTX M-9 |
| 43 | ST95 | B2 | + | + | - |
| 44 | ST69 | E | - | - | - |
| 45 | ST73 | B2 | + | + | - |
| 46 | ST62 | F | - | - | - |
| 47 | ST73 | B2 | - | + | - |
| 48 | ST131 | B2 | - | - | - |
| 49 | ST131 | B2 | - | + | CTX M-9 |

ST, sequence type, ESBL, extended-spectrum β -lactamase, BHI, brain heart infusion

Table S3: Distribution of STs, phylogenetic group, biofilm formation ability, and possession of ESBL gene of each genetically discordant *E. coli* strain

| Isolate Number | ST | phylogenetic group | biofilm formation (LB) | biofilm formation (BHI) | possession of ESBL gene |
|----------------|--------|--------------------|------------------------|-------------------------|-------------------------|
| 50 | ST357 | B2 | - | - | - |
| 51 | ST88 | A | - | + | - |
| 52 | ST95 | B2 | + | + | - |
| 53 | new ST | E | - | - | - |
| 54 | ST4623 | B1 | - | - | - |
| 55 | ST38 | E | + | - | CTX M-9 |
| 56 | ST453 | B1 | - | - | - |
| 57 | new ST | B1 | - | - | - |
| 58 | new ST | B2 | - | - | - |
| 59 | ST1611 | B1 | - | + | - |
| 60 | ST1193 | B2 | - | - | - |
| 61 | ST648 | F | - | - | - |
| 62 | ST538 | B2 | + | + | CTX M-9 |
| 63 | ST117 | F | - | + | - |
| 64 | ST131 | B2 | - | + | - |
| 65 | ST162 | B1 | - | - | - |
| 66 | ST95 | B2 | + | - | - |
| 67 | ST131 | B2 | - | - | - |
| 68 | ST131 | B2 | + | + | - |
| 69 | ST297 | B1 | - | - | - |
| 70 | ST95 | B2 | + | + | - |

ST, sequence type, ESBL, extended-spectrum β -lactamase, BHI, brain heart infusion

Table S4: Distribution of 20 virulence factor genes and VF scores of each genetically identical *E. coli* strain

| Isolate Number | <i>afaB/C</i> | <i>iucD</i> | <i>CNF1</i> | <i>sfaD/E</i> | <i>papC</i> | <i>fyuA</i> | <i>cvaC</i> | <i>fimH</i> | <i>iutA</i> | <i>ibeA</i> | <i>iha</i> | <i>ompT</i> | <i>KpsMT2</i> | <i>papG2</i> | <i>hlyA</i> | <i>TcpC</i> | <i>usp</i> | <i>iroN</i> | <i>sat</i> | <i>traT</i> | VF score |
|----------------|---------------|-------------|-------------|---------------|-------------|-------------|-------------|-------------|-------------|-------------|------------|-------------|---------------|--------------|-------------|-------------|------------|-------------|------------|-------------|----------|
| 1 | - | + | - | - | + | - | - | + | + | - | - | - | + | - | - | - | - | - | - | + | 6 |
| 2 | - | - | - | - | - | + | - | + | - | + | - | - | + | - | - | - | + | - | - | - | 5 |
| 3 | - | - | - | - | + | - | - | + | - | - | - | + | - | + | - | - | - | + | - | + | 6 |
| 4 | - | + | - | - | - | + | - | + | + | - | + | - | + | - | - | - | + | - | + | - | 8 |
| 5 | - | + | + | + | + | + | - | + | + | - | + | - | - | + | + | + | + | + | + | + | 15 |
| 6 | - | + | - | - | - | + | - | + | + | - | + | - | + | - | - | - | + | - | + | - | 8 |
| 7 | - | - | - | - | + | + | - | + | - | - | - | - | + | + | - | + | + | - | - | + | 8 |
| 8 | - | - | + | + | + | + | + | + | - | + | - | - | + | - | + | - | + | + | - | + | 12 |
| 9 | - | - | - | - | + | + | - | + | - | + | - | - | + | + | - | - | + | - | - | + | 8 |
| 10 | - | + | + | - | + | + | - | + | + | - | + | - | - | + | + | - | + | - | + | + | 12 |
| 11 | - | + | + | + | + | + | - | + | + | - | + | - | + | + | + | + | + | + | + | + | 16 |
| 12 | - | - | - | - | - | + | - | + | - | + | - | - | + | - | - | - | + | - | - | + | 6 |
| 13 | - | - | + | + | + | + | - | + | - | - | - | - | + | - | + | + | + | + | - | + | 11 |
| 14 | - | - | - | - | + | + | - | + | - | + | - | - | + | + | - | - | + | - | - | + | 8 |
| 15 | - | + | - | - | - | + | - | + | + | - | + | - | - | - | - | - | + | - | + | + | 8 |
| 16 | - | - | + | + | + | + | - | + | - | - | - | - | - | - | + | - | + | + | - | - | 8 |
| 17 | - | + | + | - | + | + | - | + | + | - | + | - | + | + | + | + | + | - | + | + | 14 |
| 18 | - | + | - | - | - | + | - | + | + | - | + | - | + | - | - | - | + | - | + | - | 8 |
| 19 | - | - | - | - | - | + | - | + | - | + | - | - | + | - | - | - | + | - | - | - | 5 |
| 20 | - | + | - | - | - | + | - | + | + | - | + | - | + | - | - | - | + | - | + | + | 9 |
| 21 | - | + | - | - | - | + | - | + | + | - | + | - | - | - | - | - | + | - | + | + | 8 |
| 22 | - | + | + | + | + | + | - | + | + | - | + | - | + | + | + | + | + | + | + | + | 16 |
| 23 | + | + | - | - | - | + | - | + | + | - | + | - | + | - | - | - | + | - | + | + | 10 |
| 24 | - | + | - | - | - | - | - | + | + | - | - | - | + | - | - | - | - | - | - | + | 5 |
| 25 | - | - | - | - | + | + | + | + | - | - | - | + | + | + | - | - | + | + | - | + | 10 |
| 26 | - | + | - | - | - | + | - | + | + | - | + | - | + | - | - | - | + | - | + | - | 8 |

| | | | | | | | | | | | | | | | | | | | | | |
|----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|----|
| 27 | - | - | - | - | - | + | - | + | - | + | - | - | + | - | - | - | + | + | - | + | 7 |
| 28 | - | + | - | - | - | + | - | + | + | - | + | - | + | - | - | - | + | - | + | - | 8 |
| 29 | - | + | - | - | - | + | - | + | + | - | + | - | + | - | - | - | + | - | + | - | 8 |
| 30 | - | - | - | - | - | + | - | + | - | - | + | - | - | - | - | - | + | - | - | + | 5 |
| 31 | - | - | - | - | + | + | - | + | - | - | - | - | + | + | - | + | + | - | - | + | 8 |
| 32 | + | + | - | - | - | + | - | + | + | - | + | - | + | - | - | - | + | - | + | + | 10 |
| 33 | - | - | - | - | + | + | - | + | - | + | - | - | + | + | - | - | + | - | - | + | 7 |
| 34 | - | - | - | - | - | + | - | + | - | - | - | - | - | - | - | - | - | - | - | + | 3 |
| 35 | - | + | - | - | - | + | - | + | + | - | + | - | + | - | - | - | + | - | + | + | 9 |
| 36 | - | + | - | - | - | + | - | + | + | - | + | - | + | - | - | - | + | - | + | + | 9 |
| 37 | + | + | - | - | - | + | - | + | + | + | + | - | + | - | - | - | + | - | + | + | 11 |
| 38 | - | + | - | - | - | + | - | + | + | - | + | - | - | - | - | - | + | - | + | + | 8 |
| 39 | - | + | - | - | - | + | - | + | + | - | - | - | + | - | - | - | - | - | - | + | 6 |
| 40 | - | - | + | + | + | + | - | + | - | + | - | - | + | - | + | - | + | + | - | + | 11 |
| 41 | - | + | - | - | + | + | - | + | + | - | + | - | + | - | - | - | + | - | + | + | 10 |
| 42 | - | + | - | - | - | + | - | + | + | - | + | - | + | - | - | - | + | - | + | + | 9 |
| 43 | - | - | + | - | + | + | - | + | - | - | - | - | - | - | + | - | + | - | - | + | 7 |
| 44 | - | + | - | - | - | + | + | + | + | - | - | + | + | - | - | - | - | + | - | + | 9 |
| 45 | - | - | + | + | + | + | - | + | - | - | - | - | + | + | + | - | + | + | - | - | 10 |
| 46 | - | + | - | - | + | + | - | + | + | - | + | - | + | + | - | - | - | - | + | + | 10 |
| 47 | - | + | - | + | - | + | - | + | + | - | + | - | + | - | - | + | + | + | + | + | 12 |
| 48 | - | + | - | - | - | + | - | + | + | - | + | - | + | - | - | - | + | - | + | + | 9 |
| 49 | - | - | - | - | - | + | - | + | - | - | - | - | - | - | - | - | + | - | - | + | 4 |

Table S5: Distribution of 20 virulence factor genes and VF scores of each genetically discordant *E. coli* strain

| Isolate Number | <i>afaB/C</i> | <i>iucD</i> | <i>CNF1</i> | <i>sfaD/E</i> | <i>papC</i> | <i>fyuA</i> | <i>cvaC</i> | <i>fimH</i> | <i>iutA</i> | <i>ibeA</i> | <i>iha</i> | <i>ompT</i> | <i>KpsMT2</i> | <i>papG2</i> | <i>hlyA</i> | <i>TcpC</i> | <i>usp</i> | <i>iroN</i> | <i>sat</i> | <i>traT</i> | VF score |
|----------------|---------------|-------------|-------------|---------------|-------------|-------------|-------------|-------------|-------------|-------------|------------|-------------|---------------|--------------|-------------|-------------|------------|-------------|------------|-------------|----------|
| 50 | - | - | - | - | - | + | - | + | - | + | - | - | + | - | - | - | + | - | - | + | 6 |
| 51 | - | + | - | - | - | + | + | + | + | - | - | + | - | - | - | - | - | + | - | + | 8 |
| 52 | - | - | - | - | + | + | - | + | - | - | - | - | + | + | - | - | + | - | - | + | 7 |
| 53 | - | - | - | - | - | - | - | + | - | - | - | - | + | - | - | - | - | - | - | - | 2 |
| 54 | - | - | - | - | - | - | - | + | - | - | - | - | - | - | - | - | - | - | - | - | 1 |
| 55 | + | - | - | - | - | + | - | - | - | - | - | - | + | - | - | - | - | - | - | + | 4 |
| 56 | - | - | - | - | - | + | - | + | - | - | - | - | + | - | - | - | + | - | - | + | 5 |
| 57 | - | - | - | - | - | + | - | + | - | - | - | - | - | - | - | - | - | - | - | - | 2 |
| 58 | - | - | - | - | - | - | - | + | - | - | - | - | - | - | - | - | - | - | - | - | 1 |
| 59 | - | - | - | - | - | - | - | + | - | - | - | - | - | - | - | - | - | - | - | - | 1 |
| 60 | - | + | - | - | - | + | - | + | + | - | + | - | + | - | - | - | + | - | + | - | 8 |
| 61 | - | + | - | - | - | - | + | + | + | - | - | + | + | - | - | - | - | + | - | + | 8 |
| 62 | - | - | - | - | - | + | - | + | - | + | - | - | - | - | - | - | + | - | - | - | 4 |
| 63 | - | + | - | - | - | - | + | + | + | - | - | + | - | - | - | - | - | + | - | + | 7 |
| 64 | - | + | - | - | - | + | - | + | + | - | + | - | + | - | - | - | + | - | + | + | 9 |
| 65 | - | + | - | - | - | - | + | + | + | - | - | + | - | - | - | - | - | + | - | + | 7 |
| 66 | - | - | - | - | + | + | - | + | - | - | - | - | + | + | - | + | + | - | - | + | 8 |
| 67 | - | + | - | - | + | + | - | + | + | + | + | - | + | - | - | - | + | - | + | - | 10 |
| 68 | - | + | - | - | - | + | - | + | + | - | + | - | + | - | - | - | + | - | + | + | 9 |
| 69 | - | - | - | - | - | - | - | + | - | - | - | - | - | - | - | - | - | - | - | - | 1 |
| 70 | - | - | - | - | + | + | - | + | - | - | - | - | + | + | - | + | + | - | - | + | 8 |

VF, virulence factor

References

1. Versalovic J, Koeuth T, Lupski JR. 1991. Distribution of repetitive DNA sequences in eubacteria and application to fingerprinting of bacterial genomes. *Nucleic Acids Res* 19:6823-31.
2. Shibata N, Kurokawa H, Doi Y, Yagi T, Yamane K, Wachino J, Suzuki S, Kimura K, Ishikawa S, Kato H, Ozawa Y, Shibayama K, Kai K, Konda T, Arakawa Y. 2006. PCR classification of CTX-M-type beta-lactamase genes identified in clinically isolated gram-negative bacilli in Japan. *Antimicrob Agents Chemother* 50:791-5.
3. Clermont O, Christenson JK, Denamur E, Gordon DM. 2013. The Clermont *Escherichia coli* phylo-typing method revisited: improvement of specificity and detection of new phylo-groups. *Environ Microbiol Rep* 5:58-65.
4. Clermont O, Bonacorsi S, Bingen E. 2000. Rapid and simple determination of the *Escherichia coli* phylogenetic group. *Appl Environ Microbiol* 66:4555-8.
5. Clermont O, Bonacorsi S, Bingen E. 2004. Characterization of an anonymous molecular marker strongly linked to *Escherichia coli* strains causing neonatal meningitis. *J Clin Microbiol* 42:1770-2.
6. Lescat M, Clermont O, Woerther PL, Glodt J, Dion S, Skurnik D, Djossou F, Dupont C, Perroz G, Picard B, Catzeffis F, Andremont A, Denamur E. 2013. Commensal *Escherichia coli* strains in Guiana reveal a high genetic diversity with host-dependant population structure. *Environ Microbiol Rep* 5:49-57.
7. Clermont O, Lescat M, O'Brien CL, Gordon DM, Tenailon O, Denamur E. 2008. Evidence for a human-specific *Escherichia coli* clone. *Environ Microbiol* 10:1000-6.
8. Doumith M, Day M, Ciesielczuk H, Hope R, Underwood A, Reynolds R, Wain J, Livermore DM, Woodford N. 2015. Rapid identification of major *Escherichia coli* sequence types causing urinary tract and bloodstream infections. *J Clin Microbiol* 53:160-6.
9. Wirth T, Falush D, Lan R, Colles F, Mensa P, Wieler LH, Karch H, Reeves PR, Maiden MC, Ochman H, Achtman M. 2006. Sex and virulence in *Escherichia coli*: an evolutionary perspective. *Mol Microbiol* 60:1136-51.
10. Le Bouguenec C, Archambaud M, Labigne A. 1992. Rapid and specific detection of the *pap*, *afa*, and *sfa* adhesin-encoding operons in uropathogenic *Escherichia coli* strains by polymerase chain reaction. *J Clin Microbiol* 30:1189-93.
11. Johnson JR, Stell AL. 2000. Extended virulence genotypes of *Escherichia coli* strains from patients with urosepsis in relation to phylogeny and host compromise. *J Infect Dis* 181:261-72.
12. Johnson JR, Brown JJ. 1996. A novel multiply primed polymerase chain reaction assay

- for identification of variant papG genes encoding the Gal(alpha 1-4)Gal-binding PapG adhesins of Escherichia coli. *J Infect Dis* 173:920-6.
13. Johnson JR, Russo TA, Tarr PI, Carlino U, Bilge SS, Vary JC, Jr., Stell AL. 2000. Molecular epidemiological and phylogenetic associations of two novel putative virulence genes, iha and iroN(*E. coli*), among Escherichia coli isolates from patients with urosepsis. *Infect Immun* 68:3040-7.
 14. Yamamoto S, Terai A, Yuri K, Kurazono H, Takeda Y, Yoshida O. 1995. Detection of urovirulence factors in Escherichia coli by multiplex polymerase chain reaction. *FEMS Immunol Med Microbiol* 12:85-90.
 15. Johnson JR, Stapleton AE, Russo TA, Scheutz F, Brown JJ, Maslow JN. 1997. Characteristics and prevalence within serogroup O4 of a J96-like clonal group of uropathogenic Escherichia coli O4:H5 containing the class I and class III alleles of papG. *Infect Immun* 65:2153-9.
 16. Schubert S, Rakin A, Karch H, Carniel E, Heesemann J. 1998. Prevalence of the "high-pathogenicity island" of Yersinia species among Escherichia coli strains that are pathogenic to humans. *Infect Immun* 66:480-5.
 17. Rodriguez-Siek KE, Giddings CW, Doetkott C, Johnson TJ, Fakhr MK, Nolan LK. 2005. Comparison of Escherichia coli isolates implicated in human urinary tract infection and avian colibacillosis. *Microbiology (Reading)* 151:2097-2110.
 18. Ananias M, Yano T. 2008. Serogroups and virulence genotypes of Escherichia coli isolated from patients with sepsis. *Braz J Med Biol Res* 41:877-83.
 19. Nakano M, Yamamoto S, Terai A, Ogawa O, Makino SI, Hayashi H, Nair GB, Kurazono H. 2001. Structural and sequence diversity of the pathogenicity island of uropathogenic Escherichia coli which encodes the USP protein. *FEMS Microbiol Lett* 205:71-6.
 20. Huang SH, Wass C, Fu Q, Prasadarao NV, Stins M, Kim KS. 1995. Escherichia coli invasion of brain microvascular endothelial cells in vitro and in vivo: molecular cloning and characterization of invasion gene ibe10. *Infect Immun* 63:4470-5.
 21. Johnson TJ, Wannemuehler Y, Doetkott C, Johnson SJ, Rosenberger SC, Nolan LK. 2008. Identification of minimal predictors of avian pathogenic Escherichia coli virulence for use as a rapid diagnostic tool. *J Clin Microbiol* 46:3987-96.
 22. Cirl C, Wieser A, Yadav M, Duerr S, Schubert S, Fischer H, Stappert D, Wantia N, Rodriguez N, Wagner H, Svanborg C, Miethke T. 2008. Subversion of Toll-like receptor signaling by a unique family of bacterial Toll/interleukin-1 receptor domain-containing proteins. *Nat Med* 14:399-406.