

**Table S1: Primers and PCR cycling conditions of this study**

Target gene	Primers sequences (5' – 3')	Product (bp)	Annealing Temp.	Reference
<b>REP-PCR</b>	REP1R: IIIICGICGICATCIGGC REP2: ICGICTTATCIGGCCTAC	Variable	40°C	[1]
<i>eaeA</i>	ATGCTTAGTGCTGGTTTAGG GCCTTCAT ATTTCGCTTTC	248	51°C	[2]
<i>bfpA</i>	AATGGTGCTTGCGCTTGCTGC GCCGCTTTATCCAACCTGGTA	326	56°C	[3]
<i>stx1</i>	ACACTGGATGATCTCAGTGG CTGAATCCCCCTCCATTATG	614	60°C	[4]
<i>stx2</i>	CCATGACAACGGACAGCAGTT CCTGTCAACTGAGCAGCACTTGG	779	60°C	
<i>bla<sub>TEM</sub></i>	CATTTCCGTGTCGCCCTTATTC CGTTCATCCATAGTTGCCTGAC	800	61°C	
<i>bla<sub>OXA-1</sub></i>	GGCACCAGATTCAACTTTCAAG GACCCCAAGTTTCCTGTAAGTG	564	61°C	
<i>bla<sub>SHV</sub></i>	AGGATTGACTGCCTTTTTG ATTTGCTGATTTGCTCG	392	54°C	[5]
<i>bla<sub>CTX-M-1</sub></i>	ATGTGCAGYACCAGTAARGTKATGGC TGGGTRAARTARGTSACCAGAAACAGCGG	593	54°C	[6]
<i>bla<sub>IMP</sub></i>	CATGGTTTGGTGGTTCCTTGT ATAATTTGGCGGACTTTGGC	488	55°C	[4]
<i>bla<sub>VIM</sub></i>	AGTGGTGAGTATCCGACA ATGAAAGTGCGTGGAGAC	280	52°C	
<i>bla<sub>NDM-1</sub></i>	GGCGGAATGGCTCATCACGA CGCAACACAGCCTGACTTTC	287	58°C	
<i>qnrA</i>	ATTCTCACGCCAGGATTTG GATCGGCAAAGGTTAGGTCA	516	53°C	
<i>qnrB</i>	GATCGTGAAAGCCAGAAAGG ACGATGCCTGGTAGTTGTCC	469	53°C	[7]
<i>qnrS</i>	ACGACATTCGTCAACTGCAA TAAATTGGCACCTGTAGGC	417	53°C	

## References

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## Supplementary Figures

NCBI Multiple Sequence Alignment Viewer, Version 1.21.0

Sequence ID	Start	Alignment	End	Organism	Country	Host
MW721313	(+) 1	<div> <div>1 10 20 30 40 50 61</div> <div> <div>ATGTGCAGCACCAAGTAAAGTTATGGCCGCGCGCCGCGGTGCTGAAGAAAAAGTGAAAGCGAAAC</div> <div> <div>blactX-M</div> <div>UBP30086.1</div> </div> </div> </div>	549	Escherichia coli	Egypt: ...	cattle
MW721311.1	(+) 1	<div> <div>1 10 20 30 40 50 61</div> <div> <div>ATGTGCAGCACCAAGTAAAGTTATGGCCGCGCGCCGCGGTGCTGAAGAAAAAGTGAAAGCGAAAC</div> <div> <div>blactX-M</div> <div>UBP30086.1</div> </div> </div> </div>	549	Escherichia coli	Egypt: ...	Homo s...
CP081589.1	(-) 3,392	<div> <div>1 10 20 30 40 50 61</div> <div> <div>ATGTGCAGCACCAAGTAAAGTTATGGCCGCGCGCCGCGGTGCTGAAGAAAAAGTGAAAGCGAAAC</div> <div> <div>K5584_01460</div> <div>O2N72863.1</div> </div> </div> </div>	2,844	Escherichia coli	Germany	
CP075059.1	(-) 62,918	<div> <div>1 10 20 30 40 50 61</div> <div> <div>ATGTGCAGCACCAAGTAAAGTTATGGCCGCGCGCCGCGGTGCTGAAGAAAAAGTGAAAGCGAAAC</div> <div> <div>H4F95_02610</div> <div>QV195937.1</div> </div> </div> </div>	62,370	Escherichia coli	China:Y...	swine
CP059120.1	(+) 57,405	<div> <div>1 10 20 30 40 50 61</div> <div> <div>ATGTGCAGCACCAAGTAAAGTTATGGCCGCGCGCCGCGGTGCTGAAGAAAAAGTGAAAGCGAAAC</div> <div> <div>H0X94_23985</div> <div>QXZ61115.1</div> </div> </div> </div>	57,953	Escherichia coli	Ghana	Homo s...
CP048916.1	(+) 52,969	<div> <div>1 10 20 30 40 50 61</div> <div> <div>ATGTGCAGCACCAAGTAAAGTTATGGCCGCGCGCCGCGGTGCTGAAGAAAAAGTGAAAGCGAAAC</div> <div> <div>G5S48_23015</div> <div>QWR75782.1</div> </div> </div> </div>	53,517	Escherichia coli	Egypt:G...	Homo s...

**Figure S1.** Sequence alignment of *bla*<sub>CTX-M-1</sub> gene of diarrheic calf isolate ID 2 (accession no.: MW721313) and worker isolate ID 3 (accession no.: MW721311) with *bla*<sub>CTX-M-15</sub> gene of other *E. coli* isolates on GenBank.

\* Red shadow: single nucleotide mutation (G to T at position 21).

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