

Table S1. The distribution of antimicrobial-resistant *E. coli* in different age groups in 2009-2010 and 2020.

[illegible]

CZ ^{a,b}	15 (20.0)	10 (16.1)	9 (9.3)	41 (46.1)	52 (56.5)	39 (43.8)	15 (25.0)	0 (0)	10 (16.1)	15 (22.7)	21 (30.9)	31 (46.3)
CXM ^{a,b}	15 (20.0)	9 (14.5)	9 (9.3)	43 (48.3)	51 (55.4)	37 (41.6)	14 (23.3)	0 (0)	10 (16.1)	14 (21.2)	19 (27.9)	28 (41.8)
CMZ ^a	2 (2.7)	5 (8.1)	4 (4.1)	18 (20.2)	31 (33.7)	22 (24.7)	1 (1.7)	0 (0)	2 (3.2)	2 (3.0)	6 (8.8)	6 (9.0)
Extended-spectrum cephalosporins												
CRO ^{a,b}	16 (21.3)	9 (14.5)	9 (9.3)	40 (44.9)	50 (54.3)	37 (41.6)	14 (23.3)	0 (0)	9 (14.5)	15 (22.7)	19 (27.9)	31 (46.3)
CAZ ^a	12 (16.0)	10 (16.1)	8 (8.2)	32 (36.0)	47 (51.1)	31 (34.8)	10 (16.7)	0 (0)	6 (9.7)	14 (21.2)	13 (19.1)	16 (23.9)
FEP ^a	9 (12.0)	4 (6.5)	4 (4.1)	18 (20.2)	18 (19.6)	19 (21.3)	10 (16.7)	0 (0)	5 (8.1)	11 (16.7)	10 (14.7)	15 (22.4)
Cephameycins												
FOX ^a	8 (10.7)	7 (11.3)	8 (8.2)	27 (30.3)	44 (47.8)	30 (33.7)	3 (4.9)	0 (0)	4 (6.5)	5 (7.6)	9 (13.2)	9 (13.4)
Fluoroquinolones												
CIP ^{a,b}	20 (26.7)	13 (21.0)	25 (25.8)	42 (47.2)	60 (65.2)	51 (57.3)	20 (33.3)	4 (23.5)	20 (32.3)	26 (39.4)	40 (58.8)	39 (58.2)
LVX ^{a,b}	15 (20.0)	9 (14.5)	18 (18.6)	34 (38.2)	50 (54.3)	43 (48.3)	16 (26.7)	1 (5.9)	13 (21.0)	18 (27.3)	33 (48.5)	36 (53.7)
Tetracyclines												
TE	46 (61.3)	36 (58.1)	52 (53.6)	54 (60.7)	54 (58.7)	52 (58.4)	29 (48.3)	8 (47.1)	27 (43.5)	36 (54.5)	35 (51.5)	33 (49.3)
Glycylcyclines												
TIG	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
Folate pathway inhibitors												
SXT ^a	41 (54.7)	30 (48.4)	36 (37.1)	47 (52.8)	54 (58.7)	54 (60.7)	32 (53.3)	6 (35.3)	24 (38.7)	26 (39.4)	34 (50.0)	24 (35.8)
Drug-resistance ^a												
MDR	39 (52.0)	29 (46.8)	36 (37.1)	54 (60.7)	64 (70.0)	57 (64.0)	36 (60.0)	7 (41.2)	29 (46.8)	36 (54.5)	39 (57.4)	40 (59.7)
XDR	1 (1.3)	2 (3.2)	2 (2.1)	5 (5.6)	11 (12.0)	5 (5.6)	0 (0)	0 (0)	2 (3.2)	1 (1.5)	5 (7.4)	4 (6.0)

^aThe distribution of antimicrobial resistance of *E. coli* isolated from different age groups in 2009-2010 showed a significant difference ($p < 0.05$).

^bThe distribution of antimicrobial resistance of *E. coli* isolated from different age groups in 2020 showed a significant difference ($p < 0.05$).

Abbreviations: AM, ampicillin; AMC, amoxicillin; AN, amikacin; CAZ ceftazidime, CIP, ciprofloxacin; CMZ, cefmetazole; CRO, ceftriaxone; CXM, cefuroxime; CZ, cefazolin; ETP, ertapenem; FEP, cefepime; FOX, ceftazidime; GM, gentamicin; LVX, levofloxacin; IPM, imipenem; MEM meropenem; SAM, ampicillin/sulbactam; SXT, sulfamethoxazole/trimethoprim; TE, tetracycline; TIG, tigecycline; TZP, piperacillin/tazobactam; I, intermediate resistant; R, resistant; MDR, multidrug-resistant; XDR, extensively drug-resistant.

Table S2. The distribution of virulence factors in *E. coli* in different age groups in 2009-2010 and 2020.

Virulence factor genes	Age group (years old) in 2009-2010						Age group (years old) in 2020					
	≤3	4-20	21-40	41-60	61-80	>80	≤3	4-20	21-40	41-60	61-80	>80
	(n=75)	(n=62)	(n=97)	(n=89)	(n=92)	(n=89)	(n=60)	(n=17)	(n=62)	(n=66)	(n=68)	(n=67)
<i>papGI</i>	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	1 (1.5)	0 (0)
<i>papGII</i> ^{a,b}	35 (46.7)	17 (27.4)	34 (35.1)	22 (24.7)	17 (18.5)	19 (21.3)	30 (50.0)	5 (29.4)	13 (30.0)	11 (16.7)	8 (11.8)	10 (14.9)
<i>papGIII</i>	17 (22.7)	6 (9.7)	23 (23.7)	16 (18.0)	14 (15.2)	9 (10.1)	4 (6.7)	1 (5.9)	8 (12.9)	13 (19.7)	7 (10.3)	8 (11.9)
<i>sfa</i>	10 (13.3)	5 (8.1)	11 (11.3)	6 (6.7)	2 (2.2)	9 (10.1)	9 (15.0)	0 (0)	9 (14.5)	11 (16.7)	6 (8.8)	8 (11.9)
<i>foc</i> ^a	8 (10.7)	13 (21.0)	12 (12.4)	9 (10.1)	5 (5.4)	6 (6.7)	12 (20.0)	1 (5.9)	10 (16.1)	7 (10.6)	5 (7.4)	5 (7.5)
<i>cnfI</i> ^{a,b}	26 (34.7)	17 (27.4)	28 (28.9)	15 (16.9)	10 (10.9)	16 (18.0)	23 (38.3)	6 (35.3)	21 (33.9)	21 (31.8)	10 (14.7)	11 (16.4)
<i>aer</i> ^b	56 (74.7)	35 (56.5)	54 (55.7)	56 (62.9)	61 (66.3)	62 (69.7)	47 (78.3)	2 (11.8)	28 (45.2)	35 (53.0)	37 (54.4)	40 (59.7)
<i>usp</i> ^{a,b}	56 (74.7)	47 (75.8)	68 (70.1)	52 (58.4)	46 (50.0)	49 (55.1)	43 (71.7)	5 (29.4)	32 (51.6)	44 (66.7)	37 (54.4)	39 (58.2)
<i>iha</i>	37 (49.3)	22 (35.5)	28 (28.9)	27 (30.3)	30 (32.6)	36 (40.4)	24 (40.0)	4 (23.5)	15 (24.2)	20 (30.3)	21 (30.9)	27 (40.3)
<i>ompT</i> ^{a,b}	65 (86.7)	56 (90.3)	84 (86.6)	64 (71.9)	63 (68.5)	68 (76.4)	50 (83.3)	5 (29.4)	44 (71.0)	52 (78.8)	48 (70.6)	54 (80.6)
<i>afa</i> ^b	39 (52.0)	36 (58.1)	44 (45.4)	58 (65.2)	57 (62.0)	50 (56.2)	45 (75.0)	2 (11.8)	39 (62.9)	47 (71.2)	44 (64.7)	40 (59.7)
<i>iRONE</i> ^b	31 (41.3)	31 (50.0)	45 (46.4)	34 (38.2)	33 (35.9)	29 (32.6)	24 (40.0)	6 (35.3)	30 (48.4)	26 (39.4)	16 (23.5)	19 (28.4)
<i>fimH</i> ^a	74 (98.7)	62 (100)	96 (99.0)	89 (100)	85 (92.4)	84 (94.4)	56 (93.3)	14 (82.4)	52 (83.9)	61 (92.4)	59 (86.8)	61 (91.0)
<i>hly</i> ^a	33 (44.0)	15 (24.2)	28 (28.9)	16 (18.0)	16 (17.4)	17 (19.1)	25 (41.7)	9 (52.9)	20 (32.3)	18 (27.3)	15 (22.1)	18 (26.9)
<i>sat</i> ^a	36 (48.0)	16 (25.8)	25 (25.8)	24 (27.0)	30 (32.6)	34 (38.2)	28 (46.7)	2 (11.8)	25 (40.3)	22 (33.3)	33 (48.5)	29 (43.3)
<i>K1</i> ^a	18 (24.0)	27 (43.5)	37 (38.1)	16 (18.0)	11 (12.0)	17 (19.1)	11 (18.3)	5 (29.4)	15 (24.2)	13 (19.7)	14 (20.6)	17 (25.4)

^aThe distribution of virulence factors in *E. coli* isolated from different age groups in 2009-2010 showed a significant difference ($p < 0.05$).

^bThe distribution of virulence factors in *E. coli* isolated from different age groups in 2020 showed a significant difference ($p < 0.05$).

Table S3. Oligonucleotide primers used in this study

Primer	Sequence (5'-3')	Reference
Virulence factors detection		
afa-F	CGGCTTTTCTGCTGAACTGGCAGGC	[1]
afa-R	CCGTCAGCCCCCACGGCAGACC	
iroN-F	AAGTCAAAGCAGGGGTGCCCCG	[2]
iroN-R	GACGCCGACATTAAGACGCAG	
usp-1	CGGCTCTTACATCGGTGCGTTG	[3]
usp-2	GACATATCCAGCCAGCGAGTTC	
foc-F	GGTGAACCGCAGAAAATAC	[4]
foc-R	GAACTGTTGGGGAAAGAGTG	
sfa-F	GGATGTTTCTTTGGGTAATCTG	[4]
sfa-R	CATTCCCTGTATTCGCATAG	
iha-F	CTGGCGGAGGCTCTGAGATCA	[2]
iha-R	TCCTTAAGCTCCCGCGGCTGA	
ompT-F	ATCTAGCCGAAGAAGGAGGC	[5]
ompT-R	CCCGGGTCATAGTGTTCATC	
papGI-F	TCGTGCTCAGGTCCGGAATTT	[6]
papGI-R	TGGCATCCCCCAACATTATCG	
papGII-F	GGGATGAGCGGGCCTTTGAT	[6]
papGII-R	CGGGCCCCCAAGTAACTCG	
papGIII-1	GGCCTGCAATGGATTTACCTGG	[6]
papGIII-2	CCACCAAATGACCATGCCAGAC	
neuA-F	ATGATTACTCGACACTGTC	[7]
neuA-R	AACAATCTCCGCTATTTTCG	
iutA-F	GGCTGGACATCATGGGAACTGG	[2]
iutA-R	CGTCGGGAACGGGTAGAATCG	
cnf1-F	AGACGATTTTATCAATGACCCC	[8]
cnf1-R	CAAAAGACAGACCAAGCAATAC	
sat-F	ACGGTCAGGGATTTACATTT	[9]
sat-R	GCTATTTGGCTGTTATGTGC	
fimH-F	CATTCGCCTGTAAAACCGCC	[10]
fimH-R	ATAACACGCCGCCATAAGCC	
hlyA-F	AGCAATGCAGATGCAGATAC	[8]
hlyA-R	AATGGACAGGAATGAGAGGG	
Phylogenetic grouping		[11]
chuA.1b	GACGAACCAACGGTCAGGAT	

chuA.2	TGCCGCCAGTACCAAAGACA
yjaA.1b	TGAAGTGTCTCAGGAGACGCTG
yjaA.2b	ATGGAGAATGCGTTCCTCAAC
TspE4C2.1	CACTATTCGTAAGGTCATCC
TspE4C2.2	AGTTTATCGCTGCGGGTCGC
AceK.f	AACGCTATTCGCCAGCTTGC
ArpA1.r	TCTCCCCATACCGTACGCTA
ArpAgpE.f	GATTCCATCTTGTCAAAATATGCC
ArpAgpE.r	GAAAAGAAAAAGAATTCCCAA
trpAgpC.1	AGTTTTATGCCCAGTGCGAG
trpAgpC.2	TCTGCGCCGGTCACGCCC
aesI-F	CCTCTACTCACCCAAAAGTC
aesI-R	ATCACGTAACCACAACGCAC

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