Table S1. PA strain information

Strain	Clade <sup>b</sup>	stx Allele(s)	Genome accession <sup>d</sup>	Phage
Name <sup>a</sup>		` '		accession <sup>e</sup>
PA2	8	stx2a	AOEL00000000	KP682371
PA3	8	stx2a, stx2c	AKLC01000000	
PA4	2.9	stx1a, stx2a	AMUA01000000	KP682372
PA5	2.9	stx1a, stx2a	AKLD01000000	KP682373
PA7	2.9		AMTQ00000000	
PA8	8	stx2a	AOEO00000000	KP682374
PA9	8	stx2a	AKLE01000000	
PA10	6	stx2c	AKLF01000000	
PA11	2.9	stx2a	AOEI00000000	KP682375
PA12	2.9	stx1a, stx2a	This study	KP682376
PA13	8	stx2a, $stx2c$	AOEK00000000	
PA14	2.9	stx1a, stx2a	AKLG01000000	
PA15	2.9	stx1a, stx2a	AKLH01000000	
PA16	2.9	stx1a, stx2a	This study	KP682377
PA17	2.9	stx1a, stx2a	This study	
PA18	*	stx1a, stx2a	This study	KP682378
PA19	8	stx2a	AOEJ00000000	
PA21	*	stx1a, stx2a	This study	KP682379
PA22	5.2	stx1a, stx2c	AKLI00000000	
PA23	2.9	stx1a, stx2a	AMUB0100000	
PA24	8	stx1a	AKLJ01000000	
PA25	8	stx2a	AKLK01000000	
PA27	2.9	stx1a, stx2a	This study	KP682380
PA28	8	stx2a, stx2c	AKLL01000000	KP682381
PA29	2.9	stx1a, stx2a	This study	KP682382
PA30	*	stx1a, stx2a	This study	KP682383
PA31	2.9	stx1a, stx2a	AKLM01000000	
PA32	2.9	stx2a	AKLN01000000	KP682384
PA33	2.9	$stx1a$ , $stx2a^{c}$	AKLO01000000	KP682385
PA34	8	stx2a	AMTR01000000	
PA35	8	stx2a, stx2c	AOES00000000	
PA36	2.9	stx1a, stx2a	This study	KP682386
PA38	6	stx2c	AMUO01000000	
PA39	8	stx2a, stx2c	AKLP01000000	
PA40	7	stx2c	AKLQ00000000	
PA41	7	stx1a, stx2c	AKLR01000000	
PA42	2.4	stx1a, stx2a	AKLS01000000	KP682387
PA44	2.9	stx1a, stx2a	This study	KP682388
PA45	2.4	stx1a, stx2a	AMUD01000000	KP682389
PA47	8	stx2a, stx2c	AOEM00000000	
PA48	9	stx1a, stx2c	AOEN01000100	
PA49	2.9	stx1a, stx2a	AMUC01000000	
PA50	*	stx1a, stx2a	This study	KP682390

PA51	*	stx1a, stx2a	This study	KP682391	
PA52	*	stx1a, stx2a	This study	KP682392	

<sup>&</sup>lt;sup>a</sup> For all 45 isolates, the date and geographic location of isolation, PFGE pattern and LSPA type were previously reported by Hartzell *et al.* (2011).

<sup>&</sup>lt;sup>b</sup> Clade types were determined *in silico* or reported previously (Hartzell *et al.*, 2011). \* Unable to assign a clade because of missing SNP positions due to sequence quality.

<sup>&</sup>lt;sup>c</sup> Strain PA33 was previously reported as an "stx2 variant" (Hartzell et al. 2011). However, the phage genome sequence reported here identified it as stx2a.

<sup>&</sup>lt;sup>d</sup> For isolates previously sequenced, GenBank accession numbers are reported. The 13 isolates sequenced during this study were submitted to the Short Read Archive under Bioproject PRJNA274145.

<sup>&</sup>lt;sup>e</sup> GenBank accession numbers for phage sequenced in this study.