

**Table S1.** Sequences of primers used to detect virulence genes, amplicon sizes and references.

Pathovar	Gene	Primers (5'- 3')	Virulence factor	Amplicon size (bp)	References
EHEC, EPEC	<i>escV</i>	ATTCTGGCTCTCTTCTTCTTTATGGCTG CGTCCCCTTTTACAAACTTCATCGC	component EscV	544	[14]
	<i>ent</i>	TGGGCTAAAAGAAGACACACTG CAAGCATCCTGATTATCTCACC	enterotoxin	629	
	<i>eaeA</i>	GACCCGGCACAAGCATAAGC CCACCTGCAGCAACAAGAGG	intimin	384	[14]
EPEC	<i>bfpB</i>	GACACCTCATTGCTGAAGTCG CCAGAACACCTCCGTTATGC	bundle-forming pilus	910	[14]
ETEC	<i>elt</i>	GAACAGGAGGTTTCTGCGTTAGGTG CTTTCAATGGCTTTTTTTTGGGAGTC	heat labile toxin LT	655	[14]
	<i>estIa</i>	CCTCTTTTAGYCAGACARCTGAATCASTTG CAGGCAGGATTACAACAAAGTTCACAG	heat-stable enterotoxin a	157	
	<i>estIb</i>	TGTCTTTTTCACCTTTCGCTC CGGTACAAGCAGGATTACAACAC	heat-stable enterotoxin b	171	
EIEC	<i>invE</i>	CGATAGATGGCGAGAAATTATATCCCG CGATCAAGAATCCCTAACAGAAGAATCAC	invasion protein	766	[14]
	<i>ipaH</i>	GAA AAC CCT CCT GGT CCA TCA GG GCC GGT CAG CCA CCC TCT GAG AGT AC	adhesin siderophore	437	
EHEC	<i>stx1</i>	ATA AAT CGC CAT TCG TTG ACT AC AGA ACG CCC ACT GAG ATC ATC	Shiga toxin 1	180	[14]
	<i>stx2</i>	GGCACTGTCTGAAACTGCTCC TCGCCAGTTATCTGACATTCTG	Shiga toxin 2	255	
	<i>hlyA</i>	GCATCATCAAGCGTACGTTCC AATGAGCCAAGCTGGTTAAGCT	hemolysin A	534	
	<i>saa</i>	CGTGATGAACAGGCTATTGC ATGGACATGCCTGTGGCAAC	STEC autoagglutinating adhesin	119	
EAEC	<i>astA</i>	TGCCATCAACACAGTATATCCG ACGGCTTTGTAGTCCTTCCAT	EAST1 toxin	102	[14]
	<i>aggR</i>	ACGCAGAGTTGCCTGATAAAG AATACAGAATCGTCAGCATCAGC	transcriptional activator	400	
	<i>pic</i>	AGCCGTTTCCGCAGAAGCC AAATGTCAGTGAACCGACGATTGG	serine protease	1,111	
NTEC	<i>cnf</i>	TTATATAGTCGTCAAGATGGA CACTAAGCTTTACAATATTGA	Cytotoxic necrotizing factor	633	[30]
APEC, UPEC	<i>irp-2</i>	AAGGATTCGCTGTTACCGGAC AACTCCTGATACAGGTGGC	yersiniabactin synthetase	413	[29]
	<i>iss</i>	ATCACATAGGATTCTGCCG CAGCGGAGTATAGATGCCA	increased serum survival	306	
	<i>pap-C</i>	TGATATCACGCAGTCAGTAGC CCGGCCATATTACATAA	papACEFG, genes of P fimbriae operon	501	
	<i>tsh</i>	ACTATTCTCTGCAGGAAGTC CTTCCGATGTTCTGAACGT	temperature-sensitive haemagglutinin	824	
	<i>cva/cvi</i>	TGGTAGAATGTGCCAGAGCAAG GAGCTGTTTGTAGCGAAGCC	colicin V	1181	
	<i>iucD</i>	ACAAAAAGTTCTATCGCTTCC CCTGATCCAGATGATGCTC	aerobactin	714	

<i>vat</i>	TCCTGGGACATAATGGTCAG GTGTCAGAACGGAATTGT	vacuolating toxin	981	[14]
<i>ompT</i>	TCATCCCCGGAAGCCTCCCTCACTACTAT TAGCGTTTGCTGCACTGGCTTCTGATAC	outer membrane prote- ase T	496	
<i>iutA</i>	GGCTGGACATCATGGGAACTGG CGTCGGGAACGGGTAGAATCG	aerobactin siderophore receptor	302	
<i>fyuA</i>	TGATTAACCCCGCGACGGGAA CGCAGTAGGCACGATGTTGTA GCGCATTGCTGATACTGTTG	yersiniabactin sidero- phore receptor	880	
<i>kpsII</i>	CATCCAGACGATAAGCATGAGCA	capsular antigen	272	[4]
<i>traT</i>	GGTGTGGTGCGATGAGCACAG CACGGTTCAGCCATCCCTGAG	complement resistance protein	290	

**Table S2.** Sequences of primers used to detect resistance genes.

Target gene	Sequence (5'–3')	Annealing tem- perature (°C)	Size of PCR product (bp)	Reference
<i>blaTEM</i>	GAG TAT TCA ACA TTT TCG T ACC AAT GCT TAA TCA GTG A	50	445	[35]
<i>blaCTX</i>	CGCCGCATACACTATTCTCAGAAATGA ACGCTCACCGGCTCCAGATTTAT		593	
<i>blaOXA</i>	ATGTGCAGyACCAGTAArGTkATGGC TGGGTrAArTArGTsACCAGAAyCAGCGG		813	
<i>blaSHV</i>	ACACAATACATATCAACTTCGC AGTGTGTTTAGAATGGTGATC		237	
<i>tetA</i>	GTG AAA CCC AAC ATA CCC C GAA GGC AAG CAG GAT GTA G	63	887	[36]
<i>tetB</i>	CCT TAT CAT GCC AGT CTT GC ACT GCC GTT TTT TCG CC		773	
<i>tetC</i>	GCTGTAGGCATAGGCTTGGT GCCGGAAGCGAGAAGAATCA		888	
<i>tetM</i>	GTG GAC AAA GGT ACA ACG AG CGG TAA AGT TCG TCA CAC AC	62	406	[23]
<i>tetO</i>	AAC TTA GGC ATT CTG GCT CAC TCC CAC TGT TCC ATA TCG TCA		515	
<i>tetK</i>	GAT CAA TTG TAG CTT TAG GTG AAG G TTT TGT TGA TTT ACC AGG TAC CAT T		155	
<i>tetL</i>	TGG TGG AAT GAT AGC CCA TT CAG GAA TGA CAG CAC GCT AA		229	
<i>aadA</i>	GTGGATGGCGGCCTGAAGCC AATGCCCAGTCGGCAGCG	63	525	[36]
<i>strA/strB</i>	ATGGTGGACCCTAAACTCT CGTCTAGGATCGAGACAAAG		893	
<i>aac(3)-II</i>	ATA TCG CGA TGC ATA CGC GG GAC GGC CTC TAA CCG GAA GG	56	877	[14]
<i>aac(3)-IV</i>	CTT CAG GAT GGC AAG TTG GT TCA TCT CGT TCT CCG CTC AT	55	286	
<i>aphA1</i>	ATG GGC TCG CGA TAA TGT C CTC ACC GAG GCA GTT CCA T	50	600	[14]
<i>aphA2</i>	GAA CAA GAT GGA TTG CAC GC GCT CTT CAG CAA TAT CAC GG	50	680	
<i>sul1</i>	CGGCGTGGGCTACCTGAACG	65	433	[36]

<i>sul2</i>	GCCGATCGCGTGAAGTTCCG CGG CAT CGT CAA CAT AAC CT TGTGCGGATGAAGTCAGCTC	721	
<i>sul3</i>	CAA CGG AAG TGG GCG TTG TGG A GCT GCA CCA ATT CGC TGA ACG	244	
<i>dfrA1</i>	TGGTAGCTATATCGAAGAATGGAGT TATGTTAGAGGCGAAGTCTTGGGTA	425	
<i>dfrA5</i>	AGCTACTCTTTAAAGCCTTGACGTA GTGTTGCTCAAAAACAACCTTCG	60	341 [37]
<i>dfrA7-17</i>	ACATTTGACTCTATGGGTGTTCTTC AAAACCTGTTCAAAAACCAAATTGAA	280	

**Table S3.** Primer sequences used to determine phylogenetic groups in *E. coli* strains.

Gene	Sequence of primers (5'-3')	PCR product	Amplicon size [bp]	Reference
<i>yjaA</i>	TGAAGTGTCAAGGAGACGCTG TGAAGTGTCAAGGAGACGCTG	stress response protein	211	
TspE4.C2	GAG TAA TGT CGG GGC ATT CA CGC GCC AAC AAA GTA TTA CG	anonymous DNA fragment	152	
<i>chuA</i>	GAC GAA CCA ACG GTC AGG AT TGC CGC CAG TAC CAA AGA CA	outer membrane hemin receptor ChuA	279	[35]
<i>svg</i>	TCCGGCTGATTACAAACCAAC CTGCACGAGGTTGTAGTCCTG	hypothetical protein, sequence lo- cated at open reading frame (ORF) specific for virulent B2 <sub>1</sub> subgroup of <i>E. coli</i>	434	
<i>uidA</i>	ATC ACC GTG GTG ACG CATGTC GC CAC CAC GAT GCC ATG TTC ATC TGC-3	glucuronidase	486	