

Supplementary Tables S1 – S17 and Figure S1

Table S1. *E. coli* strains isolated from poultry farms (Poultry farm)

| # | Strain | Farming system | Flock size | Animals age (weeks) |
|----|--------|----------------|------------|---------------------|
| 1 | BWO1 | cage | 30 000 | 36 |
| 2 | BWO2 | cage | 30 000 | 36 |
| 3 | BWO3 | cage | 30 000 | 36 |
| 4 | CJO1 | deep litter | 800 | 80 |
| 5 | CJO2 | deep litter | 800 | 80 |
| 6 | CMK2 | cage | 1 500 | 22 |
| 7 | CMO1 | cage | 1 500 | 22 |
| 8 | CMO2 | cage | 1 500 | 22 |
| 9 | DPO1 | cage | 5 000 | 30 |
| 10 | DPO2 | cage | 5 000 | 30 |
| 11 | DPO3 | cage | 5 000 | 30 |
| 12 | FD1O1 | deep litter | 8 000 | 55 |
| 13 | FD2O1 | deep litter | 10 000 | 29 |
| 14 | FD2O2 | deep litter | 10 000 | 29 |
| 15 | FD3K2 | deep litter | 6 000 | 10 |
| 16 | FD3O1 | deep litter | 6 000 | 10 |
| 17 | JAN1 | free range | 25 000 | 28 |
| 18 | JAO1 | free range | 25 000 | 28 |
| 19 | JAO2 | free range | 25 000 | 28 |
| 20 | JAO3 | free range | 25 000 | 28 |
| 21 | KAO1 | free range | 600 | 36 |
| 22 | KAO2 | free range | 600 | 36 |

| | | | | |
|----|-------|--------------------------|--------|----|
| 23 | KBO1 | free range | 100 | 45 |
| 24 | KBO2 | free range | 100 | 45 |
| 25 | MJO1 | cage | 10 000 | 52 |
| 26 | MJO2 | cage | 10 000 | 52 |
| 27 | PT1K2 | deep litter & free range | 8 600 | 26 |
| 28 | PT1N1 | deep litter & free range | 8 600 | 26 |
| 29 | PT1N2 | deep litter & free range | 8 600 | 26 |
| 30 | PT1O1 | deep litter & free range | 8 600 | 26 |
| 31 | PT1O2 | deep litter & free range | 8 600 | 26 |
| 32 | PT2K2 | deep litter & free range | 7 000 | 32 |
| 33 | PT2O1 | deep litter & free range | 7 000 | 32 |
| 34 | PT3K1 | deep litter & free range | 4 300 | 22 |
| 35 | PT3K2 | deep litter & free range | 4 300 | 22 |
| 36 | PWO1 | deep litter | 1 300 | 80 |
| 37 | PWO2 | deep litter | 1 300 | 80 |
| 38 | WWO1 | cage | 57 000 | 40 |
| 39 | WWO2 | cage | 57 000 | 40 |
| 40 | ZMK1M | cage | 12 000 | 83 |
| 41 | ZMN1M | cage | 17 000 | 37 |
| 42 | ZMN2M | cage | 17 000 | 37 |
| 43 | ZMN2S | cage | 17 000 | 37 |
| 44 | ZMN3M | cage | 17 000 | 37 |

Table S2. *E. coli* strains isolated from food samples (FOOD)

| # | Strain | Food sample |
|---|--------|----------------|
| 1 | FOOD2 | Chicken/breast |
| 2 | FOOD3 | Chicken/breast |
| 3 | FOOD5 | Chicken/breast |
| 4 | FOOD6 | Chicken/breast |

| | | |
|----|--------|----------------|
| 5 | FOOD10 | Chicken/breast |
| 6 | FOOD11 | Chicken/breast |
| 7 | FOOD12 | Pork/loin |
| 8 | FOOD13 | Pork/loin |
| 9 | FOOD15 | Pork/loin |
| 10 | FOOD16 | Chicken/breast |
| 11 | FOOD18 | Pork/loin |
| 12 | FOOD19 | Pork/loin |
| 13 | FOOD20 | Chicken |
| 14 | FOOD21 | Chicken/breast |
| 15 | FOOD22 | Chicken |
| 16 | FOOD23 | Ground/turkey |
| 17 | FOOD24 | Turkey/breast |
| 18 | FOOD25 | Pork/shoulder |
| 19 | FOOD27 | Ground/pork |
| 20 | FOOD28 | Ground/chicken |
| 21 | FOOD29 | Chicken/breast |
| 22 | FOOD30 | Turkey |
| 23 | FOOD31 | Chicken |
| 24 | FOOD33 | Ground/chicken |
| 25 | FOOD34 | Chicken |
| 26 | FOOD35 | Turkey |
| 27 | FOOD36 | Ground/pork |
| 28 | FOOD38 | Chicken |
| 29 | FOOD41 | Chicken |
| 30 | FOOD42 | Chicken/wing |
| 31 | FOOD43 | Pork/shoulder |
| 32 | FOOD44 | Chicken |
| 33 | FOOD45 | Chicken/leg |

| | | |
|----|----------|----------------|
| 34 | FOOD46 | Chicken/wing |
| 35 | FOOD48 | Chicken/breast |
| 36 | FOOD19S | Ground/beef |
| 37 | FOOD115N | Ground/pork |
| 38 | FOOD119N | Ground/beef |

Table S3. *E. coli* strains isolated from patients with urinary tract infections (UTI)

| # | Strain | Patient sex | Age |
|----|--------|-------------|-----|
| 1 | UTI1 | female | 44 |
| 2 | UTI2 | male | 64 |
| 3 | UTI3 | male | 41 |
| 4 | UTI4 | female | 70 |
| 5 | UTI5 | female | 87 |
| 6 | UTI6 | male | 24 |
| 7 | UTI7 | female | 90 |
| 8 | UTI8 | female | 30 |
| 9 | UTI9 | female | 41 |
| 10 | UTI10 | female | 60 |
| 11 | UTI11 | female | 63 |
| 12 | UTI12 | male | 35 |
| 13 | UTI13 | female | 34 |
| 14 | UTI14 | female | 16 |
| 15 | UTI15 | female | 15 |
| 16 | UTI16 | male | 80 |
| 17 | UTI17 | male | 34 |
| 18 | UTI18 | female | 31 |
| 19 | UTI19 | female | 70 |
| 20 | UTI20 | female | 39 |

| | | | |
|----|-------|--------|----|
| 21 | UTI21 | male | 40 |
| 22 | UTI22 | male | 73 |
| 23 | UTI23 | female | 86 |
| 24 | UTI24 | female | 84 |
| 25 | UTI25 | female | 66 |
| 26 | UTI26 | female | 32 |
| 27 | UTI27 | male | 60 |
| 28 | UTI28 | male | 46 |
| 29 | UTI29 | female | 32 |
| 30 | UTI30 | male | 56 |
| 31 | UTI31 | female | 38 |
| 32 | UTI32 | female | 18 |
| 33 | UTI33 | male | 16 |
| 34 | UTI34 | female | 33 |
| 35 | UTI35 | female | 33 |
| 36 | UTI36 | female | 86 |
| 37 | UTI37 | female | 62 |
| 38 | UTI38 | female | 17 |
| 39 | UTI39 | female | 28 |
| 40 | UTI40 | female | 43 |
| 41 | UTI41 | female | 73 |
| 42 | UTI42 | male | 88 |
| 43 | UTI43 | female | 84 |
| 44 | UTI44 | male | 34 |
| 45 | UTI45 | female | 82 |
| 46 | UTI46 | female | 80 |
| 47 | UTI47 | male | 65 |
| 48 | UTI48 | male | 30 |
| 49 | UTI49 | female | 23 |

| | | | |
|----|-------|------|----|
| 50 | UTI81 | male | 55 |
|----|-------|------|----|

Table S4. The list of the primers (Genomed, Warszawa, Poland) used for the determination of the phylogenetic groups of *E. coli* in the quadruplex-PCR method

| Gene | Sequence of Primers | PCR Product Size (bp) | Gene Bank ID |
|----------------|---|-----------------------|--------------|
| <i>yjaA</i> | 5' -CAAACGTGAAGTGTCAAGGAG-3' 5' -AATGCGTTCCTCAACCTGTG-3' | 288 | 948515 |
| <i>chuA</i> | 5' -CAAACGTGAAGTGTCAAGGAG-3' 5' -AATGCGTTCCTCAACCTGTG-3' | 211 | 7155958 |
| <i>TspE4C2</i> | 5' -CACTATTCGTAAGGTCATCC-3' 5' -AGTTTATCGCTGCGGGTCGC-3' | 152 | EU240725.1 |
| <i>arpA</i> | 5' -AACGCTATTCGCCAGCTTGC-3' 5' -TCTCCCCATACCGTACGCTA-3' | 400 | 7155679 |
| <i>arpA</i> | 5' -GATTCCATCTTGTCAAAATATGCC-3' 5'- GAAAAGAAAAAGAATTCCCAAGAG 3' | 301 | 944933 |
| <i>trpA</i> | 5' -AGTTTTATGCCCAGTGCGAG-3' 5' -TCTGCGCCGGTCACGCCC-3' | 219 | 912862 |
| <i>trpA</i> | 5' -CGGCGATAAAGACATCTTCAC-3' 5' -GCAACGCGGCCTGGCGGAAG-3' | 489 | 13702525 |

For the reaction, there was set up 25 µl of PCR mixture per sample containing 50 ng of template DNA, 2-U Taq polymerase DNA DreamTaq™ Green (Thermo Scientific, Vilnius, Lithuania), 2.5 µL of 10 × DNA DreamTaq™ Green Buffer (Thermo Scientific, Vilnius, Lithuania), 200-mM dNTP (Thermo Scientific, Vilnius, Lithuania) and 20 pmol each of the primers (Genomed, Warszawa, Poland). PCR amplifications were performed with parameters as follows: 95 °C for 4 min and 30 cycles of denaturation (30 s, 95 °C), annealing (20 s, 59 °C for quadruplex and phylogroup C and 20 s, 57 °C for phylogroup E), extension steps (1 min, 72 °C) and final extension (10 min, 68 °C).

Table S5. Characterization of *E. coli* isolates from poultry farms (Poultry farm – AFEC)

| Strains | Ph | Genes amplified in quadruplex PCR reactions | | | | group C | group E |
|---------|----|---|-------------|-------------|-----------------|--------------------------------|--------------------------------|
| | | <i>arpA</i> | <i>chuA</i> | <i>yjaA</i> | <i>TspE4.C2</i> | <i>arpA</i> (<i>ArpAgpC</i>) | <i>arpA</i> (<i>ArpAgpE</i>) |
| BWO1 | B1 | + | - | - | + | + | - |
| BWO2 | B2 | - | + | + | - | - | - |
| BWO3 | B1 | + | - | - | + | + | - |
| CJO1 | B1 | + | - | - | + | - | - |
| CJO2 | A | + | - | + | - | - | - |
| CMO1 | B1 | + | - | - | + | + | - |
| CMO2 | D | + | + | - | + | + | - |
| CMK2 | B1 | + | - | - | + | + | - |
| DPO1 | C | + | - | + | - | + | - |
| DPO2 | B1 | + | - | - | + | + | - |
| DPO3 | A | + | - | + | - | - | - |
| FD1O1 | A | + | - | - | - | + | - |
| FD2O1 | A | + | - | - | - | - | - |
| FD2O2 | D | + | + | - | - | + | - |
| FD3O1 | A | + | - | - | - | - | - |
| FD3K2 | B2 | - | + | - | + | + | - |
| JAO1 | F | - | + | - | - | + | - |
| JAO2 | A | + | - | + | - | - | - |
| JAO3 | A | + | - | - | - | - | - |
| JAN1 | A | + | - | - | - | + | - |
| KAO1 | A | + | - | - | - | - | - |
| KAO2 | B1 | + | - | - | + | + | - |
| KBO1 | A | + | - | - | - | - | - |
| KBO2 | A | + | - | - | - | - | - |
| MJO1 | C | + | - | + | - | + | - |

| | | | | | | | |
|-------|----|---|---|---|---|---|---|
| MJO2 | A | + | - | - | - | - | - |
| PT1O1 | B1 | + | - | - | + | + | - |
| PT1O2 | B1 | + | - | - | + | + | - |
| PT1K2 | B1 | + | - | - | + | + | - |
| PT1N1 | A | + | - | - | - | - | - |
| PT1N2 | B1 | + | - | - | + | - | - |
| PT2O1 | D | + | + | - | - | + | - |
| PT2K2 | D | + | + | - | - | + | - |
| PT3K1 | D | + | + | - | - | + | - |
| PT3K2 | E | + | + | - | - | + | + |
| PWO1 | D | + | + | - | - | + | - |
| PWO2 | C | + | - | + | - | + | - |
| WWO1 | B1 | + | - | - | + | + | - |
| WWO2 | A | + | - | - | - | + | - |
| ZMK1M | U | + | - | + | + | + | - |
| ZMN1M | B2 | - | + | + | - | + | - |
| ZMN2M | F | - | + | - | - | + | - |
| ZMN3M | D | + | + | - | - | + | - |
| ZMNS2 | F | - | + | - | - | + | - |

Ph – Phylo-group; U – Unknown;

Table S6. Characterization of *E. coli* isolates ambulatory patients with UTI symptoms (UTI)

| Strains | Ph | Genes amplified in quadruplex PCR reactions | | | | group C | group E |
|---------|----|---|-------------|-------------|-----------------|--------------------------------|--------------------------------|
| | | <i>arpA</i> | <i>chuA</i> | <i>yjaA</i> | <i>TspE4.C2</i> | <i>arpA</i> (<i>ArpAgpC</i>) | <i>arpA</i> (<i>ArpAgpE</i>) |
| UTI 1 | B2 | - | + | + | - | - | - |
| UTI 2 | B2 | - | + | + | - | - | - |
| UTI 3 | B2 | - | + | + | - | - | - |

| | | | | | | | |
|--------|----|---|---|---|---|---|---|
| UTI 4 | B2 | - | + | + | - | + | - |
| UTI 5 | B2 | - | + | + | + | + | - |
| UTI 6 | B2 | - | + | + | - | + | - |
| UTI 7 | B1 | + | - | - | + | + | - |
| UTI 8 | B2 | - | + | + | + | + | - |
| UTI 9 | B2 | - | + | - | + | + | - |
| UTI 10 | D | + | + | - | - | + | - |
| UTI 11 | B2 | - | + | + | + | + | - |
| UTI 12 | B2 | - | + | + | + | + | - |
| UTI 13 | B2 | - | + | + | - | - | - |
| UTI 14 | B1 | + | - | - | + | - | - |
| UTI 15 | F | - | + | - | - | - | - |
| UTI 16 | D | + | + | - | - | + | - |
| UTI 17 | B2 | - | + | + | + | + | - |
| UTI 18 | B2 | - | + | + | + | + | - |
| UTI 19 | B2 | - | + | + | - | - | - |
| UTI 20 | D | + | + | - | - | + | - |
| UTI 21 | B2 | - | + | + | - | - | - |
| UTI 22 | B2 | - | + | + | - | - | - |
| UTI 23 | B2 | - | + | + | - | + | - |
| UTI 24 | B2 | - | + | + | - | + | - |
| UTI 25 | B2 | - | + | + | + | + | - |
| UTI 26 | F | - | + | - | - | + | - |
| UTI 27 | F | - | + | - | - | + | - |
| UTI 28 | F | - | + | - | - | - | - |
| UTI 29 | B2 | - | + | + | - | + | - |
| UTI 30 | B2 | - | + | + | - | - | - |
| UTI 31 | B2 | - | + | + | - | + | - |
| UTI 32 | B2 | - | + | + | - | + | - |
| UTI 33 | B2 | - | + | + | - | - | - |

| | | | | | | | |
|--------|----|---|---|---|---|---|---|
| UTI 34 | B2 | - | + | + | + | + | - |
| UTI 35 | E | + | + | - | - | + | + |
| UTI 36 | D | + | + | - | - | + | - |
| UTI 37 | B2 | - | + | + | - | - | - |
| UTI 38 | B2 | - | + | + | + | + | - |
| UTI 39 | F | - | + | - | - | - | - |
| UTI 40 | B2 | - | + | + | - | - | - |
| UTI 41 | B2 | - | + | + | - | - | - |
| UTI 42 | C | + | - | + | - | + | - |
| UTI 43 | B2 | - | + | + | - | + | - |
| UTI 44 | D | + | + | - | - | + | - |
| UTI 45 | D | + | + | - | + | + | - |
| UTI 46 | D | + | + | - | - | + | - |
| UTI 47 | A | + | - | - | - | + | - |
| UTI 48 | B2 | - | + | + | + | - | - |
| UTI 49 | B2 | - | + | + | + | - | - |
| UTI 81 | C | + | - | + | - | + | + |

Ph – Phylo-group;

Table S7. Characterization of *E. coli* isolates from food (FOOD)

| Strains | Ph | Genes amplified in quadruplex PCR reactions | | | | group C | group E |
|---------|----|---|-------------|-------------|-----------------|-----------------------------------|-----------------------------------|
| | | <i>arpA</i> | <i>chuA</i> | <i>yjaA</i> | <i>TspE4.C2</i> | <i>arpA</i> (<i>ArpAgpC</i>) | <i>arpA</i> (<i>ArpAgpE</i>) |
| FOOD 2 | B1 | + | - | - | + | + | + |
| FOOD 3 | F | - | + | - | - | + | - |
| FOOD 5 | A | + | - | - | - | - | - |
| FOOD 6 | A | + | - | - | - | - | - |
| FOOD 10 | B1 | + | - | - | + | + | - |

| | | | | | | | |
|---------|----|---|---|---|---|---|---|
| FOOD 11 | F | - | + | - | - | + | - |
| FOOD 12 | A | + | - | - | - | - | - |
| FOOD 13 | A | + | - | - | - | - | - |
| FOOD 15 | A | + | - | - | - | - | - |
| FOOD 16 | U | - | - | + | + | - | - |
| FOOD 18 | A | + | - | - | - | - | - |
| FOOD 19 | A | + | - | - | - | - | - |
| FOOD 20 | B1 | + | - | - | + | + | - |
| FOOD 21 | A | + | - | - | - | - | - |
| FOOD 22 | A | + | - | - | - | - | - |
| FOOD 23 | U | + | - | + | + | + | - |
| FOOD 24 | A | + | - | - | - | - | - |
| FOOD 25 | A | + | - | - | - | + | - |
| FOOD 27 | B1 | + | - | - | + | + | - |
| FOOD 28 | B1 | + | - | - | + | + | - |
| FOOD 29 | U | + | - | + | + | + | - |
| FOOD 30 | B1 | + | - | - | + | - | - |
| FOOD 31 | A | + | - | - | - | + | - |
| FOOD 33 | A | + | - | - | - | + | - |
| FOOD 34 | E | + | + | - | + | + | + |
| FOOD 35 | B1 | + | - | - | + | + | - |
| FOOD 36 | F | - | + | - | - | - | - |
| FOOD 38 | U | + | - | + | + | + | - |
| FOOD 41 | B1 | + | - | - | + | + | - |
| FOOD 42 | F | - | + | - | - | + | - |
| FOOD 43 | A | + | - | - | - | + | + |
| FOOD 44 | A | + | - | - | - | - | - |
| FOOD 45 | A | + | - | - | - | + | - |
| FOOD 46 | A | + | - | + | - | - | - |
| FOOD 48 | A | + | - | + | - | - | - |

| | | | | | | | |
|-----------|---|---|---|---|---|---|---|
| FOOD 19 S | A | + | - | - | - | + | - |
| FOOD 115N | A | + | - | - | - | + | - |
| FOOD 119N | A | + | - | + | - | - | - |

Ph – Phylo-group; U – Unknown;

Table S8. Antibiotic resistance of *E. coli* strains isolated from various sources

| Antimicrobials | Source (number of isolates) | | |
|----------------|-----------------------------|---------------|---------------|
| | Poultry farm | FOOD | Patients/UTIs |
| | (44) n (%) | (38) n (%) | (50) n (%) |
| AMP | 19(43.2) | 18(47.4) | 19(38.0) |
| TE | 13(29.5) | 18(47.4) | 17(34.0) |
| SXT | 10(22.7) | 13(34.2) | 15(30.0) |
| CIP | 6(13.6) | 13(34.2) | 7(14.0) |
| PRL | 6(13.6) | 1(2.6) | 6(12.0) |
| C | 6(13.6) | 1(2.6) | 2(4.0) |
| AMC | 2(4.5) | 0 | 2(4.0) |
| CXM | 1(2.3) | 0 | 1(2.0) |
| GE | 1(2.3) | 0 | 0 |
| NF | 0 | 0 | 2(4.0) |
| TZP | 0 | 0 | 0 |
| CTX | 2(4.5) | 0 | 0 |
| CAZ | 0 | 0 | 0 |
| MEM | 0 | 0 | 0 |
| IPM | 0 | 0 | 0 |
| AK | 0 | 1(2.6) | 0 |

Note: AMP - Ampicillin 10, TE - Tetracycline 30, SXT - Trimethoprim-Sulfamethoxazole 1.25/23.75, CIP - Ciprofloxacin, PRL - Piperacillin 100, C - Chloramphenicol 30, AMC - Amoxicillin/clavulanic acid 20/10, CXM - Cefuroxime 30, GE - Gentamicin 10, NF - Nitrofurantoin 300, TZP - Piperacillin/Tazobactam 100/10, CTX - Cefotaxime 30, CAZ - Ceftazidime 30, MEM - Meropenem 10, IPM - Imipenem 10, AK - Amikacin 30;

Table S9. Genotypic and phenotypic characterization of E. coli isolates ambulatory patients with UTI symptoms (UTI)

| No./ patient sex | Strains | Ph | Virulence/profiles | | | | | | | | Resistance/patterns |
|------------------------|---------|----|--------------------|-------------|------------|------------|------------|---------------|------------|------------|------------------------|
| | | | Adhesins | | | Toxins | | Miscellaneous | | | |
| | | | <i>fimH</i> | <i>papC</i> | <i>iha</i> | <i>vat</i> | <i>pic</i> | <i>irp2</i> | <i>iss</i> | <i>usp</i> | |
| 1/F | UTI 40 | B2 | ■ | | | ■ | ■ | ■ | | ■ | |
| 2/F | UTI 10 | D | ■ | | | | | ■ | | ■ | AMP |
| 3/F | UTI 11 | B2 | ■ | | ■ | | | ■ | | ■ | CIP |
| 4/F | UTI 13 | B2 | ■ | ■ | ■ | ■ | ■ | ■ | ■ | ■ | |
| 5/F | UTI 14 | B1 | ■ | | ■ | | | ■ | ■ | ■ | TE |
| 6/F | UTI 15 | F | ■ | | | ■ | | ■ | ■ | ■ | TE |
| 7/F | UTI 18 | B2 | ■ | ■ | ■ | ■ | ■ | ■ | | ■ | |
| 8/F | UTI 19 | B2 | ■ | ■ | | | ■ | ■ | | ■ | |
| 9/F | UTI 20 | D | ■ | ■ | ■ | ■ | ■ | ■ | ■ | ■ | |
| 10/F | UTI 23 | B2 | ■ | ■ | | ■ | | ■ | | ■ | |
| 11/F | UTI 24 | B2 | ■ | ■ | ■ | | | ■ | | ■ | AMP/TE/C |
| 12/F | UTI 25 | B2 | ■ | ■ | | | | ■ | | ■ | |
| 13/F | UTI 26 | F | ■ | ■ | | | | ■ | | ■ | |
| 14/F | UTI 29 | B2 | ■ | ■ | | ■ | ■ | ■ | | ■ | AMP/TE |
| 15/F | UTI 31 | B2 | ■ | ■ | | ■ | ■ | ■ | | ■ | AMP/SXT |
| 16/F | UTI 32 | B2 | ■ | ■ | | ■ | ■ | ■ | | ■ | AMP/SXT |
| 17/F | UTI 34 | B2 | ■ | ■ | ■ | ■ | ■ | ■ | | ■ | |
| 18/F | UTI 35 | E | ■ | ■ | | ■ | ■ | ■ | ■ | ■ | AMP, TE, SXT, CIP, PRL |
| 19/F | UTI 36 | D | ■ | ■ | | ■ | ■ | ■ | ■ | ■ | AMP/TE/SXT/CIP |
| 20/F | UTI 37 | B2 | ■ | ■ | | ■ | | ■ | | ■ | |
| 21/F | UTI 38 | B2 | ■ | ■ | | ■ | | ■ | | ■ | |
| 22/F | UTI 39 | F | ■ | ■ | | ■ | | ■ | | ■ | |
| 23/F | UTI 4 | B2 | ■ | ■ | | ■ | ■ | ■ | | ■ | |
| 24/F | UTI 41 | B2 | ■ | ■ | | ■ | | ■ | | ■ | TE |
| 25/F | UTI 43 | B2 | ■ | ■ | ■ | ■ | | ■ | | ■ | AMP/TE/PRL |
| 26/F | UTI 45 | D | ■ | ■ | | ■ | ■ | ■ | ■ | ■ | TE/SXT |
| 27/F | UTI 46 | D | ■ | | | | | ■ | ■ | ■ | AMP/PRL |

| | | | | | | | | | | | |
|---------------|---------------|----|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------------------|
| 28/F | UTI 49 | B2 | ■ | | ■ | ■ | | ■ | ■ | ■ | SXT |
| 29/F | UTI 5 | B2 | ■ | ■ | ■ | ■ | ■ | ■ | | ■ | |
| 30/F | UTI 7 | B1 | ■ | | | ■ | | ■ | ■ | ■ | AMP/TE/SXT/CIP |
| 31/F | UTI 8 | B2 | ■ | ■ | ■ | ■ | | ■ | | ■ | |
| 32/F | UTI 9 | B2 | | | | ■ | | ■ | ■ | ■ | AMP/TE/SXT |
| 33/F | UTI 1 | B2 | ■ | ■ | ■ | ■ | ■ | ■ | | ■ | SXT |
| n(%) 33(66.0) | | | 32 | 24 | 12 | 25 | 15 | 33 | 11 | 33 | MDR(n=6) |
| 34/M | UTI 12 | B2 | ■ | ■ | ■ | ■ | ■ | ■ | | ■ | AMP/AMC/SX/PRL |
| 35/M | UTI 16 | D | ■ | | | | | ■ | | ■ | AMP/SXT |
| 36/M | UTI 17 | B2 | ■ | | | ■ | ■ | ■ | | ■ | |
| 37/M | UTI 21 | B2 | ■ | ■ | | ■ | | ■ | | ■ | |
| 38/M | UTI 22 | B2 | ■ | ■ | ■ | ■ | ■ | ■ | | ■ | NF |
| 39/M | UTI 27 | F | ■ | ■ | | | | ■ | | ■ | |
| 40/M | UTI 28 | F | ■ | ■ | | ■ | | ■ | | ■ | AMP |
| 41/M | UTI 3 | B2 | ■ | ■ | | ■ | ■ | ■ | | ■ | |
| 42/M | UTI 30 | B2 | ■ | ■ | | ■ | | ■ | ■ | ■ | AMP |
| 43/M | UTI 33 | B2 | ■ | ■ | ■ | ■ | ■ | ■ | ■ | ■ | |
| 44/M | UTI 42 | C | ■ | ■ | | ■ | ■ | ■ | ■ | ■ | AMP/TE/SXT/CIP/NF |
| 45/M | UTI 44 | D | ■ | ■ | | | | ■ | ■ | ■ | AMP/SXT |
| 46/M | UTI 47 | A | ■ | | | | | | ■ | | AMC/TE/SXT/CIP/PRL/C |
| 47/M | UTI 48 | B2 | ■ | ■ | | ■ | | ■ | | ■ | TE |
| 48/M | UTI 6 | B2 | ■ | ■ | | | | ■ | | ■ | TE |
| 49/M | UTI 81 | C | ■ | | | ■ | ■ | | | ■ | TE/SXT/CIP/PRL/ESBL+ |
| 50/M | UTI 2 | B2 | ■ | ■ | | ■ | ■ | ■ | | ■ | AMP/TE |
| n(%) 17(34.0) | | | 17 | 13 | 3 | 12 | 8 | 15 | 5 | 16 | MDR(n=4) |
| Total n(%) | 50 (100.0) | | 49 (98.0) | 37 (74.0) | 15 (30.0) | 37 (74.0) | 23 (46.0) | 48 (96.0) | 16 (32.0) | 49 (98.0) | MDR total n=10 (20.0) |

Patient

sex: F – female, M – male; Ph – Phylogroup; U – Unknown

Note: MDR–multidrug resistance; AMP–ampicillin, TE–tetracycline, SXT–trimethoprim/sulfamethoxazole, CIP–ciprofloxacin, PRL–piperacillin, C–chloramphenicol, AMC–amoxicillin/clavulanic acid, CXM–cefuroxime, NF–nitrofurantoin;

Table S10. Genotypic and phenotypic characterization of *E. coli* isolates from food (FOOD)

| No./ Source of meet | Strains | Ph | Virulence/profiles | | | | | | | | Resistance/patterns |
|---------------------------|----------|----|--------------------|-------------|------------|------------|------------|---------------|------------|------------|---------------------|
| | | | Adhesins | | | Toxins | | Miscellaneous | | | |
| | | | <i>fimH</i> | <i>papC</i> | <i>iha</i> | <i>vat</i> | <i>pic</i> | <i>irp2</i> | <i>iss</i> | <i>usp</i> | |
| 1/h | FOOD10 | B1 | ■ | | | | | | | ■ | AMP/TE |
| 2/h | FOOD11 | F | ■ | | | ■ | ■ | ■ | ■ | ■ | AMP/TE/CIP |
| 3/h | FOOD16 | U | | ■ | | | | ■ | | ■ | CIP |
| 4/h | FOOD2 | B1 | ■ | | | | | | | ■ | |
| 5/h | FOOD20 | B1 | ■ | ■ | | | ■ | ■ | ■ | ■ | CIP |
| 6/h | FOOD21 | A | ■ | ■ | | | ■ | ■ | | ■ | |
| 7/h | FOOD22 | A | ■ | ■ | | | ■ | ■ | | ■ | |
| 8/h | FOOD28 | B1 | ■ | ■ | ■ | | ■ | | ■ | ■ | AMP/TE/CIP |
| 9/h | FOOD29 | U | ■ | ■ | | | ■ | | ■ | ■ | |
| 10/h | FOOD3 | F | ■ | | | ■ | ■ | ■ | ■ | ■ | AMP/TE |
| 11/h | FOOD31 | A | ■ | ■ | | | ■ | | ■ | | |
| 12/h | FOOD33 | A | ■ | ■ | | | ■ | ■ | ■ | | AMP/TE/SXT/CIP |
| 13/h | FOOD34 | E | | ■ | | | ■ | | ■ | ■ | AMP/TE/SXT/CIP |
| 14/h | FOOD38 | U | ■ | ■ | | | ■ | ■ | ■ | | |
| 15/h | FOOD41 | B1 | ■ | ■ | | | ■ | ■ | ■ | | AMP/TE/SXT/CIP/C |
| 16/h | FOOD42 | F | ■ | ■ | | ■ | ■ | ■ | ■ | | TE/CIP |
| 17/h | FOOD44 | A | ■ | ■ | | | ■ | ■ | ■ | | AMP/TE/SXT/CIP |
| 18/h | FOOD45 | A | ■ | | | | | ■ | ■ | | AMP/TE/SXT/CIP |
| 19/h | FOOD46 | A | ■ | ■ | ■ | | ■ | ■ | ■ | | AMP/SXT |
| 20/h | FOOD48 | A | ■ | ■ | | | ■ | | ■ | ■ | AMP/TE/SXT/CIP |
| 21/h | FOOD5 | A | | | | | | | | | |
| 22/h | FOOD6 | A | | | | | | | | ■ | |
| n(%) | 22(57.9) | | 18 | 15 | 2 | 3 | 16 | 13 | 15 | 13 | MDR(n=8) |

| | | | | | | | | | | | |
|---------------|-------------|----|--------------|--------------|-------------|-------------|--------------|--------------|--------------|--------------|--------------------------|
| 23/p | FOOD115N | A | ■ | ■ | | | ■ | ■ | ■ | | AMP/TE/SXT/CIP |
| 24/p | FOOD12 | A | ■ | | | | | | | ■ | |
| 25/p | FOOD13 | A | ■ | | | | ■ | ■ | | ■ | |
| 26/p | FOOD15 | A | ■ | | | | | | ■ | ■ | |
| 27/p | FOOD18 | A | ■ | ■ | | | ■ | ■ | ■ | ■ | |
| 28/p | FOOD19 | A | ■ | ■ | | | ■ | ■ | | ■ | |
| 29/p | FOOD25 | A | ■ | ■ | | | | ■ | ■ | ■ | |
| 30/p | FOOD27 | B1 | ■ | ■ | ■ | | ■ | ■ | ■ | ■ | |
| 31/p | FOOD36 | F | ■ | ■ | | | ■ | | ■ | | AMP/TE/SXT/CIP |
| 32/p | FOOD43 | A | ■ | ■ | | | ■ | ■ | ■ | | AMP/TE |
| n(%) | 10(26.3) | | 10 | 7 | 1 | 0 | 7 | 7 | 7 | 7 | MDR(n=2) |
| 33/t | FOOD23 | U | ■ | ■ | | ■ | ■ | ■ | | ■ | |
| 34/t | FOOD24 | A | ■ | ■ | | | | | ■ | ■ | AMP/TE/SXT/CIP |
| 35/t | FOOD30 | B1 | ■ | ■ | ■ | | ■ | | ■ | ■ | AMP |
| 36/t | FOOD35 | B1 | ■ | ■ | ■ | | ■ | | ■ | | AMP/TE/SXT/CIP/PRL/AK |
| n(%) | 4(10.5) | | 4 | 4 | 2 | 1 | 3 | 1 | 3 | 3 | MDR(n=2) |
| 37/b | FOOD119N | A | ■ | ■ | ■ | | ■ | | ■ | | TE/SXT/CIP |
| 38/b | FOOD19S | A | ■ | ■ | ■ | | ■ | ■ | ■ | | AMP/TE/SXT/CIP |
| n(%) | 2(5.3) | | 2 | 2 | 2 | 0 | 2 | 1 | 2 | 0 | MDR(n=2) |
| Total (n)% | 38 (100) | | 34 (89.5) | 28 (73.7) | 7 (18.4) | 4 (10.5) | 28 (73.7) | 22 (57.9) | 27 (71.1) | 23 (60.5) | MDR total n=14 (36.8) |

Type of meat: h–chicken, p–pork, t–turkey, b–beef;

Ph – Phylogroup; U – Unknown

Note: MDR–multidrug resistance; AMP–ampicillin, TE–tetracycline, SXT–trimethoprim/sulfamethoxazole, CIP–ciprofloxacin, PRL–piperacillin, C–chloramphenicol, AMC–amoxicillin/clavulanic acid, AK–amikacin;

Table S11. Genotypic and phenotypic characterization of *E. coli* isolates from poultry farms (Poultry farm – AFEC))

| No./ Farming system | Strains | Ph | Virulence/profiles | | | | | | | | Resistance/patterns |
|---------------------------|---------|----|--------------------|-------------|------------|------------|------------|---------------|------------|------------|---------------------|
| | | | Adhesins | | | Toxins | | Miscellaneous | | | |
| | | | <i>fimH</i> | <i>papC</i> | <i>iha</i> | <i>vat</i> | <i>pic</i> | <i>irp2</i> | <i>iss</i> | <i>usp</i> | |
| 1/f | JA01 | F | ■ | ■ | | | | ■ | ■ | | |
| 2/f | JA02 | A | ■ | ■ | | | ■ | ■ | ■ | ■ | |
| 3/f | JA03 | A | ■ | ■ | | | ■ | ■ | ■ | ■ | |
| 4/f | JAN1 | A | ■ | | | | | ■ | ■ | | |
| 5/f | KA01 | A | ■ | ■ | | | | | | | |
| 6/f | KA02 | B1 | ■ | ■ | | | ■ | ■ | ■ | ■ | |
| 7/f | KB01 | A | ■ | | | | | | | ■ | |
| 8/f | KB02 | A | ■ | ■ | | | ■ | ■ | ■ | ■ | |
| n(%) | 8(18.2) | | 8 | 6 | 0 | 0 | 4 | 6 | 6 | 5 | MDR(n=0) |
| 9/df | PT101 | B1 | ■ | | | | | | ■ | ■ | AMP/GE |
| 10/df | PT102 | B1 | ■ | | | | ■ | ■ | ■ | ■ | AMP |
| 11/df | PT1K2 | B1 | ■ | | | | ■ | ■ | ■ | ■ | AMP/TE/SXT/CIP/C |
| 12/df | PT1N1 | A | ■ | | | | | | | | AMP/TE/PRL |
| 13/df | PT1N2 | B1 | ■ | | | | ■ | ■ | ■ | ■ | AMP/TE/PRL |
| 14/df | PT201 | D | ■ | | | | | | | | |
| 15/df | PT2K2 | D | ■ | ■ | | ■ | ■ | ■ | ■ | ■ | |
| 16/df | PT3K1 | D | ■ | | | | | | | ■ | |
| 17/df | PT3K2 | E | ■ | ■ | | | ■ | ■ | ■ | ■ | AMP/TE/CIP/C |
| n(%) | 9(20.5) | | 9 | 2 | 0 | 1 | 5 | 5 | 6 | 7 | MDR(n=4) |
| 18/d | CJ01 | B1 | ■ | | | | | | | | |
| 19/d | CJ02 | A | ■ | ■ | | ■ | ■ | ■ | ■ | ■ | AMP/TE/PRL |
| 20/d | FD101 | A | ■ | | | | ■ | ■ | | | |
| 21/d | FD201 | A | ■ | | | | | ■ | | | AMP/CIP/C |
| 22/d | FD202 | D | ■ | ■ | | | ■ | ■ | ■ | ■ | TE/SXT/ESBL+ |
| 23/d | FD301 | A | ■ | | | | | ■ | ■ | | AMP/TE/SXT/CIP |

| | | | | | | | | | | | |
|---------------|-------------|----|--------------|--------------|------------|------------|--------------|--------------|--------------|--------------|---------------------------|
| 24/d | FD3K2 | B2 | ■ | | | | ■ | ■ | ■ | ■ | TE/SXT/CIP/C/ESBL+ |
| 25/d | PW01 | D | ■ | | | | | | ■ | | AMP/TE/SXT |
| 26/d | PW02 | C | ■ | ■ | | | ■ | ■ | ■ | ■ | |
| n(%) | 9(20.5) | | 9 | 3 | 0 | 1 | 5 | 7 | 6 | 4 | MDR(n=6) |
| 27/c | BW01 | B1 | | ■ | | | | | ■ | | AMP |
| 28/c | BW02 | B2 | ■ | ■ | | | ■ | ■ | ■ | ■ | |
| 29/c | BW03 | B1 | ■ | | | | ■ | ■ | ■ | ■ | |
| 30/c | CM01 | B1 | | | | | | ■ | ■ | | AMP/SXT/C |
| 31/c | CM02 | D | ■ | ■ | | | ■ | ■ | ■ | ■ | AMP/TE/SXT/PRL |
| 32/c | CMK2 | B1 | ■ | ■ | | | ■ | ■ | ■ | | AMP/TE/SXT/PRL |
| 33/c | DP01 | C | ■ | ■ | | | | | | | |
| 34/c | DP02 | B1 | ■ | ■ | ■ | | ■ | ■ | ■ | ■ | TE/SXT |
| 35/c | DP03 | A | ■ | | | | ■ | ■ | ■ | ■ | AMP |
| 36/c | MJ01 | C | ■ | ■ | | | | ■ | | | |
| 37/c | MJ02 | A | ■ | ■ | | | ■ | ■ | ■ | | |
| 38/c | WW01 | B1 | ■ | | | | | ■ | | | AMP |
| 39/c | WW02 | A | ■ | ■ | | | ■ | ■ | ■ | ■ | |
| 40/c | ZMK1M | U | ■ | | | | | | | | |
| 41/c | ZMN1M | B2 | ■ | ■ | | | | ■ | ■ | ■ | |
| 42/c | ZMN2M | F | ■ | ■ | | ■ | ■ | ■ | ■ | ■ | |
| 43/c | ZMN2S | F | ■ | ■ | | | ■ | ■ | ■ | ■ | |
| 44/c | ZMN3M | D | ■ | | | ■ | ■ | ■ | ■ | ■ | AMP/TE/SXT/CIP/C |
| n(%) | 18(40.9) | | 16 | 12 | 1 | 2 | 11 | 15 | 14 | 10 | MDR(n=4) |
| Total n(%) | 44 (100) | | 42 (95.5) | 23 (52.3) | 1 (2.3) | 4 (9.1) | 25 (56.8) | 33 (75.0) | 32 (72.7) | 26 (59.1) | MDR total n=14 (31.8%) |

Farming system: c – cage, d –deep litter, f – free-range, df – deep litter and free-range;

Ph – Phylogroup; U – Unknown

Note: MDR–multidrug resistance; AMP-ampicillin, TE-tetracycline, SXT-trimethoprim/sulfamethoxazole, CIP-ciprofloxacin, PRL-piperacillin, C-chloramphenicol, AMC-amoxicillin/clavulanic acid, CXM-cefuroxime, GE-gentamicin, CTX-cefotaxime;

Table S12. ERIC-PCR profiles and STs (MLST) with the highest number of similarities among *E. coli* isolates

| Cluster/ ERIC | Strains/ MLST (ST) | Virulence/profiles | | | | | | | | Resistance/patterns |
|------------------|------------------------|--------------------|------------|-------------|------------|-------------|------------|------------|------------|------------------------|
| | | <i>fimH</i> | <i>usp</i> | <i>irp2</i> | <i>vat</i> | <i>papC</i> | <i>pic</i> | <i>iss</i> | <i>iha</i> | |
| EI | WW01/ST1049 | ■ | | ■ | | | | | | AMP |
| | FOOD 28(h)/U | ■ | ■ | | | ■ | ■ | ■ | ■ | AMP/TE/CIP |
| EII | KA01/U | ■ | | | | ■ | | | | - |
| | FOOD 29(h)/U | ■ | ■ | | | ■ | ■ | ■ | | - |
| EIII | CM02/U | ■ | ■ | ■ | | ■ | ■ | ■ | | AMP/TE/SXT/PRL |
| | DP01/U | ■ | | | | ■ | | | | - |
| | UTI 16/ST69 | ■ | ■ | ■ | | | | | | AMP/SXT |
| EIV | CJ01/ST2534 | ■ | | | | | | | | - |
| | FOOD 23(t)/U | ■ | ■ | ■ | ■ | ■ | ■ | | | - |
| EV | UTI 28/U | ■ | ■ | ■ | ■ | ■ | | | | AMP |
| | FOOD 21(h)/ST536 | ■ | ■ | ■ | | ■ | ■ | | | - |
| EVI | PT1N1/U | ■ | | | | | | | | AMP/SXT |
| | FOOD 25(p)/ ST10888 | ■ | ■ | ■ | | ■ | | ■ | | - |
| EVII | MJ01/U | ■ | | ■ | | ■ | | | | - |
| | FOOD 35(t)/U | ■ | | | | ■ | ■ | ■ | ■ | AMP/TE/CIP/ SXT/PRL/AK |
| EVIII | WW02/ST212 | ■ | ■ | ■ | | ■ | ■ | ■ | | - |
| | FOOD 10(h)/ ST6073 | ■ | ■ | | | | | | | AMP/TE |
| EIX | FD202/ST5451 | ■ | ■ | ■ | | ■ | ■ | ■ | | TE/SXT/ESBL+ |
| | FD3K2/ST624 | ■ | ■ | ■ | | | ■ | ■ | | TE/CIP/SXT/C/ESBL+ |

| | | | |
|-----|--------------------|---------------|-------------------|
| | UTI 9/ST354 | ■ ■ ■ ■ ■ | AMP/TE/SXT |
| | UTI 31/ST404 | ■ ■ ■ ■ ■ ■ | AMP/SXT |
| EX | UTI 7/U | ■ ■ ■ ■ ■ | AMP/TE/CIP/SXT |
| | FOOD 38(h)/U | ■ ■ ■ ■ ■ ■ | - |
| EXI | UTI 42/U | ■ ■ ■ ■ ■ ■ ■ | AMP/TE/CIP/NF/SXT |
| | FOOD 19s(b)/ST5295 | ■ ■ ■ ■ ■ ■ ■ | AMP/TE/CIP/SXT |

Note: ■ – positive result (presence of gene); ST – sequence type (MLST); U – unknown ST;
AMP-ampicillin, TE-tetracycline, SXT-trimethoprim/sulfamethoxazole, CIP-ciprofloxacin, PRL-piperacillin, C-chloramphenicol, AMC-amoxicillin/clavulanic acid, CXM-cefuroxime, NF-nitrofurantoin, CTX-cefotaxime, AK-amikacin;
Type of meat: h-chicken, p-pork, t-turkey, b-beef;

Table S13. The allelic profiles of seven housekeeping genes: *adh*, *gyrB*, *fumC*, *icd*, *mdh*, *purA* and *recA* (variants of alleles marked in blue, which repeat among the tested strains) of 25 *E. coli* strains isolated from poultry farms, food, and patients with UTI symptoms. The sequence types (ST) highlighted in red (seven housekeeping genes) and sequence types highlighted in green (six housekeeping genes)

| ID | MLST (7) | MLST (6) | <i>icd</i> | <i>fumC</i> | <i>gyrB</i> | <i>purA</i> | <i>adk</i> | <i>mdh</i> | <i>recA</i> |
|-------------|----------|----------|------------|-------------|-------------|-------------|------------|------------|-------------|
| FOOD 10(h) | U | ST6073 | 619 | 19 | 14 | 12 | 842 | 11 | 2 |
| FOOD 19s(b) | ST5295 | ST5295 | 1 | 126 | 5 | 8 | 64 | 8 | 6 |
| FOOD 21(h) | U | ST536 | 95 | 107 | 1 | 8 | 502 | 69 | 20 |
| FOOD 23(t) | U | U | 1 | 7 | 5 | 18 | 842 | 8 | 2 |
| FOOD 25(p) | ST10888 | ST10888 | 1273 | 11 | 5 | 8 | 112 | 8 | 86 |
| FOOD 28(h) | U | U | 18 | 19 | 33 | 122 | 457 | 9 | 6 |
| FOOD 29(h) | U | U | 8 | 11 | 4 | 8 | 232 | 8 | 49 |
| FOOD 35(t) | U | U | 26 | 65 | 32 | 8 | 502 | 9 | 2 |
| FOOD 38(h) | U | U | 613 | 11 | 4 | 8 | 623 | 8 | 49 |
| UTI 7 | U | U | 1 | 65 | 5 | 13 | 457 | 9 | 6 |
| UTI 9 | ST354 | ST354 | 29 | 88 | 78 | 58 | 85 | 59 | 62 |
| UTI 16 | ST69 | ST69 | 6 | 35 | 27 | 5 | 21 | 5 | 4 |
| UTI 28 | U | U | 13 | 40 | 311 | 28 | 53 | 36 | 29 |
| UTI 31 | ST404 | ST404 | 14 | 14 | 10 | 7 | 14 | 17 | 74 |
| UTI 42 | U | U | 8 | 11 | 135 | 8 | 864 | 8 | 2 |
| DPO1(c) | U | U | 8 | 81 | 4 | 8 | 623 | 12 | 2 |
| CMO2(c) | U | U | 6 | 35 | 27 | 5 | 864 | 5 | 4 |
| FD3K2(d) | ST624 | ST624 | 96 | 4 | 87 | 58 | 92 | 70 | 91 |
| FD202(d) | ST5451 | ST5451 | 342 | 3 | 234 | 5 | 35 | 5 | 302 |
| CJO1(d) | ST2534 | ST2534 | 88 | 19 | 15 | 193 | 137 | 7 | 7 |
| KA01(f) | U | U | 88 | 4 | 15 | 8 | 457 | 80 | 14 |
| MJO1(c) | U | U | 564 | 1054 | 60 | 8 | 174 | 509 | 677 |
| PT1N1(df) | U | U | 1 | 65 | 5 | 13 | 457 | 9 | 6 |
| WWO1(c) | U | ST1049 | 16 | 4 | 14 | 5 | 46 | 24 | 14 |
| WWO2(c) | U | ST212 | 18 | 29 | 4 | 8 | 502 | 11 | 6 |

Note: U – unknown ST; Farming system: c – cage, d –deep litter, f – free-range, df – deep litter and free-range;
Type of meat: h–chicken, p–pork, t–turkey, b–beef;

Table S14. STs (MLST) and phylogroups (Clermont) among 25 *E. coli* isolates

| MLST/ Branch | Strains/ ST/Ph | Virulence/profiles | | | | | | | | Resistance/patterns |
|-----------------|------------------------|--------------------|------------|-------------|------------|-------------|------------|------------|------------|------------------------|
| | | <i>fimH</i> | <i>usp</i> | <i>irp2</i> | <i>vat</i> | <i>papC</i> | <i>pic</i> | <i>iss</i> | <i>iha</i> | |
| I | WW02/ST212/A | ■ | ■ | ■ | | ■ | ■ | ■ | | - |
| | FOOD 21(h)/ ST536/A | ■ | ■ | ■ | | ■ | ■ | | | - |
| | FOOD 35(t)/U/B1 | ■ | | | | ■ | ■ | ■ | ■ | AMP/TE/CIP/ SXT/PRL/AK |
| | DP01/U/C | ■ | | | | ■ | | | | - |
| II | PT1N1/U/A | ■ | | | | | | | | AMP/TE/PRL |
| | KA01/U/A | ■ | | | | ■ | | | | - |
| | UTI 7/U/B1 | ■ | ■ | ■ | ■ | | | ■ | | AMP/TE/CIP/SXT |
| | CJ01/ST2534/B1 | ■ | | | | | | | | - |
| | FOOD 28(h)/U/B1 | ■ | ■ | | | ■ | ■ | ■ | ■ | AMP/TE/CIP |
| III | UTI 9/ST354/B2 | | ■ | ■ | ■ | | | ■ | | AMP/TE/SXT |
| | FD3K2/ST624/B2 | ■ | ■ | ■ | | | ■ | ■ | | TE/CIP/SXT/C/ESBL+ |
| | UTI 28/U/F | ■ | ■ | ■ | ■ | ■ | | | | AMP |
| | UTI 31/ST404/B2 | ■ | ■ | ■ | ■ | ■ | ■ | | | AMP/SXT |
| IV | FD202/ ST5451/D | ■ | ■ | ■ | | ■ | ■ | ■ | | TE/SXT/ESBL+ |
| | CM02/U/D | ■ | ■ | ■ | | ■ | ■ | ■ | | AMP/TE/SXT/PRL |

| | | | |
|---|------------------------------|---------------|-------------------|
| V | UTI 16/ST69/ D | ■ ■ ■ | AMP, SXT |
| | WW01/ST1049/ B1 | ■ ■ | AMP |
| | FOOD 10(h)/ST6073/ B1 | ■ ■ | AMP/TE |
| | FOOD 38(h)/U/U | ■ ■ ■ ■ ■ | - |
| | FOOD 29(h)/U/U | ■ ■ ■ ■ ■ | - |
| | UTI 42/U/C | ■ ■ ■ ■ ■ ■ ■ | AMP/TE/CIP/NF/SXT |
| | FOOD 23(t)/U/U | ■ ■ ■ ■ ■ ■ | - |
| | FOOD 19s(b)/ST5295/ A | ■ ■ ■ ■ ■ ■ ■ | AMP/TE/CIP/SXT |
| | FOOD 25(p)/ST10888/ A | ■ ■ ■ ■ ■ | - |

Note: ■ – presence of gene; ST – sequence type (MLST); Ph – Phylogroup;

U – unknown; AMP-ampicillin, TE-tetracycline, SXT-trimethoprim/sulfamethoxazole, CIP-ciprofloxacin, PRL-piperacillin, C-chloramphenicol, AMC-amoxicillin/clavulanic acid, CXM-cefuroxime, NF-nitrofurantoin, CTX-cefotaxime, AK-amikacin;

Type of meat: h-chicken, p-pork, t-turkey, b-beef;

Table S15. Statistical association between VGs of *E. coli* isolates derived from poultry farms (n=44) – Phi coefficient

| <i>fimH</i> | <i>papC</i> | <i>iha</i> | <i>irp2</i> | <i>iss</i> | <i>usp</i> | <i>vat</i> | <i>pic</i> |
|-------------|-------------|------------|-------------|------------|------------|------------|------------|
| <i>fimH</i> | 0.01 | 0.03 | 0.12 | 0.13 | 0.26 | 0.07 | 0.25 |
| | <i>papC</i> | 0.14 | 0.29 | 0.33* | 0.22 | 0.14 | 0.36* |
| | | <i>iha</i> | 0.09 | 0.09 | 0.13 | 0.04 | 0.13 |
| | | | <i>irp2</i> | 0.59* | 0.37* | 0.18 | 0.66* |
| | | | | <i>iss</i> | 0.53* | 0.19 | 0.60* |
| | | | | | <i>usp</i> | 0.26 | 0.67* |
| | | | | | | <i>vat</i> | 0.27 |
| | | | | | | | <i>pic</i> |

Phi coefficient values:

Very strong associations between variables $\phi > 0.7$; strong associations $0.5 < \phi < 0.7$; moderate associations $0.3 < \phi < 0.5$; weak associations $\phi < 0.3$

Table S16. Statistical association between VGs of *E. coli* isolates derived from UTI (n=50) - Phi coefficient

| <i>fimH</i> | <i>papC</i> | <i>iha</i> | <i>irp2</i> | <i>iss</i> | <i>usp</i> | <i>vat</i> | <i>pic</i> |
|-------------|-------------|------------|-------------|------------|------------|------------|------------|
| <i>fimH</i> | 0.24 | 0.09 | 0.03 | 0.21* | 0.02 | 0.08 | 0.13 |
| | <i>papC</i> | 0.09 | 0.34* | 0.28* | 0.24 | 0.27 | 0.27 |
| | | <i>iha</i> | 0.13 | 0.02 | 0.09 | 0.09 | 0.18 |
| | | | <i>irp2</i> | 0.08 | 0.70* | 0.11 | 0.02 |
| | | | | <i>iss</i> | 0.21 | 0.01 | 0.03 |
| | | | | | <i>usp</i> | 0.24 | 0.13 |
| | | | | | | <i>vat</i> | 0.46* |
| | | | | | | | <i>pic</i> |

Phi coefficient values:

Very strong associations between variables $\phi > 0.7$; strong associations $0.5 < \phi < 0.7$; moderate associations $0.3 < \phi < 0.5$; weak associations $\phi < 0.3$

Table S17. Statistical association between VGs of *E. coli* isolates derived from food (n=38) - Phi coefficient

| <i>fimH</i> | <i>papC</i> | <i>iha</i> | <i>irp2</i> | <i>iss</i> | <i>usp</i> | <i>vat</i> | <i>pic</i> |
|-------------|-------------|------------|-------------|------------|------------|------------|------------|
| <i>fimH</i> | 0.18 | 0.16 | 0.23 | 0.35* | 0.10 | 0.12 | 0.38* |
| | <i>papC</i> | 0.28 | 0.22 | 0.41* | 0.24 | 0.18 | 0.59* |
| | | <i>iha</i> | 0.14 | 0.30 | 0.17 | 0.16 | 0.28 |
| | | | <i>irp2</i> | 0.04 | 0.14 | 0.29 | 0.34* |
| | | | | <i>iss</i> | 0.40* | 0.03 | 0.41* |
| | | | | | <i>usp</i> | 0.10 | 0.24 |
| | | | | | | <i>vat</i> | 0.20 |

pic

Phi coefficient values:

Very strong associations between variables $\phi > 0.7$; strong associations $0.5 < \phi < 0.7$

moderate associations $0.3 < \phi < 0.5$; weak associations $\phi < 0.3$

Figure S1. Dendrogram generated from ERIC-PCR banding pattern of 132 *E. coli* isolated from poultry farms, food and patients with UTI symptoms. The process was performed in a volume of 25 μ L, including 2.5 μ L of 10x Taq buffer, 2.5 μ L of each dNTP Mix, 0.6 μ L of forward and reverse primers, 1 μ g of template DNA, 0.62 U of DreamTag DNA polymerase, and nuclease-free water. The reaction products were isolated with 1% agarose gel electrophoresis (Amresco) and visualized with GelDoc XR (Biorad). The similarity analysis was performed with Dice coefficient and UPGMA method.