

Supplementary Materials

Table S1. Drug combinations and dosage regimens.

Combination Number	Drug A with Dose	Drug B with Dose
i.	Co-amoxiclav (1 mL/10 kg body weight, IM)	Gentamicin (3.3 mg/kg BW, IM)
ii.	Oxytetracycline (17 mg/kg BW)	
iii.	Gentamicin (6.6 mg/15 kg BW, IM)	Enrofloxacin (2.5 mg/kg BW, IM)
iv.	Gentamicin (6.6 mg/15 kg BW, IM)	
v.	Enrofloxacin (20 mL, IU)	Metronidazole (100 mL, IU)
vi.	Amoxicillin (25mL, IU)	Streptomycin (2g, IU)
vii.	Amoxicillin (25mL, IU)	Metronidazole (100 mL, IU)
viii.	Amoxicillin (25mL, IU)	Gentamicin (10mL, IU)

BW, body weight; IM, intramuscular; IU, Intrauterine.

Table S2. MIC comparison of tested antibiotics against *E. coli*.

Antibiotics	Mean + Std.	95% Confidence Interval for Mean		<i>p</i> -value
		Lower Bound	Upper Bound	
Amoxicillin	13.54+4.77	8.5322	18.5512	0.0000
Calamox	7.70+4.40	3.0819	12.3261	
Metronidazole	166.67+75.69	87.2336	246.0998	
Enrofloxacin	2.20+1.37	0.7705	3.6403	
Streptomycin	11.59+4.11	7.2718	15.9053	
Gentamicin	3.02+2.55	0.3447	5.6937	
Oxytetracycline	17.07+7.78	8.9102	25.2333	

Seq	ATCAACCGAGATTCCCCAGTAGCGGCGAGCGAACGGGGAGGAGCCCAGAGCCTGAATCA	60
Seq1	ATCAACCGAGATTCCCCAGTAGCGGCGAGCGAACGGGGAGGAGCCCAGAGCCTGAATCA	60
Seq2	ATCAACCGAGATTCCCCAGTAGCGGCGAGCGAACGGGGAGGAGCCCAGAGCCTGAATCA	60
Seq3	ATCAACCGAGATTCCCCAGTAGCGGCGAGCGAACGGGGAGGAGCCCAGAGCCTGAATCA	60
Seq4	ATCAACCGAGATTCCCCAGTAGCGGCGAGCGAACGGGGAGGAGCCCAGAGCCTGAATCA	60

Seq	GTGTGTGTGTTAGTGGAAGCGTCTGGAAAGGCGCGGATACAGGGTGACAGCCCCGTACA	120
Seq1	GTGTGTGTGTTAGTGGAAGCGTCTGGAAAGGCGCGGATACAGGGTGACAGCCCCGTACA	120
Seq2	GTGTGTGTGTTAGTGGAAGCGTCTGGAAAGGCGCGGATACAGGGTGACAGCCCCGTACA	120
Seq3	GTGTGTGTGTTAGTGGAAGCGTCTGGAAAGGCGCGGATACAGGGTGACAGCCCCGTACA	120
Seq4	GTGTGTGTGTTAGTGGAAGCGTCTGGAAAGGCGCGGATACAGGGTGACAGCCCCGTACA	120

Seq	CAAAAAAATGCACATACTGTGAGCTCGATGAGTAGGGCGGGACACGTGGTATCCTGTCT	180
Seq1	CAAAAAAATGCACATACTGTGAGCTCGATGAGTAGGGCGGGACACGTGGTATCCTGTCT	180
Seq2	CAAAAAAATGCACATACTGTGAGCTCGATGAGTAGGGCGGGACACGTGGTATCCTGTCT	180
Seq3	CAAAAAAATGCACATACTGTGAGCTCGATGAGTAGGGCGGGACACGTGGTATCCTGTCT	180
Seq4	CAAAAAAATGCACATACTGTGAGCTCGATGAGTAGGGCGGGACACGTGGTATCCTGTCT	180

Seq	GAATATGGGGGACCATCCTCCAAGGCTAAATACTCCTGACTGACCGATAGTGA	233
Seq1	GAATATGGGGGACCATCCTCCAAGGCTAAATACTCCTGACTGACCGATAGTGA	233
Seq2	GAATATGGGGGACCATCCTCCAAGGCTAAATACTCCTGACTGACCGATAGTGA	233
Seq3	GAATATGGGGGACCATCCTCCAAGGCTAAATACTCCTGACTGACCGATAGTGA	233
Seq4	GAATATGGGGGACCATCCTCCAAGGCTAAATACTCCTGACTGACCGATAGTGA	233

Figure S1. Multiple sequence alignment of *E. coli* 23S ribosomal protein (reference and local isolates PK nucleotide sequences).

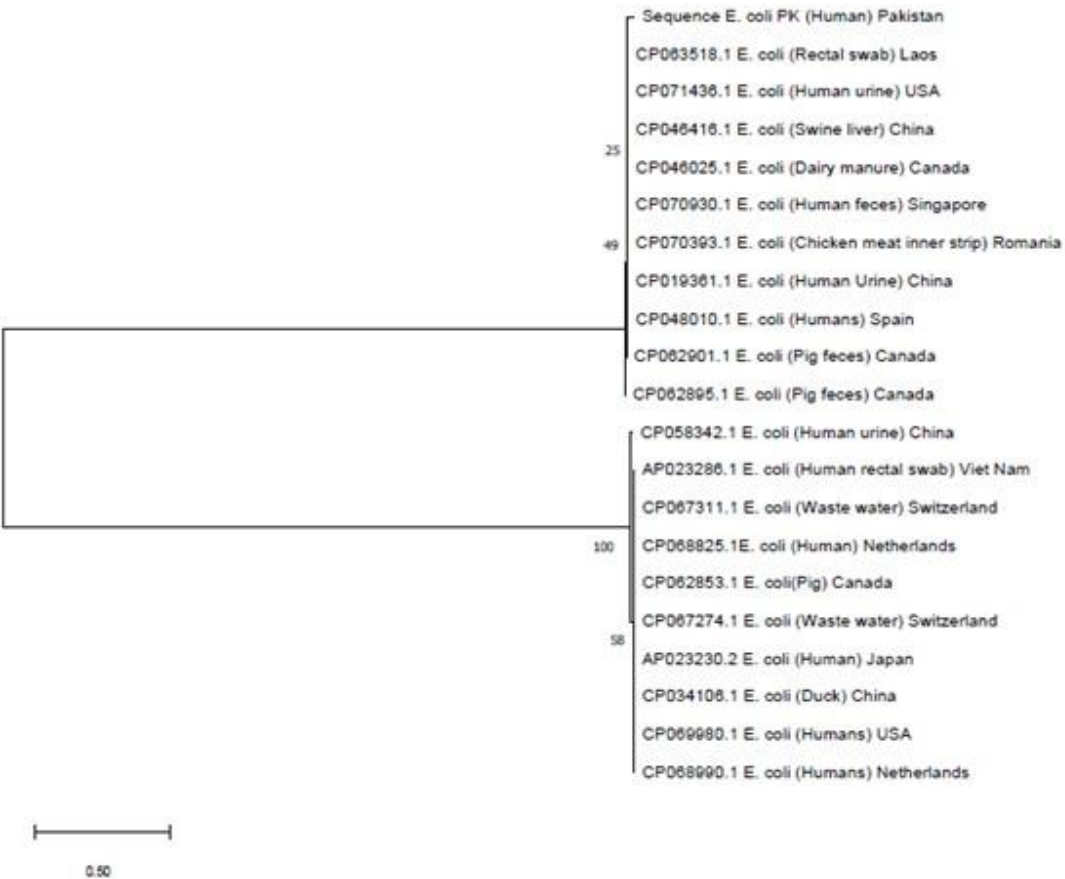


Figure S2. Phylogenetic tree of *E. coli* 23S ribosomal gene (nucleotide sequences). Analysis has been performed among different source samples of *E. coli* 23S ribosomal gene from different countries with our isolated sequenced samples. The branch length (numbers) are representing the nucleotide substitutions per 100 nucleotide sites.

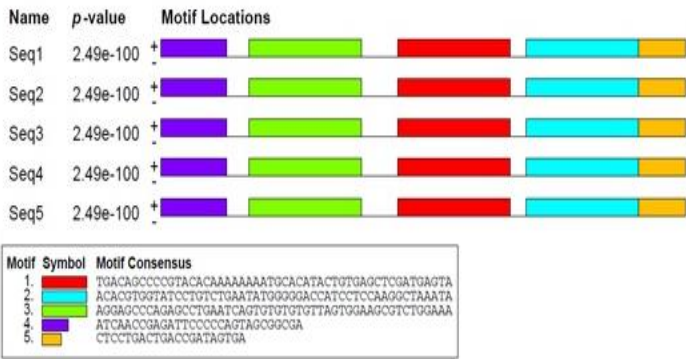


Figure S3. Motifs locations in gene sequences (1 to 5), sequence of individual motif and *p*-value of motifs in sequence 1 to 5.



Figure S4. Structural analysis of 23S *E. coli* ribosomal gene from Pakistan.