

Phylogenomics of Shiga Toxin producing *Escherichia coli* O157:H7: assessing the risk of severe human disease in light of recent strain replacement in the cattle population in the United Kingdom

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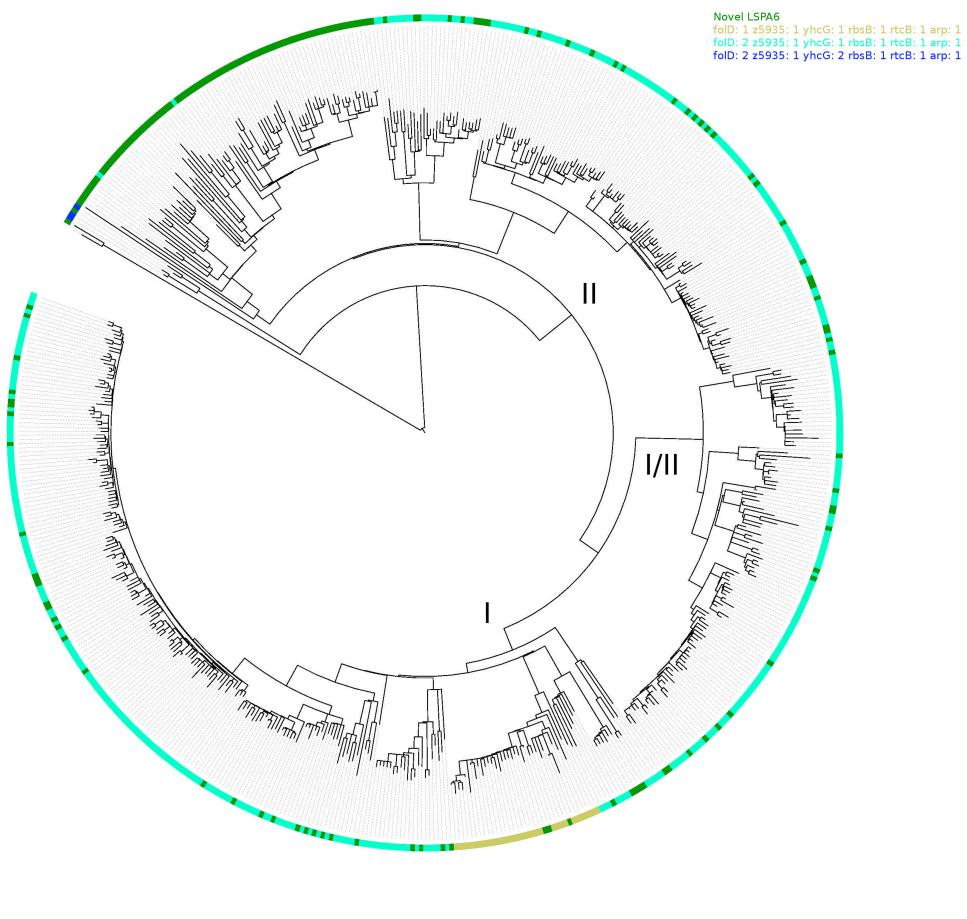
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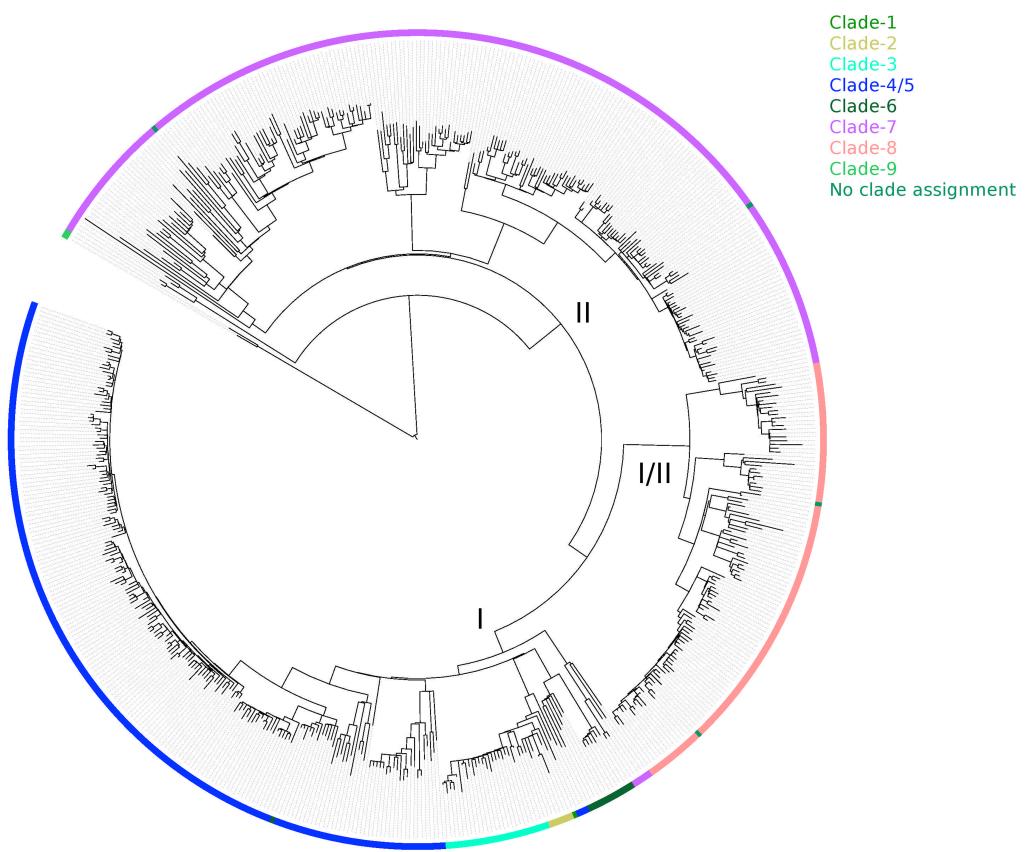
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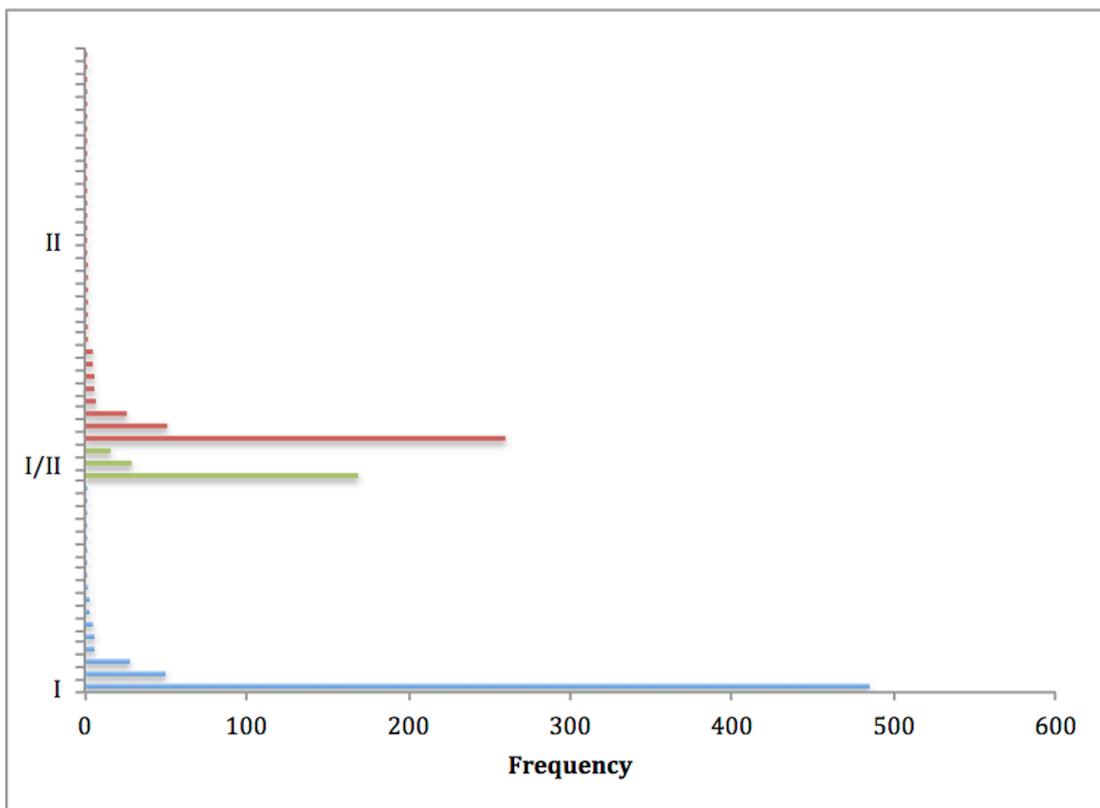
Supplementary Figure 1a.

Maximum likelihood phylogeny of 584 STEC O157:H7 $\Delta 25$ SNP representatives depicting the three lineages. The outer circle is coloured by LSPA-6 type.



Supplementary Figure 1b.

Maximum likelihood phylogeny of 584 STEC O157:H7 $\Delta 25$ SNP representatives depicting the three lineages. The outer circle is coloured by Manning Clade type.



Supplementary Figure 2.

Bar chart showing the number of isolates in each $\Delta 250$ SNP cluster.

Lineage	Intra Cluster Recombination	Donor to Lineage I	Donor to Lineage II	Donor to Lineage I/II
I (828)	19.3%	56.0%	20.3%	4.4%
I/II (384)	29.7%	15.1%	13.5%	41.7%
II (1088)	18.6%	16.5%	59.9%	5.0%

Supplementary Table 1.

Table showing the direction of recombination for each of the three lineages of STEC O157:H7. The number in brackets represents the total number of donor segments per lineage.

Lineage II-a	80	Lineage II-b	40	Lineage II-c	250
stx 2c	65	stx 2c	20	stx 1a/2c	234
yehV-sbcA	53	yehV-sbcA-argW	15	yehV-sbcA	156
OTHER	12	yehV-sbcA	4	yehV-sbcA-argW	61
stx negative	6	stx negative	8	OTHER	17
negative	5	negative	8	stx 1a/2a/2c	6
yehV	1	stx 2a	5	yehV-sbcA	4
stx 2a/2c	4	yehV-sbcA-argW	4	yecE-yehV-sbcA	2
yecE-yehV-sbcA	2	yehV-sbcA	1	stx 1a	5
wrbA-yehV-sbcA	1	stx 1a/2c	4	yehV	5
Z2577-yecE-yehV-sbcA	1	sbcA-argW	2	stx 2a/2c	3
stx 1a/2c	3	yecE-sbcA-argW	1	yehV-sbcA	3
yehV-sbcA-argW	2	yehV-sbcA-argW	1	stx 2a	1
yehV-sbcA	1	stx 2a/2c	3	yehV-sbcA-argW	1
stx 2a	2	yehV-sbcA-argW	3	stx 2c	1
yecE-yehV-sbcA	2			yehV-sbcA	1

Supplementary Table 2:

The proportion of stx sub-type and occupied stx-associated bacteriophage insertion site (SBI) for each sub-lineage of lineage II. Those SBI's that less than 10% of the total were grouped into an 'other' category.

Lineage I/II	167
stx 2a/2c	109
yehV-sbcA-argW	88
OTHER	21
stx 2a	55
yehV-argW	44
yehV-sbcA-argW	6
OTHER	5
stx 2c	3
yecE-yehV-sbcA	2
yehV-argW	1

Supplementary Table 3:

The proportion of stx sub-type and occupied stx-associated bacteriophage insertion site (SBI) for lineage I/II. Those SBI's that less than 10% of the total were grouped into an 'other' category.

Lineage I-a	41	Lineage I-b	30	Lineage I-c	467
stx 1a/2a	26	stx 2c	26	stx 2a/2c	344
wrbA-yehV	23	yecE-yehV-sbcA	15	yehV-sbcA-argW	265
OTHER	3	yecE-wrbA-yehV-sbcA	6	OTHER	79
stx 2a/2c	6	OTHER	5	stx 2a	88
yehV-sbcA	6	stx 2a/2c	1	yehV-sbcA-argW	48
stx 2c	5	yecE-yehV-sbcA-argW	1	yecE-yehV	22
yehV-sbcA	4	stx negative	3	OTHER	18
yecE-yehV-sbcA	1	negative	3	stx 2c	30
stx 2a	2			yehV-sbcA	17
wrbA-yehV	1			yehV-sbcA-argW	5
yecE-wrbA	1			OTHER	8
stx 1a	1			stx 1a/2c	3
yehV	1			sbcA	1
stx negative	1			yehV-sbcA	1
negative	1			Z2577-yecE-wrbA-yehV-sbcA	1
				stx negative	2
				yehV-sbcA-argW	2

Supplementary Table 4:

The proportion of stx sub-type and occupied stx-associated bacteriophage insertion site (SBI) for lineage I. Those SBI's that less than 10% of the total were grouped into an 'other' category.

Supplementary Table 5:

All 1129 genomes analysed in this study summarised in terms of Lineage, SNP cluster, SBI, stx type, Manning Clade and LSPA-6 type.

