

**Supplementary data**  
**Genomic Comparison Reveals Natural Occurrence of Clinically  
Relevant Multi-Drug Resistant Extended-Spectrum  $\beta$ -lactamase  
producing *Escherichia coli***

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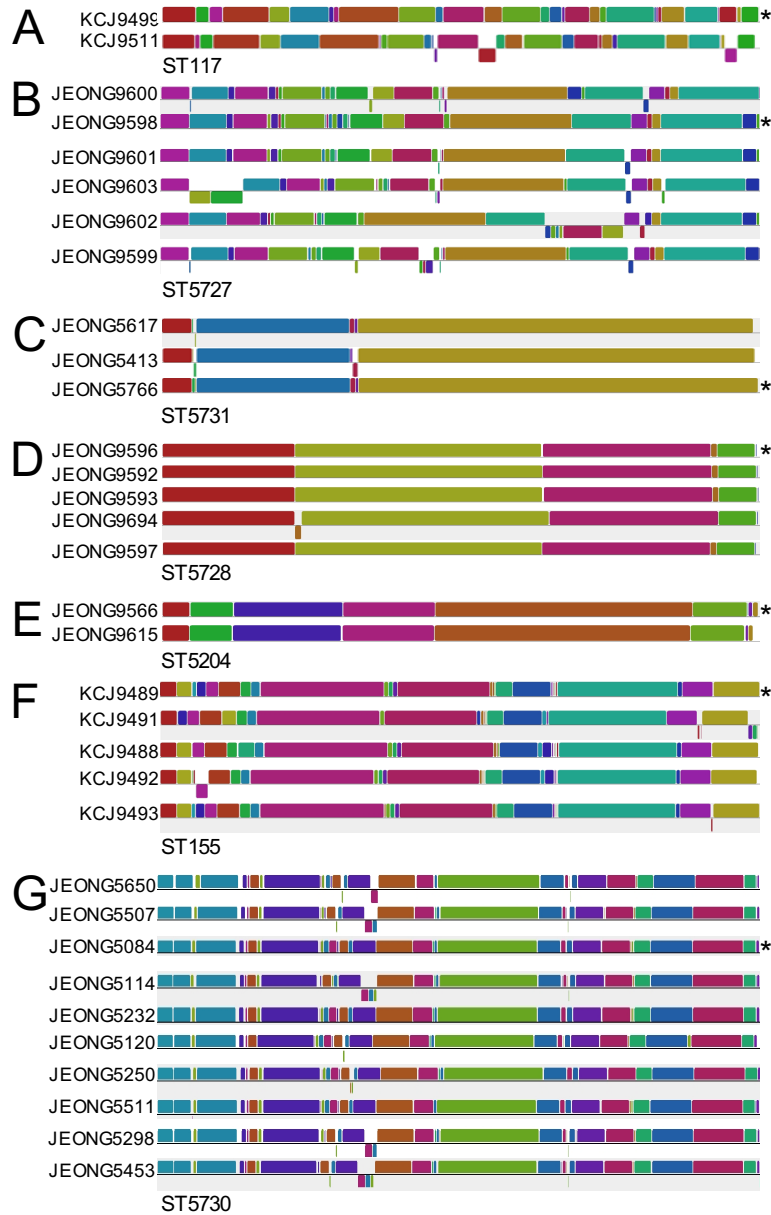
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**Running Title: Natural occurrence of ESBL *E.coli***

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Table S1. Genome sequencing information of strains used in this study

Strain Name	Accession number	Description of Isolation Source	Genome Size (bp)	Contig number	N50	References
JEONG5084	<a href="#">NSED00000000</a>	Feces of beef cattle from BRU	5,169,803	404	42,853	This Study
JEONG5114	<a href="#">NSEE00000000</a>	Feces of beef cattle from BRU	5,156,802	468	37,061	This Study
JEONG5120	<a href="#">NSEF00000000</a>	Feces of beef cattle from BRU	5,083,504	681	18,827	This Study
JEONG5232	<a href="#">NSEG00000000</a>	Feces of beef cattle from BRU	5,119,940	591	24,586	This Study
JEONG5250	<a href="#">NSEH00000000</a>	Feces of beef cattle from BRU	5,134,425	576	30,286	This Study
JEONG5298	<a href="#">NSEI00000000</a>	Feces of beef cattle from BRU	5,206,665	440	45,176	This Study
JEONG5413	<a href="#">NSEJ00000000</a>	Feces of beef cattle from BRU	4,821,355	247	85,136	This Study
JEONG5446	<a href="#">NSEK00000000</a>	Feces of beef cattle from BRU	5,607,261	417	62,828	This Study
JEONG5453	<a href="#">NSEL00000000</a>	Feces of beef cattle from BRU	5,214,502	364	58,096	This Study
JEONG5507	<a href="#">NSEM00000000</a>	Feces of beef cattle from BRU	5,189,762	458	42,281	This Study
JEONG5511	<a href="#">NSEN00000000</a>	Feces of beef cattle from BRU	5,132,836	555	27,714	This Study
JEONG5617	<a href="#">NSEO00000000</a>	Feces of beef cattle from BRU	4,797,640	172	90,738	This Study
JEONG5650	<a href="#">NSEP00000000</a>	Feces of beef cattle from BRU	5,081,214	437	48,231	This Study
JEONG5766	<a href="#">NSEQ00000000</a>	Feces of beef cattle from BRU	4,806,311	103	213,321	This Study
JEONG5776	<a href="#">NSER00000000</a>	Feces of beef cattle from BRU	5,300,733	133	155,776	This Study
JEONG9566	<a href="#">PKKV00000000</a>	Feces of beef cattle from NFREC	4,660,015	213	69,758	This Study
JEONG9567	<a href="#">PKKU00000000</a>	Feces of beef cattle from NFREC	4,812,461	130	110,948	This Study
JEONG9592	<a href="#">PKKW00000000</a>	Feces of beef cattle from NFREC	4,622,443	59	282,672	This Study
JEONG9593	<a href="#">QDJW00000000</a>	Feces of beef cattle from NFREC	4,623,655	56	240,083	This Study
JEONG9594	<a href="#">QDJX00000000</a>	Feces of beef cattle from NFREC	4,615,016	119	81,805	This Study
JEONG9596	<a href="#">QDJY00000000</a>	Feces of beef cattle from NFREC	4,604,110	170	64,951	This Study
JEONG9597	<a href="#">QDKF00000000</a>	Feces of beef cattle from NFREC	4,612,956	147	67,266	This Study
JEONG9598	<a href="#">PKKX00000000</a>	Feces of beef cattle from NFREC	4,919,012	141	86,030	This Study
JEONG9599	<a href="#">QDJZ00000000</a>	Feces of beef cattle from NFREC	4,931,346	96	111,796	This Study
JEONG9600	<a href="#">QDKA00000000</a>	Feces of beef cattle from NFREC	4,930,684	110	122,732	This Study
JEONG9601	<a href="#">QDKB00000000</a>	Feces of beef cattle from NFREC	4,912,261	221	49,238	This Study
JEONG9602	<a href="#">QDKC00000000</a>	Feces of beef cattle from NFREC	4,914,792	204	56,569	This Study
JEONG9603	<a href="#">QDKD00000000</a>	Feces of beef cattle from NFREC	4,905,796	246	52,734	This Study
JEONG9615	<a href="#">QDKE00000000</a>	Feces of beef cattle from NFREC	4,629,950	309	35,221	This Study
KCJ9488	<a href="#">QGNB00000000</a>	Feces of beef cattle from BRU	4,850,507	113	179,208	This Study
KCJ9489	<a href="#">QGNC00000000</a>	Feces of beef cattle from BRU	4,852,703	106	288,589	This Study
KCJ9491	<a href="#">QGND00000000</a>	Feces of beef cattle from BRU	4,847,940	120	211,772	This Study
KCJ9492	<a href="#">QGNE00000000</a>	Feces of beef cattle from BRU	4,851,025	109	193,455	This Study
KCJ9493	<a href="#">QGNF00000000</a>	Feces of beef cattle from BRU	4,824,226	299	39,007	This Study
KCJ9499	<a href="#">QGNS00000000</a>	Feces of beef cattle from BRU	5,173,529	154	89,182	This Study
KCJ9511	<a href="#">QNGG00000000</a>	Feces of beef cattle from BRU	5,226,877	194	83,425	This Study



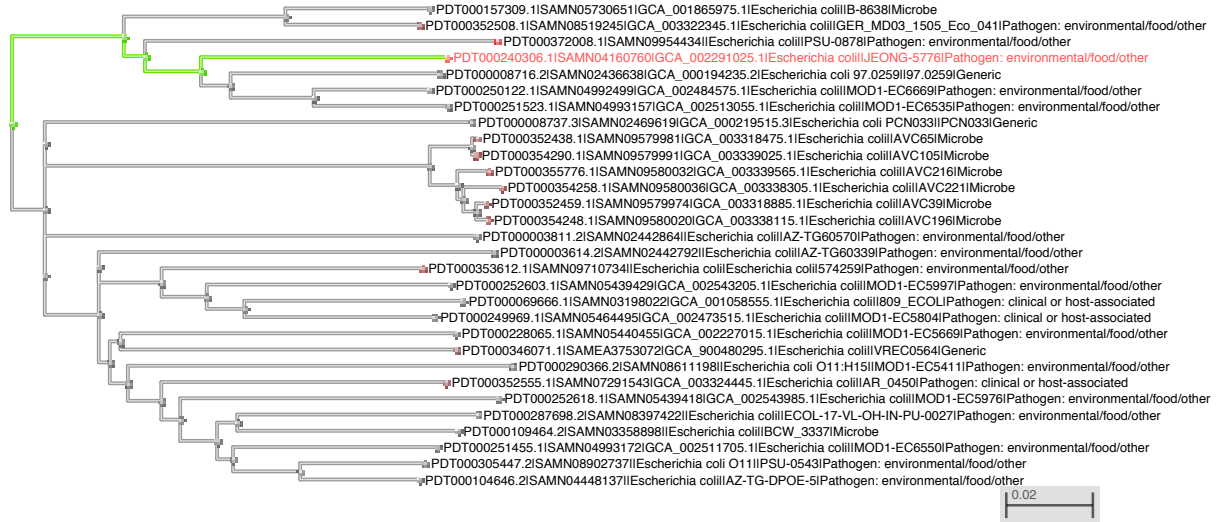
**Fig S1. Whole genome alignment of isolates in the same phylogenetic clade.** Whole genome sequences of strains within the same clade/ST were aligned using progressiveMauve with default setting. A strain with an asterisk (\*) in each sub-figure (A-G) was the reference genome in each alignment. Blocks with the same color indicate the homologous regions among/between strains in each sub-figure. An upper block indicates that the genomic region is in the same direction as the homologous region in the reference genome, while a bottom block represents an inverted genomic region.



C



D



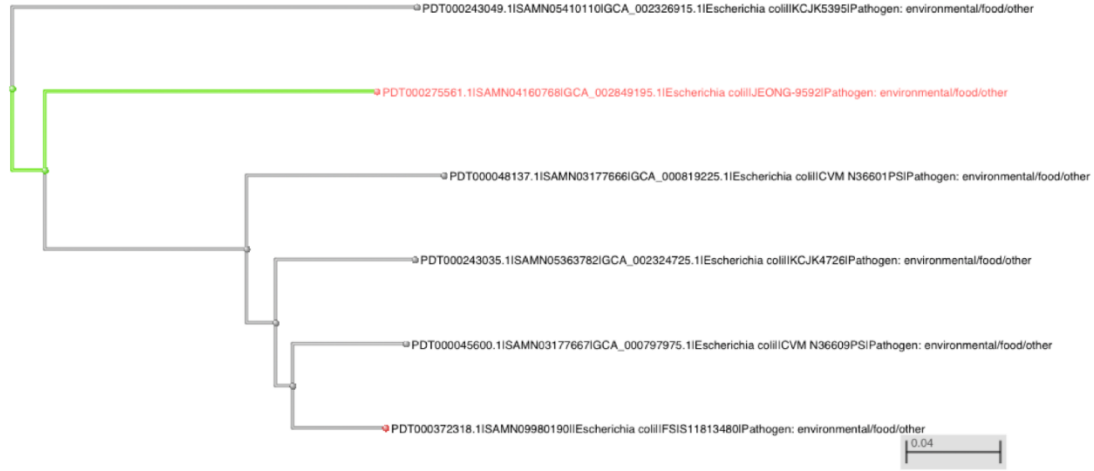
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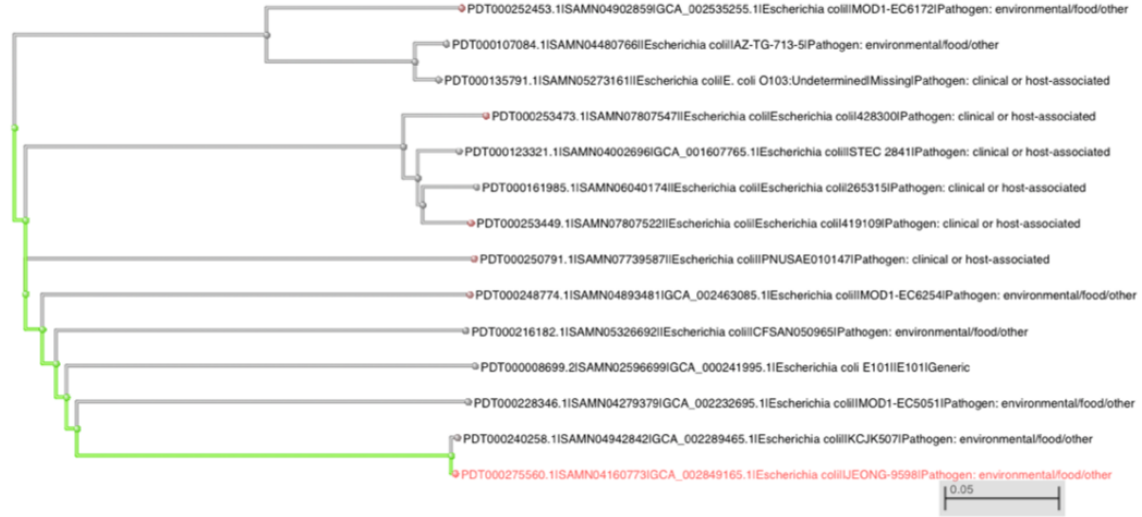
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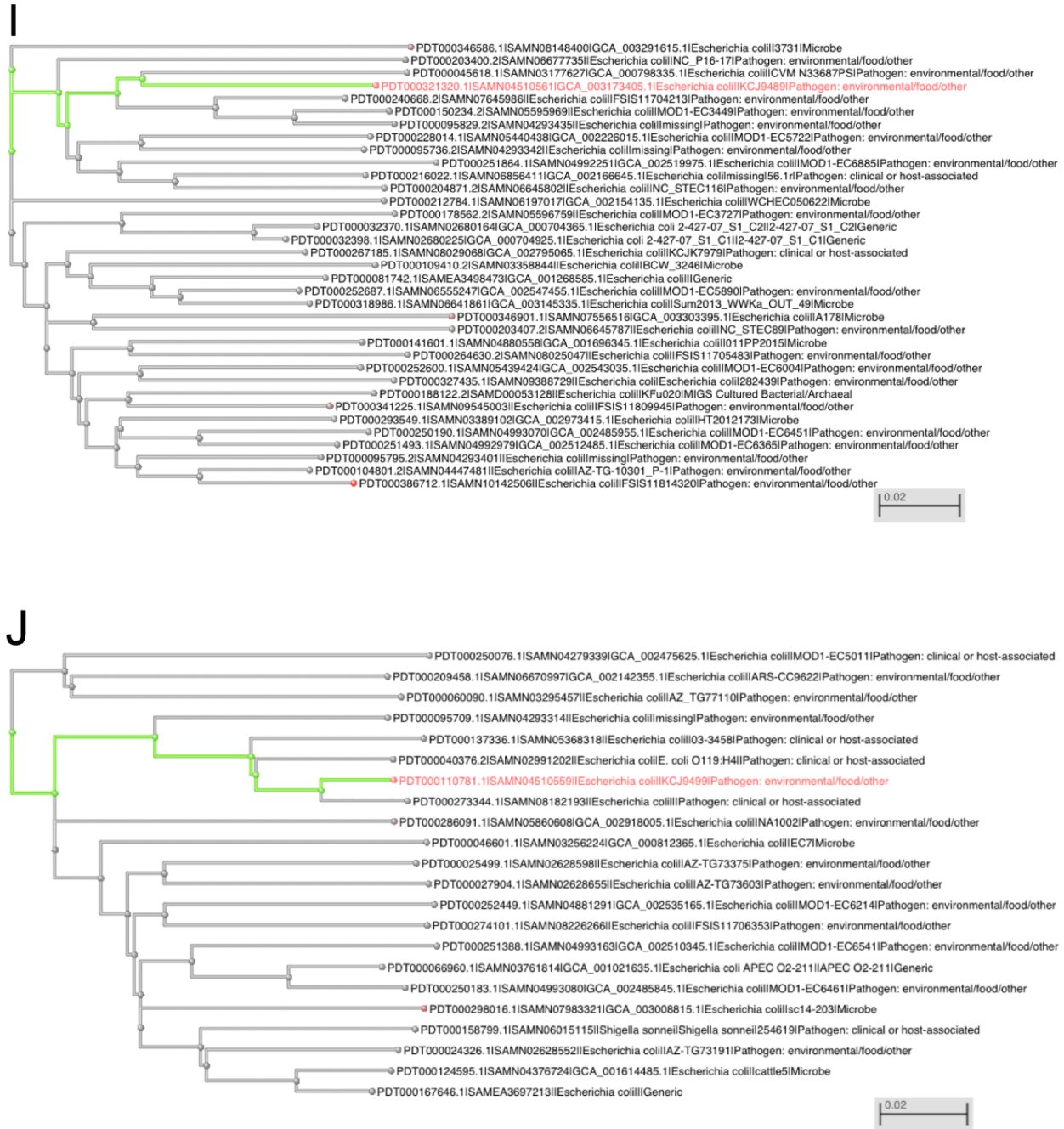


G



H





**Fig S2. Phylogenetic trees of multidrug resistant *E. coli* isolates with other global lineages.**

Phylogenetic trees analyses was conducted using the GenomeTrakr database to identify clonal variants of the representative MDR *E. coli* isolates selected from the clades in Figure 2. Strains in red color are A) JEONG5232 (ST5730), B) JEONG5446 (ST306), C) JEONG5766 (ST5731), D) JEONG5776 (ST973), E) JEONG9566 (ST5204), F) JEONG9567 (ST10), G) JEONG9592



(ST5728), H) JEONG9598 (ST5727), I) KCJ9489 (ST155), and J) KCJ9499 (ST117).

Phylogenetic trees were generated using the Genome Workbench (1). The scale bars represent the mean numbers of nucleotide substitution per site.

## Supplementary Reference

1. NCBI. 2017. Database Resources of the National Center for Biotechnology Information. *Nucleic Acids Res* 45:D12-D17.