

A novel shiga toxigenic *E. coli* sequence type harbouring multidrug resistance isolated from raw milk

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Supplementary File

Gene	Primer Sequence (5'-3')	Amplicon size (bp)
<i>bla</i> _{TEM}	F: CGCCGCATACACTATTCTCAGAATGA R: ACGCTCACCGGCTCCAGATTTAT	445
<i>bla</i> _{SHV}	F: ATGCGTTATATTCGCCTGTG R: TGCTTTGTTATTCGGGCCAA	747
<i>bla</i> _{VIM}	F: GATGGYGTTTGGTCGCATATCKCAAC R: CGAATGCGCAGCACCRGGATAGAA	390
<i>bla</i> _{CTX-M}	F: CGCTTTGCGATGTGCAG R: ACCGCGATATCGTTGGT	550

Table S1: Primer sequences used for genotypic analysis of antibiotic resistant genes in MDR STEC

Sequence Type	Serotype	Related Outbreaks
ST 10	K-12	Wild type strain
ST 11	O157:H7	Food borne
ST 33	O91:H14	Food borne
ST 73	CFT073	Uropathogenic strain
ST 75	STEC1589	Clinical Strain
ST 17	RMM13322	Raw milk
ST 3570	O86	Epidemic Strain
ST 5975	O113	Food borne
ST 446	O22	Food borne

Table S2: *E. coli* serotypes used for comparative analysis with corresponding Sequence Types (ST)

<i>E. coli</i> strains	*ps	*θ	*π	*D
K12	0.80	0.25	0.30	0.92
O157:H7	0.73	0.23	0.27	0.83
O22	0.78	0.25	0.31	1.12
O86	0.83	0.26	0.30	0.63
O91:H14	0.71	0.22	0.25	0.62
RMM13322	0.81	0.25	0.30	0.79
O113	0.80	0.25	0.31	1.03
STEC1589	0.79	0.25	0.30	0.89
CFT073	0.80	0.25	0.27	0.39
Novel ST	0.82	0.26	0.31	0.87

*ps = S (number of segregating sites)/n (total number of sites), *θ = (ps/a1), *π = nucleotide diversity, *D = Tajima's D test value

Table S3: Tajima's D Test that shows the evolutionary significance of Novel ST