

SUPPLEMENTAL MATERIAL

Johnson J.R. et al. Rapid emergence, subsidence, and molecular detection of *Escherichia coli* sequence type 1193-*fimH64* (ST1193-*H64*), a new disseminated multidrug-resistant commensal and extraintestinal pathogen.

Table S1. Virulence genes of *Escherichia coli* isolates from sequence type ST1193-*H64* or other ST14 complex (STc14) STs.

Virulence gene			Prevalence of virulence gene ^a (column %)		P value
Functional category	Specific gene ^{a,b,c,d,e}	Definition	Other STc14 isolates (n = 37)	ST1193- <i>H64</i> (n = 83 or 117)	
Adhesin	F10 <i>papA</i> allele	Antigenic variant, P fimbriae	31 (85)	87 (100)	0.006
	<i>papA/C/EF/G</i> II	<i>pap</i> operon (P fimbriae)	6 (16)	0 (0)	0.001
	<i>sfa/focDE</i>	S and F1C fimbriae	4 (11)	0 (0)	0.008
	<i>focG</i>	F1C adhesin	3 (8)	0 (0)	0.03
	<i>afa/draBC</i>	Dr-binding adhesin	16 (43)	0 (0)	< 0.001
Toxin	<i>hlyD</i>	alpha hemolysin	4 (11)	1 (1)	0.03
	<i>sat</i>	secreted autotransporter toxin	30 (81)	80 (96)	0.009
Siderophore	<i>iroN</i>	salmochelins receptor	5 (14)	0 (0)	0.002
	<i>ireA</i>	siderophore receptor	5 (14)	1 (1)	0.01
Protectin	K1 (<i>kpsM</i> allele)	group 2 capsule variant	0 (0)	62 (75)	< 0.001
	K5 (<i>kfiC</i>)	group 2 capsule variant	34 (92)	20 (24)	< 0.001
	<i>traT</i>	serum-resistance associated	24 (65)	2 (2)	< 0.001
	O75 <i>rfb</i>	O75 antigen	35 (95)	127 (100)	.0498
	O18 <i>rfb</i>	O18 antigen	2 (5)	0 (0)	.0498
Miscellaneous	<i>ibeA</i>	invasion of brain endothelium	7 (19)	0 (0)	< 0.001
	<i>clbB/N</i>	colibactin synthesis	31 (84)	0 (0)	< 0.001

^aGenes shown are those that differed significantly in prevalence between ST1193 vs. other STc14 STs.

^bGenes detected in all isolates (prevalence, 100%): *fimH*, *yfcV*, *fyuA*, *usp*, *ompT*, and *malX*.

^cOther genes detected in ≥ 1 isolate but without a significant prevalence difference between ST1193 vs. other STc14 STs (respective prevalence): *afaE8* (3% vs. 0%), *iha* (87% vs. 93%), *hra* (3% vs. 0%), *cnf1* (3% vs. 0%), *cdtB* (3% vs. 0%), *pic* (3% vs. 0%), *vat* (0% vs. 99%), *iutA* (87% vs. 93%), *chuA* (100% vs. 89%), and *kpsM* II (95% vs. 99%).

^dGenes sought but not detected: *sfaS*, *bmaE*, *clpG*, *gafD*, *hlyF*, *tsh*, *astA*, *kpsM* III, K15, *rfc*, *cvaC*, *iss*, and H7 *fliC*.

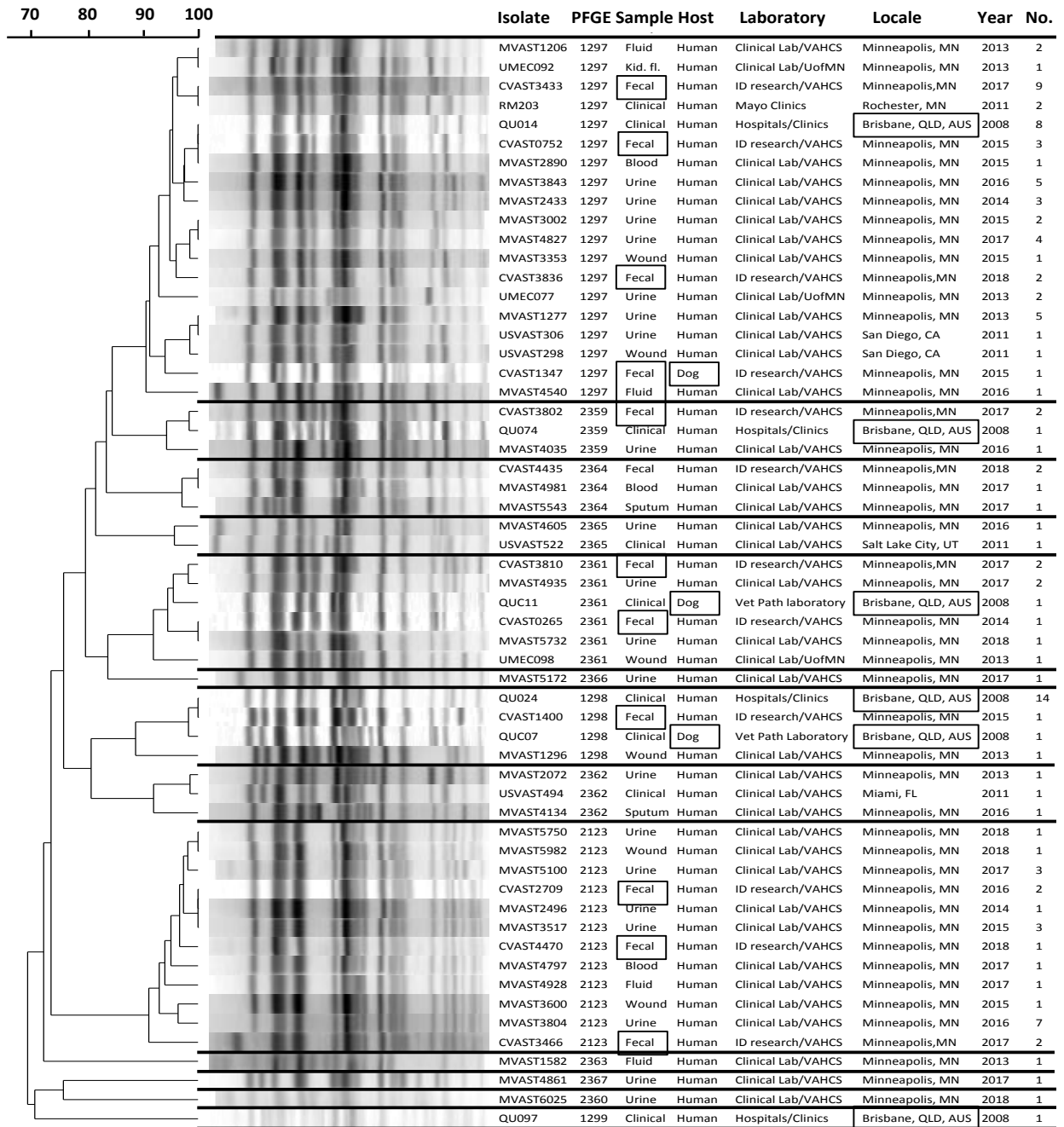


Fig. S1. Pulsed-field gel electrophoresis profiles of *Escherichia coli* ST1193-H64 isolates. Scale is percent profile similarity according to Dice coefficients. Dendrogram is based on one arbitrarily selected representative for each unique combination of pulsotype, specimen type (Sample), host, laboratory, locale, and year. Horizontal lines separate different pulsotypes (defined at the 94% profile similarity level in comparison with the index profile for a given pulsotype). Boxes indicate: in the Sample column, fecal isolates (others are clinical isolates); in the Host column, dog isolates (others are from humans); and in the locale column, Australian isolates (others are from the USA). **Definitions:** AUS, Australia; ID, Infectious Diseases; Kid., kidney; fl., fluid; Lab, laboratory; No, total number of isolates with the particular combination of characteristics; PFGE, pulsotype; QLD, Queensland; VAHCS, Veterans Affairs Health Care System; Vet Path, veterinary pathology.

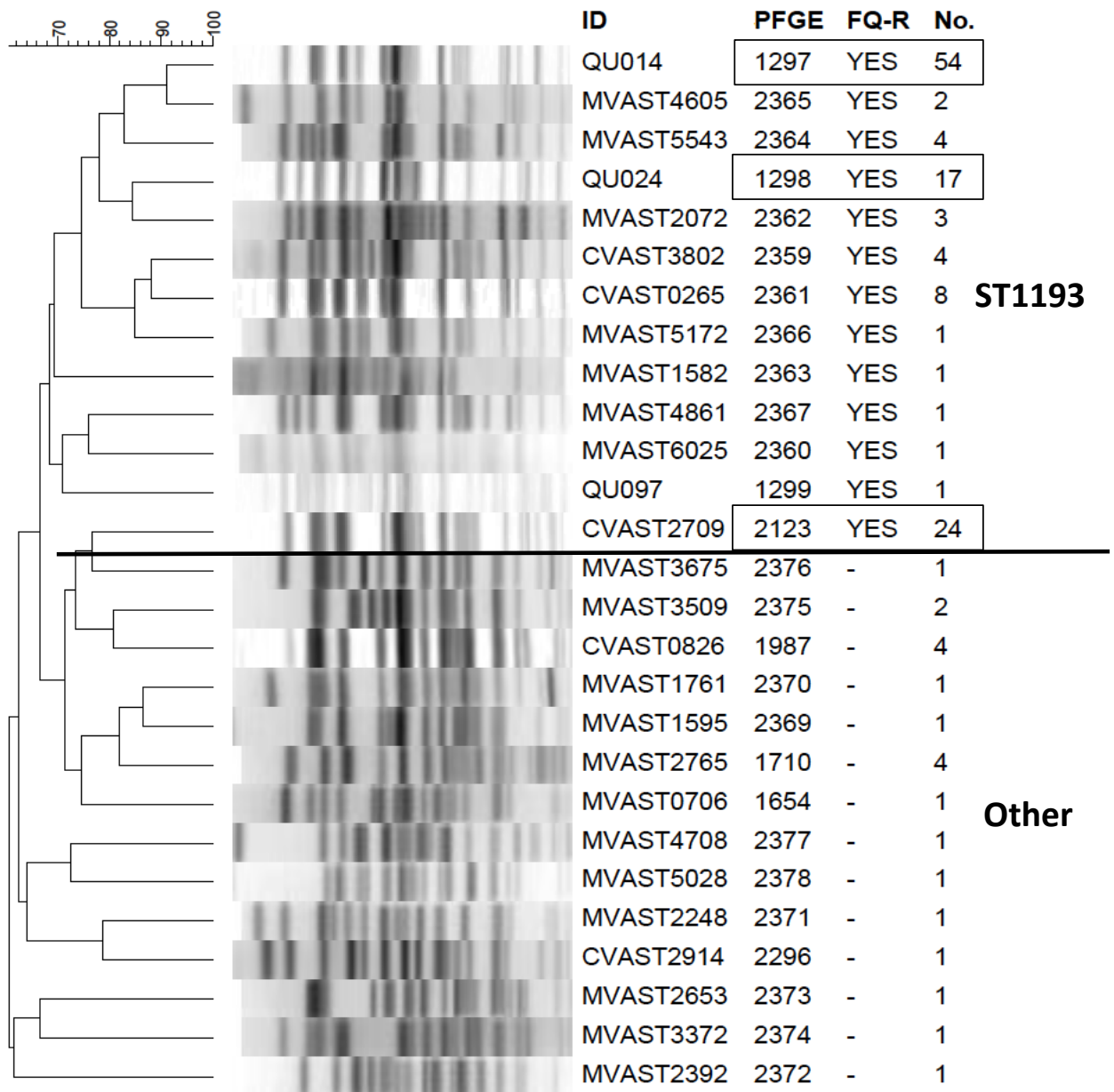


Fig. S2. Pulsed-field gel electrophoresis profiles of index *Escherichia coli* isolates from ST1193-H64 vs. other STs from the ST14 complex. Scale is percent profile similarity according to Dice coefficients. Dendrogram is based on the index profile for each pulsotype. Horizontal line separates ST1193-H64 isolates from other ST14 complex isolates. Boxes: three most prevalent pulsotypes (1297, 1298, 2123). **Definitions:** ID, identifier; PFGE, pulsotype; FQ-R, fluoroquinolone-resistant; No., total number of study isolates represented by the particular pulsotype; -, not FQ-R; Other, non-ST1193-H64.