Immunological Pathogenesis of Bovine *E. coli* Infection in a Model of *C. elegans*

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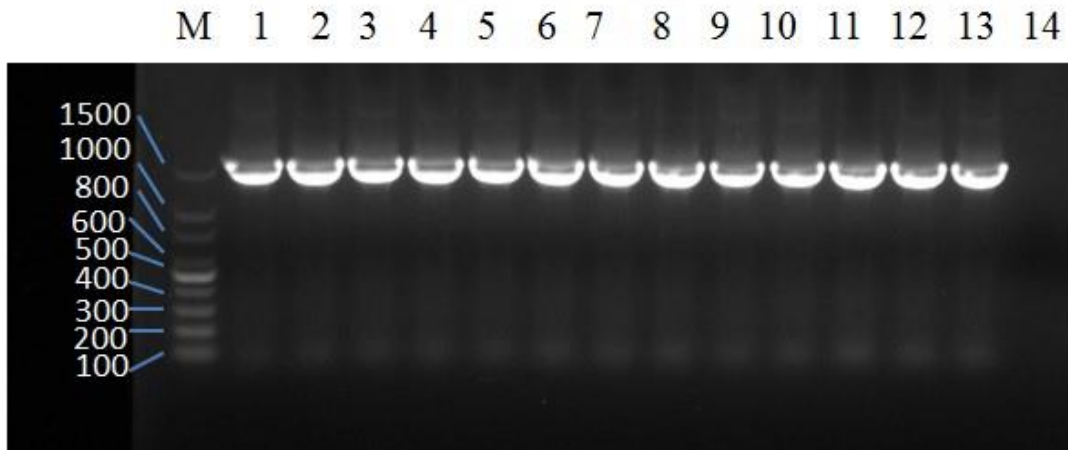
Figure S20. 16SrDNA PCR amplification results of 13 strains of bovine *Escherichia coli.* The blue lines represent the different bands of the marker

(M,marker.1-13, 13 strains of bovine Escherichia coli.14,control.)

Percent Identity

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21		
1	■	99.3	99.4	99.3	99.9	99.7	99.6	99.3	99.2	97.3	99.2	99.6	99.4	100.0	99.2	98.5	99.3	99.1	100.0	100.0	100.0	1	GX11.seq
2	0.7	■	99.8	99.9	99.3	99.0	99.6	100.0	99.8	97.7	99.7	99.3	99.3	99.3	99.9	99.1	99.2	99.6	99.2	99.2	99.3	2	GX12.seq
3	0.6	0.2	■	99.7	99.3	99.1	98.5	98.9	99.6	99.6	99.3	99.3	99.2	99.3	99.7	98.3	99.1	98.9	99.0	99.3	99.4	3	GX13.seq
4	0.7	0.1	0.3	■	99.3	97.1	97.0	97.8	98.9	96.4	97.8	99.2	98.8	99.3	99.8	98.3	98.8	98.9	98.9	99.3	99.3	4	JF690890.seq
5	0.1	0.7	0.7	0.7	■	99.7	99.7	99.3	99.3	98.0	99.2	99.6	99.3	99.7	99.2	98.5	99.2	99.1	99.7	99.7	99.9	5	JN129482.seq
6	0.3	1.0	0.9	3.0	0.3	■	99.0	98.5	96.6	93.1	99.0	99.2	98.6	99.7	98.6	97.4	98.6	98.6	99.6	99.7	99.7	6	JX136950.seq
7	0.4	0.4	1.5	3.0	0.3	1.0	■	99.2	98.7	95.3	97.1	99.0	99.3	99.4	99.3	98.6	99.3	99.2	99.3	99.4	99.6	7	KF963260.seq
8	0.7	0.0	1.1	2.3	0.7	1.6	0.8	■	99.5	96.0	97.2	98.7	99.2	99.3	99.6	98.8	99.2	99.4	99.1	99.2	99.3	8	KT152814.seq
9	0.8	0.2	0.4	1.2	0.7	3.5	1.4	0.5	■	96.5	98.7	99.3	99.1	99.1	99.6	98.9	99.2	99.5	99.1	99.1	99.2	9	MH158272.seq
10	2.8	2.4	0.4	3.7	2.0	7.2	4.8	4.1	3.6	■	95.7	99.0	96.5	97.4	97.3	95.8	96.3	96.4	96.8	97.2	97.3	10	FJ997270.seq
11	0.8	0.3	0.7	2.2	0.8	1.0	3.0	2.9	1.4	4.4	■	98.9	99.1	99.1	99.4	98.2	99.1	98.7	98.8	99.2	99.2	11	GQ157251.seq
12	0.4	0.7	0.7	0.8	0.4	0.8	1.0	1.3	0.7	1.0	1.1	■	99.3	99.5	99.4	98.3	99.4	98.8	99.1	99.5	99.6	12	GX01.seq
13	0.6	0.7	0.8	1.2	0.7	1.4	0.7	0.8	0.9	3.6	0.9	0.7	■	99.4	98.9	98.3	100.0	98.8	99.3	99.4	99.4	13	GX02.seq
14	0.0	0.7	0.7	0.7	0.3	0.3	0.6	0.7	0.9	2.7	0.9	0.5	0.6	■	99.2	98.4	99.3	99.0	99.9	99.9	100.0	14	GX03.seq
15	0.8	0.1	0.3	0.2	0.8	1.4	0.7	0.4	0.4	2.7	0.7	0.6	1.1	0.8	■	99.2	98.9	99.8	99.1	99.1	99.2	15	GX04.seq
16	1.5	0.9	1.7	1.7	1.5	2.6	1.4	1.2	1.1	4.3	1.9	1.8	1.8	1.6	0.8	■	98.2	99.4	98.6	98.6	98.5	16	GX05.seq
17	0.7	0.8	0.9	1.2	0.8	1.4	0.7	0.8	0.8	3.8	0.9	0.6	0.0	0.7	1.1	1.8	■	98.8	99.3	99.3	99.3	17	GX06.seq
18	0.9	0.4	1.1	1.1	0.9	1.4	0.8	0.6	0.5	3.7	1.3	1.2	1.2	1.0	0.2	0.6	1.2	■	99.1	99.1	99.1	18	GX07.seq
19	0.0	0.8	1.0	1.1	0.3	0.4	0.7	0.9	0.9	3.3	1.2	0.9	0.7	0.1	0.9	1.4	0.7	0.9	■	100.0	100.0	19	GX08.seq
20	0.0	0.8	0.7	0.7	0.3	0.3	0.6	0.8	0.9	2.9	0.8	0.5	0.6	0.1	0.9	1.5	0.7	0.9	0.0	■	100.0	20	GX09.seq
21	0.0	0.7	0.6	0.7	0.1	0.3	0.4	0.7	0.8	2.8	0.8	0.4	0.6	0.0	0.8	1.5	0.7	0.9	0.0	0.0	■	21	GX10.seq
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21		

Divergence

Figure S21. 16S rDNA Molecular Biological Identification Results of *Escherichia coli.* JF690890,JN129482,JX136950,KF963260,KT152814,MH158272,FJ997270,GQ157251 were *Escherichia coli* from different sources downloaded from NCBI as reference.