

Genomic Characterization of *hlyF*-positive Shiga toxin–Producing *Escherichia coli*, Italy and the Netherlands, 2000–2019

Appendix 1

Appendix 1 Table 1. Genomic sequencing depth and assembly statistics of genomic sequences of *hlyF*-positive Shiga toxin–producing *Escherichia coli*, Italy and the Netherlands, 2000–2019

Strain	Sequencing depth*	Estimated contigs coverage†	No. contigs	N50
ED0448	95x	1.05x	177	123196
ED0463B	107x	1.05x	191	93269
ED0655	59x	1.06x	188	93733
ED0656	109x	1.08x	198	75535
ED0696	68x	1.05x	225	87928
ED0812	78x	1.09x	209	67677
ED0813	84x	1.07x	191	87938
ED0840	118x	1.09x	204	90781
ED0884	108x	1.1x	202	86312
ED0918	75x	1.06x	167	110175
ED1000	74x	1.08x	193	83903
ED1001	169x	1.1x	208	75640
ED1029	200x	1.08x	190	86691
ED1049	139x	1.08x	188	108440
ED1152	153x	1.09x	215	70160
ED1213	94x	1.09x	203	105660
ED1232	174x	1.06x	204	73316
ED1269	110x	1.08x	225	104490
ED1273	132x	1.09x	206	109870
ED1283	79x	1.09x	203	83131
ED1284	67x	1.09x	194	74252
ED1304	77x	1.09x	182	87927
ED1308	83x	1.06x	200	65716
ED1319	52x	1.07x	192	87931
ED1374	141x	1.05x	184	86314
ED1381	126x	1.06x	205	68640
ED1382	251x	1.08x	165	72686
ED1386	139x	1.05x	185	104629
EF0453	131x	1.06x	211	70199
EF0475	144x	1.06x	171	72821
NL1700223	101x	1.08x	438	143394
NL1700566	111x	1.08x	479	68240
NL1700800	63x	1.12x	759	93204
NL1700844	77x	1.11x	744	93004
NL1701143	63x	1.1x	720	91144
NL1701173	78x	1.08x	752	87756
NL1701358	85x	1.02x	302	209789
NL1701474	66x	1.06x	464	79826
NL1701620	111x	1.03x	327	106777
NL1800002	86x	1.11x	769	74413
NL1800025	107x	1.02x	405	66939
NL1800037	98x	1.06x	447	71815
NL1800064	168x	1.09x	792	72748
NL1800080	204x	1.09x	849	72727
NL1800418	89x	1.11x	709	92328
NL1800531	93x	1.13x	836	72973
NL1800673	112x	1.05x	338	190511
NL1800717	106x	1.06x	510	190511
NL1800739	138x	1.11x	750	91090

Strain	Sequencing depth*	Estimated contigs coverage†	No. contigs	N50
NL1800740	146x	1.09x	692	91999
NL1900008	95x	1.11x	359	134460
NL1900697	410x	1.11x	461	101567
NL1900824	193x	1.11x	510	94172

*Sequencing depth value indicates the total length of all reads divided by the estimated length of the *E. coli* genome (i.e., 5 Mb).

†Estimated contigs coverage is calculated by dividing the number of assembled nucleotides by the estimated genome size (i.e., 5 Mb).

Appendix 1 Table 2. Genomic characterization of Shiga toxin-producing *Escherichia coli* strains with extraintestinal pathogenic *E. coli*-associated virulence genes, the Netherlands and Italy, 2000–2019*

Strain	Serotype	ST (phylo- group)	Gene							Origin	Patient diagnosis	Year (country)
			<i>stx</i>	<i>eae</i>	<i>hlyF</i>	<i>ompT</i>	<i>iro</i> <i>BCDEN</i>	<i>iss</i>	<i>ehxA</i>			
ED0448	O186:H2	301 (B1)	<i>stx</i> _{2a}	<i>eae</i> - _q	+	+	+	+	+	H	HUS	2000 (IT)
ED0463B	O186:H2	301 (B1)	<i>stx</i> _{2a}	<i>eae</i> - _q	+	+	+	+	+	Beef liver	NA	2001 (IT)
ED0655	O80:H2	301 (B1)	<i>stx</i> _{2a}	<i>eae</i> - _q	+	+	+	+	+	H	HUS	2007 (IT)
ED0656	O186:H2	301 (B1)	<i>stx</i> _{2a}	<i>eae</i> - _q	+	+	+	+	+	H	HUS	2007 (IT)
ED0696	O80:H2	301 (B1)	<i>stx</i> _{2a}	<i>eae</i> - _q	+	+	+	+	+	H	HUS	2009 (IT)
ED0812	O80:H2	301 (B1)	<i>stx</i> _{2a}	<i>eae</i> - _q	+	+	+	+	+	H	HC	2011 (IT)
ED0813	O80:H2	301 (B1)	<i>stx</i> _{2a}	<i>eae</i> - _q	+	+	+	+	+	H	HC	2011 (IT)
ED0840	O80:H2	301 (B1)	<i>stx</i> _{2a}	<i>eae</i> - _q	+	+	+	+	+	H	HUS	2012 (IT)
ED0884	O80:H2	301 (B1)	<i>stx</i> _{2a}	<i>eae</i> - _q	+	+	+	+	+	H	HC	2013 (IT)
ED0918	O80:H2	301 (B1)	<i>stx</i> _{2a}	<i>eae</i> - _q	+	+	+	+	+	H	HUS	2013 (IT)
ED1000	O80:H2	301 (B1)	<i>stx</i> _{2a}	<i>eae</i> - _q	+	+	+	+	+	H	HUS	2014 (IT)
ED1001	O80:H2	301 (B1)	<i>stx</i> _{2a}	<i>eae</i> - _q	+	+	+	+	+	H	HUS	2014 (IT)
ED1029	O80:H2	301 (B1)	<i>stx</i> _{2a}	<i>eae</i> - _q	+	+	+	+	+	H	HUS	2015 (IT)
ED1049	O80:H2	301 (B1)	<i>stx</i> _{2a}	<i>eae</i> - _q	+	+	+	+	+	H	NA	2015 (IT)
ED1152	O80:H2	301 (B1)	<i>stx</i> _{2a}	<i>eae</i> - _q	+	+	+	+	+	H	HC	2016 (IT)
ED1213	O80:H2	301 (B1)	<i>stx</i> _{2a}	<i>eae</i> - _q	+	+	+	+	+	H	HUS	2017 (IT)
ED1232	O80:H2	301 (B1)	<i>stx</i> _{2a}	<i>eae</i> - _q	+	+	+	+	+	H	HC	2017 (IT)
ED1269	O80:H2	301 (B1)	<i>stx</i> _{2a}	<i>eae</i> - _q	+	+	+	+	+	H	NA	2018 (IT)
ED1273	O80:H2	301 (B1)	<i>stx</i> _{2a}	<i>eae</i> - _q	+	+	+	+	+	H	NA	2018 (IT)
ED1283	O26:H11	21(B1)	<i>stx</i> _{2a}	<i>eae</i> - β 1	+	+	+	+	+	H	HUS	2018 (IT)
ED1284	O26:H11	21(B1)	<i>stx</i> _{2a}	<i>eae</i> - β 1	+	+	+	+	+	H	HUS	2018 (IT)
ED1304	O80:H2	301 (B1)	<i>stx</i> _{2a}	<i>eae</i> - _q	+	+	+	+	+	H	HUS	2018 (IT)
ED1308	O80:H2	301 (B1)	<i>stx</i> _{2a}	<i>eae</i> - _q	+	+	+	+	+	H	HUS	2018 (IT)
ED1319	O80:H2	301 (B1)	<i>stx</i> _{2d}	<i>eae</i> - _q	+	+	+	+	+	H	HUS	2018 (IT)
ED1374	O80:H2	301 (B1)	<i>stx</i> _{2a}	<i>eae</i> - _q	+	+	+	+	+	Raw bovine milk	NA	2019 (IT)
ED1381	O80:H2	301 (B1)	<i>stx</i> _{2a}	<i>eae</i> - _q	+	+	+	+	+	H	HUS	2019 (IT)
ED1382	O80:H2	301 (B1)	<i>stx</i> _{2a}	<i>eae</i> - _q	+	+	+	+	+	H	HUS	2019 (IT)
ED1386	O80:H2	301 (B1)	<i>stx</i> _{2a}	<i>eae</i> - _q	+	+	+	-	+	H	HUS	2019 (IT)
EF0453	O80:H2	301 (B1)	<i>stx</i> _{2f}	<i>eae</i> - _q	+	+	+	+	+	H	HUS	2013 (IT)
EF0475	O55:H9	301 (B1)	<i>stx</i> _{2f}	<i>eae</i> - _q	+	+	+	+	+	H	HUS	2014 (IT)
NL1700223	O8:H9	88(Un)	<i>stx</i> _{2e}	-	+	+	+	+	-	H	NA	2017 (NL)
NL1700566	O152:H8	13(B1)	<i>stx</i> _{1a}	-	+	+	+	+	-	H	NA	2017 (NL)
NL1700800	O80:H2	301 (B1)	<i>stx</i> _{2a}	<i>eae</i> - _q	+	+	+	+	+	H	NA	2017 (NL)
NL1700844	O80:H2	301 (B1)	<i>stx</i> _{2a}	<i>eae</i> - _q	+	+	+	+	+	H	HC	2017 (NL)
NL1701143	O45:H2	301 (B1)	<i>stx</i> _{2a}	<i>eae</i> - _q	+	+	+	+	+	H	NA	2017 (NL)
NL1701173	O80:H2	301 (B1)	<i>stx</i> _{2d}	<i>eae</i> - _q	+	+	+	+	+	H	NA	2017 (NL)
NL1701358	O115:H52	8691 (B2)	<i>stx</i> _{2f}	<i>eae</i> - λ 3	+	+	-	+	-	H, hosp.	D	2017 (NL)
NL1701474	O152:H8	13(B1)	<i>stx</i> _{1a}	-	+	+	+	+	-	H	NA	2017 (NL)
NL1701620	O8:H9	767 (B1)	<i>stx</i> _{2e}	-	+	+	+	+	-	H, hosp.	D	2017 (NL)
NL1800002	O80:H2	301 (B1)	<i>stx</i> _{2d}	<i>eae</i> - _q	+	+	+	+	+	H	NA	2018 (NL)
NL1800025	O48:H45	656 (B1)	<i>stx</i> _{2b}	-	+	+	+	+	-	H	NA	2018 (NL)
NL1800037	O152:H8	13(B1)	<i>stx</i> _{1a}	-	+	+	+	+	-	H	NA	2018 (NL)
NL1800064	O80:H2	301 (B1)	<i>stx</i> _{2d}	<i>eae</i> - _q	+	+	+	+	+	H, hosp.	HC	2018 (NL)
NL1800080	O80:H2	301 (B1)	<i>stx</i> _{2d}	<i>eae</i> - _q	+	+	+	+	+	H	NA	2018 (NL)
NL1800418	O45:H2	301 (B1)	<i>stx</i> _{2a}	<i>eae</i> - _q	+	+	+	+	+	H, hosp.	HC	2018 (NL)
NL1800531	O80:H2	301 (B1)	<i>stx</i> _{2f}	<i>eae</i> - _q	+	+	+	+	+	H	D	2018 (NL)
NL1800673	O8:H9	88(Un)	<i>stx</i> _{2e}	-	+	+	+	+	-	H	D	2018 (NL)
NL1800717	O8:H9	88(Un)	<i>stx</i> _{2e}	-	+	+	+	+	-	H	NA	2018 (NL)
NL1800739	O80:H2	301 (B1)	<i>stx</i> _{2a}	<i>eae</i> - _q	+	+	+	+	+	H	D	2018 (NL)
NL1800740	O45:H2	301 (B1)	<i>stx</i> _{2a}	<i>eae</i> - _q	+	+	+	+	+	H	NA	2018 (NL)

Strain	Serotype	ST (phylo- group)	Gene							Origin	Patient diagnosis	Year (country)
			<i>stx</i>	<i>eae</i>	<i>hlyF</i>	<i>ompT</i>	<i>iro</i>		<i>iss</i>			
NL1900008	O91:H14	33(B1)	<i>stx</i> _{1a}	-	+	+	+	+	-	H	NA	2019 (NL)
NL1900697	O45:H2	301 (B1)	<i>stx</i> _{2a}	<i>eae</i> - ^z	+	+	+	+	+	H	D	2019 (NL)
NL1900824	O80:H2	301 (B1)	<i>stx</i> _{2d}	<i>eae</i> - ^z	+	+	+	+	+	H, hosp.	D	2019 (NL)

*D, diarrhea; H, human; HC, hemorrhagic colitis; HUS, hemolytic uremic syndrome; hosp., hospitalized; IT, Italy; NA, not available; NL, the Netherlands; ST, sequence type; Un, unknown; +, positive; -, negative.

Appendix 1 Table 3. Antimicrobial resistance genes associated with pR444_A plasmid that were identified in Shiga toxin-producing *Escherichia coli* strains with extraintestinal pathogenic *E. coli*-associated virulence genes, the Netherlands and Italy, 2000–2019*

Strain	Serotype	Sequence		AMR genes						
		type	<i>stx</i>	<i>aph(3')-I</i>	<i>ant(3'')-I</i>	<i>dfrA</i>	<i>str</i>	<i>sul</i>	<i>bla</i> _{TEM-1}	<i>tet</i>
ED0448	O186:H2	301	<i>stx</i> _{2a}	<i>aph(3')-Ia</i>	-	-	<i>strAB</i>	<i>sul2</i>	<i>bla</i> _{TEM-1}	<i>tet(A)</i>
ED0463B	O186:H2	301	<i>stx</i> _{2a}	<i>aph(3')-Ia</i>	-	<i>dfrA1</i>	<i>strAB</i>	<i>sul2</i>	<i>bla</i> _{TEM-1}	<i>tet(A)</i>
ED0655	O80:H2	301	<i>stx</i> _{2a}	<i>aph(3')-Ia</i>	-	-	<i>strAB</i>	<i>sul2</i>	<i>bla</i> _{TEM-1}	<i>tet(A)</i>
ED0656	O186:H2	301	<i>stx</i> _{2a}	<i>aph(3')-Ia</i>	-	<i>dfrA1</i>	<i>strAB</i>	<i>sul2</i>	<i>bla</i> _{TEM-1}	-
ED0696	O80:H2	301	<i>stx</i> _{2a}	<i>aph(3')-Ia</i>	-	-	<i>strAB</i>	<i>sul2</i>	<i>bla</i> _{TEM-1}	<i>tet(A)</i>
ED0812	O80:H2	301	<i>stx</i> _{2a}	-	<i>ant(3'')-Ia</i>	-	-	<i>sul2</i>	-	<i>tet(A)</i>
ED0813	O80:H2	301	<i>stx</i> _{2a}	-	<i>ant(3'')-Ia</i>	-	-	<i>sul2</i>	-	<i>tet(A)</i>
ED0840	O80:H2	301	<i>stx</i> _{2a}	<i>aph(3')-Ia</i>	-	-	<i>strAB</i>	<i>sul2</i>	<i>bla</i> _{TEM-1}	<i>tet(A)</i>
ED0884	O80:H2	301	<i>stx</i> _{2a}	<i>aph(3')-Ia</i>	-	-	<i>strAB</i>	<i>sul2</i>	<i>bla</i> _{TEM-1}	<i>tet(A)</i>
ED0918	O80:H2	301	<i>stx</i> _{2a}	<i>aph(3')-Ia</i>	-	-	<i>strAB</i>	<i>sul2</i>	<i>bla</i> _{TEM-1}	<i>tet(A)</i>
ED1000	O80:H2	301	<i>stx</i> _{2a}	<i>aph(3')-Ia</i>	-	-	<i>strAB</i>	<i>sul2</i>	<i>bla</i> _{TEM-1}	<i>tet(A)</i>
ED1001	O80:H2	301	<i>stx</i> _{2a}	<i>aph(3')-Ia</i>	-	-	<i>strAB</i>	<i>sul2</i>	<i>bla</i> _{TEM-1}	<i>tet(A)</i>
ED1029	O80:H2	301	<i>stx</i> _{2a}	<i>aph(3')-Ia</i>	-	-	<i>strAB</i>	<i>sul2</i>	-	<i>tet(A)</i>
ED1049	O80:H2	301	<i>stx</i> _{2a}	<i>aph(3')-Ia</i>	-	-	<i>strAB</i>	<i>sul2</i>	<i>bla</i> _{TEM-1}	<i>tet(A)</i>
ED1152	O80:H2	301	<i>stx</i> _{2a}	<i>aph(3')-Ia</i>	-	<i>dfrA17</i>	<i>strAB</i>	<i>sul2</i>	-	<i>tet(A)</i>
ED1213	O80:H2	301	<i>stx</i> _{2a}	-	<i>ant(3'')-Ia</i>	-	-	<i>sul2</i>	-	<i>tet(A)</i>
ED1232	O80:H2	301	<i>stx</i> _{2a}	<i>aph(3'')-Ib</i>	-	-	<i>strAB</i>	<i>sul2</i>	-	-
ED1269	O80:H2	301	<i>stx</i> _{2a}	<i>aph(3')-Ia</i>	-	-	<i>strAB</i>	<i>sul2</i>	<i>bla</i> _{TEM-1}	<i>tet(A)</i>
ED1273	O80:H2	301	<i>stx</i> _{2a}	-	<i>ant(3'')-Ia</i>	-	-	<i>sul2</i>	-	<i>tet(A)</i>
ED1283	O26:H11	21	<i>stx</i> _{2a}	<i>aph(3'')-Ib</i>	-	<i>dfrA1</i>	<i>strAB</i>	<i>sul2</i>	<i>bla</i> _{TEM-1}	<i>tet(A)</i>
ED1284	O26:H11	21	<i>stx</i> _{2a}	<i>aph(3'')-Ib</i>	-	<i>dfrA1</i>	<i>strAB</i>	<i>sul2</i>	<i>bla</i> _{TEM-1}	<i>tet(A)</i>
ED1304	O80:H2	301	<i>stx</i> _{2a}	<i>aph(3')-Ia</i>	-	-	<i>strAB</i>	<i>sul2</i>	<i>bla</i> _{TEM-1}	<i>tet(A)</i>
ED1308	O80:H2	301	<i>stx</i> _{2a}	<i>aph(3')-Ia</i>	-	-	<i>strAB</i>	<i>sul2</i>	<i>bla</i> _{TEM-1}	<i>tet(A)</i>
ED1319	O80:H2	301	<i>stx</i> _{2d}	<i>aph(3')-Ia</i>	-	<i>dfrA5</i>	<i>strAB</i>	<i>sul2</i>	<i>bla</i> _{TEM-1}	<i>tet(C)</i>
ED1374	O80:H2	301	<i>stx</i> _{2a}	<i>aph(3')-Ia</i>	-	-	<i>strAB</i>	<i>sul2</i>	<i>bla</i> _{TEM-1}	<i>tet(A)</i>
ED1381	O80:H2	301	<i>stx</i> _{2a}	<i>aph(3')-Ia</i>	-	-	<i>strAB</i>	<i>sul2</i>	<i>bla</i> _{TEM-1}	<i>tet(A)</i>
ED1382	O80:H2	301	<i>stx</i> _{2a}	-	<i>ant(3'')-Ia</i>	-	-	<i>sul2</i>	-	<i>tet(A)</i>
ED1386	O80:H2	301	<i>stx</i> _{2a}	<i>aph(3')-Ia</i>	-	-	<i>strAB</i>	<i>sul1</i>	<i>bla</i> _{TEM-1}	<i>tet(A)</i>
EF0453	O80:H2	301	<i>stx</i> _{2f}	<i>aph(3')-Ia</i>	-	-	<i>strAB</i>	<i>sul2</i>	<i>bla</i> _{TEM-1}	<i>tet(A)</i>
EF0475	O55:H9	301	<i>stx</i> _{2f}	<i>aph(3'')-Ib</i>	-	-	<i>strAB</i>	<i>sul2</i>	<i>bla</i> _{TEM-1}	-
NL1700223	O8:H9	88	<i>stx</i> _{2e}	-	-	<i>dfrA5</i>	-	-	-	-
NL1700566	O152:H8	13	<i>stx</i> _{1a}	-	-	-	-	-	-	-
NL1700800	O80:H2	301	<i>stx</i> _{2a}	<i>aph(3')-Ia</i>	-	-	<i>strAB</i>	<i>sul2</i>	-	<i>tet(A)</i>
NL1700844	O80:H2	301	<i>stx</i> _{2a}	<i>aph(3')-Ia</i>	-	<i>dfrA5</i>	<i>strAB</i>	<i>sul2</i>	<i>bla</i> _{TEM-1}	<i>tet(A)</i>
NL1701143	O45:H2	301	<i>stx</i> _{2a}	<i>aph(3')-Ia</i>	-	-	<i>strAB</i>	<i>sul2</i>	<i>bla</i> _{TEM-1}	<i>tet(A)</i>
NL1701173	O80:H2	301	<i>stx</i> _{2d}	<i>aph(3')-Ia</i>	-	<i>dfrA5</i>	<i>strAB</i>	<i>sul2</i>	<i>bla</i> _{TEM-1}	-
NL1701358	O115:H52	8691	<i>stx</i> _{2f}	-	-	-	-	-	-	-
NL1701474	O152:H8	13	<i>stx</i> _{1a}	-	-	-	-	-	-	-
NL1701620	O8:H9	767	<i>stx</i> _{2e}	-	-	<i>dfrA17</i>	-	-	<i>bla</i> _{TEM-1}	<i>tet(A)</i>
NL1800002	O80:H2	301	<i>stx</i> _{2d}	<i>aph(3')-Ia</i>	-	<i>dfrA5</i>	<i>strAB</i>	<i>sul2</i>	<i>bla</i> _{TEM-1}	<i>tet(A)</i>
NL1800025	O48:H45	656	<i>stx</i> _{2b}	<i>aph(3'')-Ib</i>	-	-	<i>strAB</i>	<i>sul2</i>	-	<i>tet(A)</i>
NL1800037	O152:H8	13	<i>stx</i> _{1a}	-	-	-	-	-	-	-
NL1800064	O80:H2	301	<i>stx</i> _{2d}	<i>aph(3')-Ia</i>	-	<i>dfrA5</i>	<i>strAB</i>	<i>sul2</i>	<i>bla</i> _{TEM-1}	-
NL1800080	O80:H2	301	<i>stx</i> _{2d}	<i>aph(3')-Ia</i>	-	<i>dfrA5</i>	<i>strAB</i>	<i>sul2</i>	<i>bla</i> _{TEM-1}	-
NL1800418	O45:H2	301	<i>stx</i> _{2a}	<i>aph(3')-Ia</i>	-	-	<i>strAB</i>	<i>sul2</i>	-	<i>tet(A)</i>
NL1800531	O80:H2	301	<i>stx</i> _{2f}	<i>aph(3')-Ia</i>	-	-	<i>strAB</i>	<i>sul2</i>	<i>bla</i> _{TEM-1}	<i>tet(A)</i>
NL1800673	O8:H9	88	<i>stx</i> _{2e}	<i>aph(3'')-Ib</i>	-	<i>dfrA5</i>	<i>strAB</i>	<i>sul2</i>	<i>bla</i> _{TEM-1}	-
NL1800717	O8:H9	88	<i>stx</i> _{2e}	<i>aph(3'')-Ib</i>	-	<i>dfrA5</i>	<i>strAB</i>	<i>sul2</i>	<i>bla</i> _{TEM-1}	-
NL1800739	O80:H2	301	<i>stx</i> _{2a}	-	-	-	-	<i>sul2</i>	-	<i>tet(A)</i>
NL1800740	O45:H2	301	<i>stx</i> _{2a}	<i>aph(3')-Ia</i>	-	-	<i>strAB</i>	<i>sul2</i>	<i>bla</i> _{TEM-1}	<i>tet(A)</i>
NL1900008	O91:H14	33	<i>stx</i> _{1a}	-	-	-	-	-	-	<i>tet(A)</i>
NL1900697	O45:H2	301	<i>stx</i> _{2a}	<i>aph(3')-Ia</i>	-	-	<i>strAB</i>	<i>sul2</i>	<i>bla</i> _{TEM-1}	<i>tet(A)</i>
NL1900824	O80:H2	301	<i>stx</i> _{2d}	<i>aph(3')-Ia</i>	-	-	<i>strAB</i>	<i>sul2</i>	<i>bla</i> _{TEM-1}	-

**aph(3')-I* and *ant(3'')-I* encode resistance to aminoglycosides; *dfrA* encodes resistance to trimethoprim; *sul* encodes resistance to sulfonamides; *bla*_{TEM} encodes resistance to β-lactams; *tet* encodes resistance to tetracyclines.

Appendix 1 Table 4. Main characteristics of the 50 *Escherichia coli* genomes downloaded from GenBank and RefSeq*

Strain	Accession no.	Serotype	Sequence type		Source	Country (city or state)	Year
				(Phylogroup)			
2013C-4991	GCF_003018815.1	O80:H2	301	(B1)	Human, NA	NA	2013
31707	GCF_003122965.2	O80:H2	301	(B1)	Human, HUS	France (Paris)	2017
364060-17	GCF_003028275.1	O80:H2	301	(B1)	NA	Switzerland (Zurich)	2017
364061-17	GCF_003028045.1	O80:H2	301	(B1)	NA	Switzerland (Zurich)	2017
364062-17	GCF_003028145.1	O80:H2	301	(B1)	NA	Switzerland (Zurich)	2017
364064-17	GCF_003028245.1	O80:H2	301	(B1)	NA	Switzerland (Zurich)	2017
364068-17	GCF_003027955.1	O80:H2	301	(B1)	NA	Switzerland (Zurich)	2017
364069-17	GCF_003028095.1	O80:H2	301	(B1)	NA	Switzerland (Zurich)	2017
364073-17	GCF_003027915.1	O80:H2	301	(B1)	NA	Switzerland (Zurich)	2017
364075-17	GCF_003028075.1	O80:H2	301	(B1)	NA	Switzerland (Zurich)	2017
364077-17	GCF_003028035.1	O80:H2	301	(B1)	NA	Switzerland (Zurich)	2017
364082-17	GCF_003027965.1	O80:H2	301	(B1)	NA	Switzerland (Zurich)	2017
36549	GCF_003122855.2	O80:H2	301	(B1)	Human, HUS	France (Paris)	2017
37619	GCF_003123295.1	O80:H2	301	(B1)	Human, HUS	France (Paris)	2017
40963	GCF_003123255.1	O80:H2	301	(B1)	Human, HUS	France (Paris)	2017
CB12623	GCF_003123165.2	O80:H2	301	(B1)	Human, HUS	Switzerland (Berne)	2017
CM15-2	GCF_004664645.1	O8:H16	2217	(B1)	Ground beef	Argentina (Tandil)	1998
EH1752	GCF_013413115.1	O80:H2	301	(B1)	Human, D	Belgium	2008
EH1764	GCF_013413035.1	O80:H2	301	(B1)	Human, D	Belgium	2008
EH2262	GCF_013413055.1	O80:H2	301	(B1)	Human, D	Belgium	2013
EH2400	GCF_013413045.1	O80:H2	301	(B1)	Human, D	Belgium	2014
EH2436	GCF_013413065.1	O80:H2	301	(B1)	Human, NA	Belgium	2014
EH2644	GCF_013412965.1	O80:H2	301	(B1)	Human, HUS	Belgium	2015
EH2786	GCF_013413335.1	O80:H2	301	(B1)	Human, NA	Belgium	2016
EH2808	GCF_013412955.1	O80:H2	301	(B1)	Human, HUS	Belgium	2016
EH2882	GCF_013413375.1	O80:H2	301	(B1)	Calf, D	Belgium	1987
EH3138	GCF_013412915.1	O80:H2	301	(B1)	Human, HC	Belgium	2018
EH3154	GCF_013413215.1	O80:H2	301	(B1)	Calf, Ent	Belgium	2018
EH3155	GCF_013413175.1	O80:H2	301	(B1)	Calf, Ent	Belgium	2018
EH3160	GCF_013413135.1	O80:H2	301	(B1)	Calf, Ent	Belgium	2018
EH3168	GCF_013412945.1	O80:H2	301	(B1)	Human, HC	Belgium	2018
EH3172	GCF_013412895.1	O80:H2	301	(B1)	Human, D	Belgium	2018
EH3173	GCF_013412825.1	O80:H2	301	(B1)	Human, NA	Belgium	2018
EH3180	GCF_013412835.1	O80:H2	301	(B1)	Human, NA	Belgium	2018
EH3205	GCF_013412845.1	O80:H2	301	(B1)	Human, D	Belgium	2019
EH3212	GCF_013412765.1	O80:H2	301	(B1)	Human, HUS	Belgium	2019
EH3257	GCF_013412765.1	O80:H2	301	(B1)	Human, HUS†	Belgium	2019
EH3278	GCF_013412755.1	O80:H2	301	(B1)	Human, HUS	Belgium	2019
EH3307	GCF_013413315.1	O80:H2	301	(B1)	Calf, D	Belgium	2016
EH3310	GCF_013413285.1	O80:H2	301	(B1)	Calf, D	Belgium	2016
EH3311	GCF_013413275.1	O80:H2	301	(B1)	Calf, D	Belgium	2016
EH3315	GCF_013413235.1	O80:H2	301	(B1)	Calf, D	Belgium	2017
EH3320	GCF_013413165.1	O80:H2	301	(B1)	Calf, D	Belgium	2017
EH3338	GCF_013413145.1	O80:H2	301	(B1)	Calf, Sept	Belgium	2018
H39-78	GCF_003123395.1	O80:H2	301	(B1)	Cattle, NA	France (Lyon)	2017
LMFS-V-JF-008	GCA_014451005.1	O103:H2	17	(B1)	Surface water	Canada (Sumas Prairie)	2015
LMFS-V-JF-010	GCF_014050405.1	O109:H5	647	(B2)	Surface water	Canada (Sumas Prairie)	2015
NGE.clc	GCF_001191215.1	O45:H16	2217	(B1)	Cow, NA	USA (Kansas)	2001
OLC1061	GCF_002134035.1	O128ab:H2	25	(B1)	NA	Canada	2012
RM11911	GCF_008761495.2	O45:H16	2217	(B1)	Water	USA (California)	2010

*RefSeq, www.ncbi.nlm.nih.gov/RefSeq. All strains were positive for *stx* and *hlyF* genes. HC, hemorrhagic colitis; HUS, hemolytic uremic syndrome;

NA, not available; D, diarrhea;

Sept, septicemia; Ent, enteritis.

†Fatal disease.

Appendix 1 Table 5. Statistics output of core genome multilocus sequence typing analysis of *hlyF*-positive Shiga toxin-producing *Escherichia coli* strains used in this study*

Genome	Exact match	Allele inferred	Locus not found	Possible locus on tip	Noninformative paralogous hits	Alleles larger than mode	Alleles smaller than mode
2013C-4991	2341	0	6	1	6	0	6
31707	2342	0	8	0	7	0	3
364060-17	2339	0	9	6	5	0	1
364061-17	2348	0	4	1	7	0	0
364062-17	2348	0	4	0	7	0	1
364064-17	2348	0	5	0	7	0	0
364068-17	2350	0	4	0	6	0	0
364069-17	2349	0	3	1	7	0	0
364073-17	2349	0	2	0	7	0	2
364075-17	2350	0	3	0	7	0	0
364077-17	2349	0	4	0	7	0	0
364082-17	2349	0	3	0	7	0	1
36549	2348	0	3	2	7	0	0
37619	2306	0	38	9	7	0	0
40963	2294	0	39	19	7	1	0
CB12623	2344	0	5	4	5	0	2
CM15-2	2352	0	4	1	1	0	2
ED0448	2344	0	6	1	5	0	4
ED0463B	2338	0	12	3	5	0	2
ED0655	2346	0	6	0	6	0	2
ED0656	2339	0	12	2	4	0	3
ED0696	2346	0	6	1	6	0	1
ED0812	2336	0	9	3	6	0	6
ED0813	2344	0	6	0	7	0	3
ED0840	2342	0	6	1	7	0	4
ED0867	2338	0	12	2	6	0	2
ED0884	2344	0	4	2	6	0	4
ED0918	2350	0	3	0	4	0	3
ED1000	2343	0	7	0	6	0	4
ED1001	2338	0	8	2	7	0	5
ED1029	2347	0	6	0	6	0	1
ED1049	2348	0	4	0	7	0	1
ED1152	2344	0	5	2	7	0	2
ED1213	2342	0	6	2	6	0	4
ED1232	2344	0	6	3	5	0	2
ED1269	2303	0	47	0	7	1	2
ED1273	2346	0	4	0	7	0	3
ED1283	2348	0	0	5	5	0	2
ED1284	2347	0	3	4	4	0	2
ED1301	2343	0	7	0	7	1	2
ED1304	2341	0	10	3	4	0	2
ED1308	2339	0	14	1	5	0	1
ED1319	2336	0	8	0	7	0	9
ED1374	2338	0	14	1	5	0	2
ED1381	2341	0	4	2	7	0	6
ED1382	2346	0	6	2	5	0	1
ED1386	2346	0	5	0	5	0	4
EF0453	2342	0	8	2	6	0	2
EF0475	2342	0	6	1	6	1	4
EH1752	2351	0	3	0	6	0	0
EH1764	2350	0	3	0	7	0	0
EH2262	2351	0	2	0	6	0	1
EH2400	2350	0	3	0	7	0	0
EH2436	2346	0	7	0	6	0	1
EH2644	2349	0	3	0	7	0	1
EH2786	2351	0	2	1	6	0	0
EH2808	2346	0	7	0	6	0	1
EH2882	2350	0	3	0	5	0	2
EH3138	2351	0	2	0	6	0	1
EH3154	2348	0	6	0	5	0	1
EH3155	2350	0	4	0	6	0	0
EH3160	2350	0	4	0	6	0	0
EH3168	2349	0	4	1	6	0	0
EH3172	2349	0	4	0	7	0	0
EH3173	2350	0	3	0	7	0	0
EH3180	2350	0	3	0	7	0	0

Genome	Exact match	Allele inferred	Locus not found	Possible locus on tip	Noninformative paralogous hits	Alleles larger than mode	Alleles smaller than mode
EH3205	2344	0	11	0	5	0	0
EH3212	2349	0	3	1	7	0	0
EH3257	2349	0	3	1	7	0	0
EH3278	2349	0	3	1	7	0	0
EH3307	2339	0	15	0	5	0	1
EH3310	2349	0	3	0	7	0	1
EH3311	2342	0	9	0	7	1	1
EH3315	2342	0	9	0	7	1	1
EH3320	2349	0	3	0	7	0	1
EH3338	2350	0	4	0	6	0	0
H39-78	2347	0	4	1	7	0	1
LMFS-V-JF-008	2354	0	0	0	6	0	0
LMFS-V-JF-010	2351	0	6	0	1	0	2
NGE.clc	2343	0	10	1	3	0	3
NL1700223	2356	0	2	0	2	0	0
NL1700566	2348	0	4	3	2	1	2
NL1700800	2353	0	2	0	5	0	0
NL1700844	2349	0	4	0	7	0	0
NL1701143	2349	0	3	1	6	0	1
NL1701173	2349	0	5	0	6	0	0
NL1701358	2271	0	80	0	4	1	4
NL1701474	2350	0	4	2	2	1	1
NL1701620	2352	0	4	1	3	0	0
NL1800002	2345	0	8	1	6	0	0
NL1800025	2338	0	14	2	2	0	4
NL1800037	2350	0	4	2	2	1	1
NL1800064	2350	0	4	0	6	0	0
NL1800080	2350	0	4	0	6	0	0
NL1800418	2352	0	2	1	5	0	0
NL1800531	2349	0	4	0	7	0	0
NL1800673	2352	0	5	0	2	0	1
NL1800717	2352	0	5	0	2	0	1
NL1800739	2352	0	2	0	6	0	0
NL1800740	2352	0	2	1	5	0	0
NL1900008	2349	0	7	0	2	0	2
NL1900697	2350	0	3	1	5	0	1
NL1900824	2349	0	4	0	6	0	1
OLC1061	2351	0	5	1	3	0	0
RDEx444	2338	0	10	0	7	0	5
RM11911	2341	0	9	0	2	2	6

*Analysis conducted with the chewBBACA tool (<https://doi.org/10.1099/mgen.0.000166>).