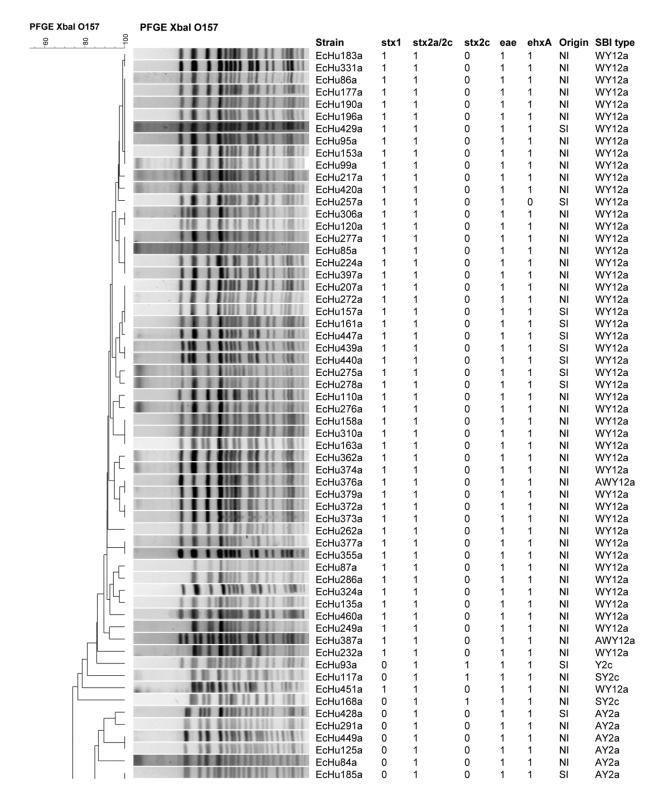
## Geographic Divergence of Bovine and Human Shiga Toxin–Producing *Escherichia* coli O157:H7 Genotypes, New Zealand

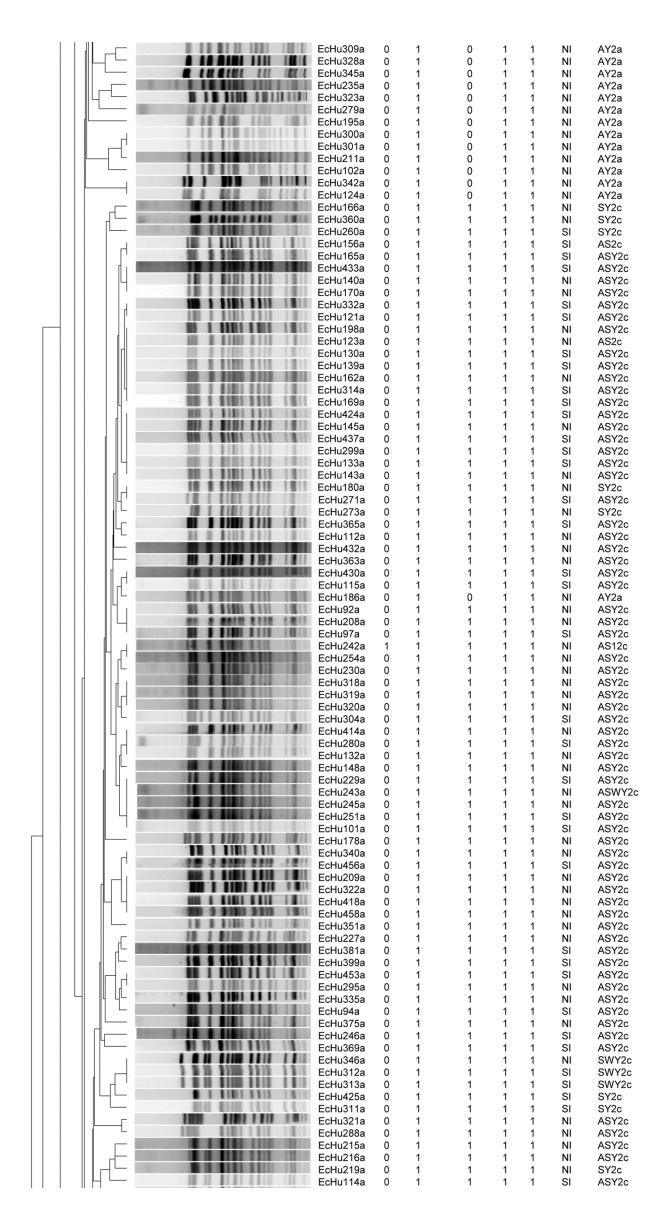
## **Technical Appendix**

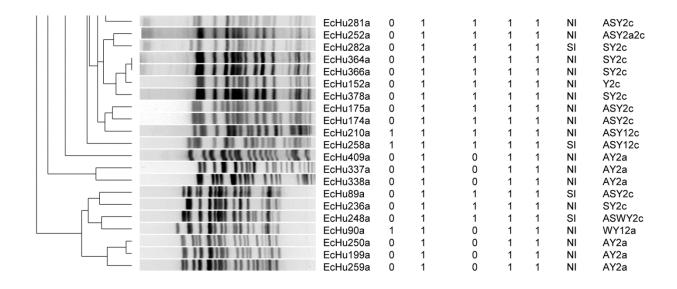
Technical Appendix Figure 1 (below and following pages). PFGE profile comparison of 363 human Shiga toxin–producing *Escherichia coli* O157:H7 isolates using UPGMA cluster analysis (Dice similarity coefficient, 1% band matching tolerance). Virulence genes (*stx*1, *stx*2a/2c, *stx*2c, *eae*, *ehx*A) present (1) or absent (0). Island of origin (Origin) presented as North Island (NI) or South Island (SI) of New Zealand, and genotypes of isolates as Shiga toxin (Stx)-encoding bacteriophage insertion (SBI) types.

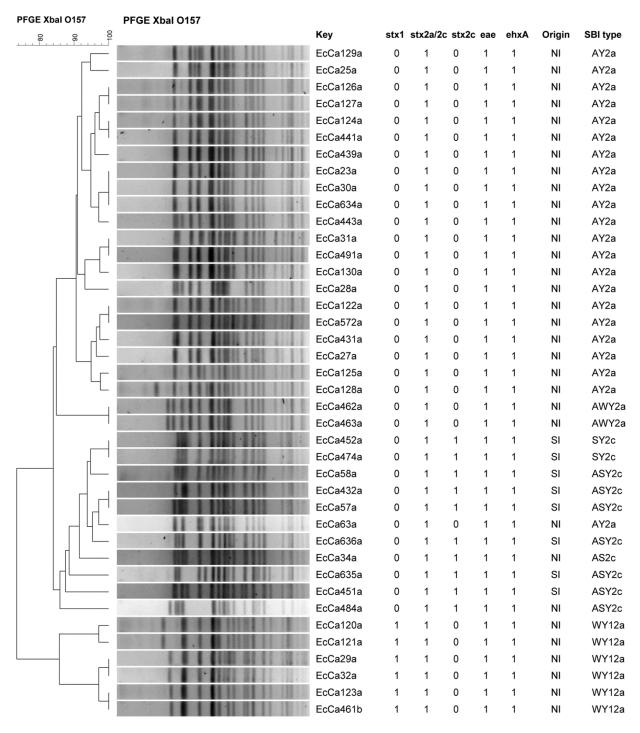


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0.111111111111	EcHu417a	0	1	0	1 1	NI	AY2a
0 11010111111	EcHu441a	0	1	0	1 1	NI	AY2a
10 0 0101111111111111111111111111111111	EcHu442a	0	1	0	1 1	NI	AY2a
# F # # # # # # # # # # # # # # # # # #	EcHu294a	0	1	0	1 1	NI	AY2a
	EcHu270a	0	1	0	1 1	NI	AY2a
10 C B1 C	EcHu261a	0	1	0	1 1	NI	AY2a
- 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	EcHu285a	0	1	0	1 1	NI	AY2a
B 0 0 0 0 0 0 1 1 1	EcHu298a	0	1	0	1 1	NI	AY2a
	EcHu401a	0	1	0	1 1	NI	AY2a
	EcHu181a	0	1	0	1 1	NI	AY2a
0 10 01011 IN 11	EcHu357a	0	1	0	1 1	NI	AY2a
B 10 01811 1181	EcHu358a	0	1	0	1 1	SI	AY2a
	EcHu131a	0	1	0	1 1	SI	AY2a
B 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	EcHu408a	Ö	1	0	1 1	NI	AY2a
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	EcHu274a	0	1	0	1 1	NI	AY2a
	EcHu202a	0	1	0	1 1	NI	AY2a
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1 11 1111	EcHu205a	0	1	0	1 1	NI	AY2a
9 19 8191 1111	EcHu384a	0	1	0	1 1	SI	AY2a
	EcHu419a	0	1	0	1 1	NI	AY2a
# 10 Bimi 1111	EcHu353a	0	1	0	1 1	NI	AY2a
# 13 BIN1 1111	EcHu380a	0	1	0	1 1	NI	AY2a
# 18 @101 1111	EcHu383a	0	1	0	1 1	SI	AY2a
- 0 10 0101 1111	EcHu434a	0	1	0	1 1	SI	AY2a
<b>0 00 00</b> 00 0000	EcHu448a	0	1	0	1 1	NI	AY2a
	EcHu269a	0	1	0	1 1	SI	AY2a
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1 11 111	EcHu218a	0	1	0	1 1		
						NI	AY2a
	EcHu226a	0	1	0	1 1	NI	AY2a
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	EcHu241a	0	1	0	1 1	NI	AWY2a
	EcHu244a	0	1	0	1 1	NI	AY2a
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1 1 1 1 1 1 1 1 1 1	EcHu316a	0	1	0	1 1	NI	AY2a
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0 10 01m1 1111	EcHu334a	0	1	0	1 1	NI	AY2a
	EcHu390a	0	1	0	1 1	NI	AY2a
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OI 00 OLER 1888	EcHu356a	0	1	0	1 1	NI	AY2a
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40 44 4 5401 1 551	EcHu247a	0	1	0	1 1	NI	AY2a
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	EcHu404a	0	1	0	1 1	NI	AY2a
18 1 10 10 10 1 1 1 1 1	EcHu423a	0	1	0	1 1	NI	AY2a
W 18 8193 1311	EcHu427a	0	1	0	1 1	NI	AY2a
W 18 8101 1111	EcHu348a	0	1	0	1 1	NI	AY2a
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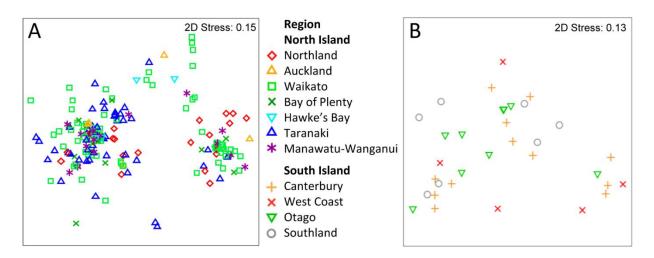
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Technical Appendix Figure 2. PFGE profile comparison of 40 bovine Shiga toxin–producing *Escherichia coli* O157:H7 isolates using UPGMA cluster analysis (Dice similarity coefficient, 1% band matching tolerance). Virulence genes (*stx*1, *stx*2a/2c, *stx*2c, *eae*, *ehx*A) present (1) or absent (0). Island of origin (Origin) presented as North Island (NI) or South Island (SI) of New Zealand, and genotypes of isolates as Shiga toxin-encoding bacteriophage insertion (SBI) types.



Technical Appendix Figure 3. Multidimensional scaling plots showing the genotypic clustering of bovine meat Shiga toxin–producing *Escherichia coli* O157:H7 isolates originating from the North Island (n = 200, 1 isolate excluded) and South Island (n = 33, 1 isolate excluded) of New Zealand. The plots were determined on the basis of the isolates' pulsed-field gel electrophoresis profiles. Clusters associated with regions are presented for isolates from the North Island (A) and the South Island (B).

	NZ Cattle	NZ Human	AU Cattle	AU Human	US Cattle	US Human
NZ Cattle (n = 40)		0.74 – 0.93	0.00 - 0.13	0.04 - 0.20	0.16 - 0.41	0.18 - 0.41
NZ Human (n = 363)	0.92		0.04 – 0.09	0.06 - 0.18	0.21 – 0.33	0.23 – 0.34
AU Cattle (n = 205)	0.06	0.06		0.57 – 0.79	0.27 – 0.43	0.05 – 0.13
AU Human (n = 79)	0.11	0.12	0.69		0.24 – 0.44	0.08 - 0.21
US Cattle (n = 143)	0.28	0.27	0.35	0.35		0.51 – 0.69
US Human (n = 179)	0.30	0.29	0.09	0.15	0.61	

Technical Appendix Figure 4. Proportional similarity index (PSI) values assessing the similarity of frequency distributions of Shiga toxin-encoding bacteriophage insertion (SBI) types among human and bovine Shiga toxin-producing *Escherichia coli* O157:H7 isolates originating from New Zealand (NZ), Australia (AU), and the United States (US). PSI values are presented in the lower half of the matrix with corresponding bootstrapped 95% confidence intervals in the upper half. Increased font size of PSI value shows higher degree of similarity.