



Isolate ID	Clade <sup>1</sup>	<i>rpoB</i> AT <sup>2</sup>	MLST Type	SR/RefSeq Accession	Growth at 6°C <sup>3</sup>	Hemolytic <sup>3</sup>	PI- PLC <sup>3,4</sup>	Lecithinase <sub>3</sub>	NheB <sup>3,5</sup>	Hbl-L2 <sup>3,5</sup>	<i>hblA</i> <sup>3</sup>	<i>hblC</i> <sup>3</sup>	<i>hblD</i> <sup>3</sup>	<i>nheA</i> <sup>3</sup>	<i>nheB</i> <sup>3</sup>	<i>nheC</i> <sup>3</sup>	<i>cytK</i> <sup>3</sup>	<i>entFM</i> <sup>3</sup>	Cytotoxicity Average <sup>6</sup>
FSL K6-0268	IV	409	230	SRR5185034	-	+	+	+	+	-	+	+	+	+	+	+	+	+	0.01
FSL K6-1030	IV	556	1191	SRR4661783	-	-	-	+	+	-	+	-	+	+	+	+	+	+	0.00
FSL M8-0139	IV	424	138	SRR5185026	-	-	+	+	+	-	-	-	-	+	+	+	+	+	0.00
FSL R5-0184	IV	277	927	SRR5185020	-	+	+	+	+	+	+	+	+	+	+	+	+	+	1.00
FSL R5-0585	IV	278	1143	SRR5185019	-	+	+	+	+	-	+	+	+	+	+	+	+	+	0.01
FSL R5-0859	IV	158	1099	SRR5185016	-	+	+	+	+	+	+	+	+	+	+	+	+	+	0.00
FSL W7-1101	IV	296	1100	SRR5185011	-	+	+	+	+	+	+	+	+	+	+	+	+	+	0.30
FSL W7-1334	IV	304	265	SRR5185009	-	+	+	+	-	+	+	+	+	+	+	+	-	+	0.00
FSL W8-0640	IV	154	1089	SRR2541688	-	+	+	+	+	+	+	+	+	+	+	+	+	+	0.00
FSL W8-0824	IV	92	24	SRR2541693	-	+	+	+	+	+	+	+	+	+	+	+	+	+	0.64
ATCC 14579 <sup>T</sup>	IV	158	4	NC_004722.1	-	+	+	+	+	+	+	+	+	+	+	+	+	+	0.99
ATCC 10792 <sup>T</sup>	IV	689	10	NC_005957.1	-	+	+	+	+	+	+	+	+	+	+	+	+	+	0.76
FSL M8-0214	V	412	223	SRR5185025	-	+	+	+	+	+	+	+	+	+	+	+	-	+	0.42
FSL H8-0482	V	129	223	SRR2541601	-	+	+	+	+	-	+	+	+	+	+	+	-	+	0.01
BCT-7112 <sup>T</sup>	V	129	111	NC_022781.1	-	+	+	+	+	+	+	+	+	+	+	+	-	+	0.02
FSL H7-0683	VI	75	222	SRR4064645	+	-	+	+	-	-	+	+	+	+	+	+	-	+	0.00
FSL E2-0214	VI	531	410	SRR4661781	+	+	+	+	-	-	+	+	+	-	+	+	-	+	0.00
FSL H7-0926	VI	90	667	SRR2541537	+	+	+	+	-	-	+	+	+	+	+	+	-	+	0.00
FSL H8-0485	VI	132	1142	SRR5189059	+	-	+	+	+	-	-	+	+	+	+	+	-	+	0.00
FSL H8-0492	VI	134	1098	SRR4661790	+	-	+	+	-	-	+	+	+	+	+	+	-	+	0.00
FSL J3-0123	VI	513	1095	SRR5189058	+	+	+	+	+	-	+	+	+	+	+	+	-	+	0.00
FSL M7-0109	VI	273	410	SRR5189057	+	+	+	+	+	-	+	+	+	-	+	+	-	+	0.00
FSL M7-0669	VI	3	655	SRR5189065	+	+	+	+	+	-	+	+	+	-	+	+	-	+	0.00

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FSL M7-1219	VI	97	1092	SRR5189064	+	+	+	+	+	-	+	+	+	+	+	+	-	+	0.00
FSL R5-0708	VI	257	1144	SRR5189062	+	+	+	+	+	-	+	+	+	+	+	+	-	+	0.00
FSL W7-1108	VI	342	673	SRR5189056	+	+	+	+	+	-	+	+	+	+	+	+	-	+	0.00
DSM 2048 <sup>T</sup>	VI	3	116	NZ_CP009692.1	+	+	+	+	+	-	+	+	+	-	+	+	-	+	0.00
WSBC 10204 <sup>T</sup>	VI	3	196	NZ_CP009746.1	+	-	+	+	+	-	+	+	+	+	+	+	-	+	0.00
NVH 391-98 <sup>T</sup>	VII	688	930	NC_009674.1	-	+	-	+	-	-	-	-	-	-	-	-	+	+	0.25

<sup>1</sup> Phylogenetic group determined based on concatenated 7-gene MLST sequences.

<sup>2</sup> AT refers to *rpoB* allelic type; determined based on 632 nucleotide sequence of *rpoB*.

<sup>3</sup> “+” denotes the bacterial isolate was positive for a given virulence factor, “-” denotes the virulence factor was not detected. Data presented are based on PCR amplification of target genes.

<sup>4</sup> PI-PLC refers to phosphoinositide phospholipase C activity as determined by plating isolates on *Bacillus cereus*/*Bacillus thuringiensis* chromogenic plating medium.

<sup>5</sup> Lecithinase activity determined by plating isolate on Bacara agar.

<sup>6</sup> Proportion of HeLa cells that were positive for propidium iodide staining, following a 30 minute co-incubation with supernatants (5% v/v) from bacterial cultures grown at 37°C. Results are averaged from two independent experiments.

**Table S2.** P-values of statistical analyses of associations between virulence factors and phylogenetic clades and cytotoxicity

Association tested <sup>1,2</sup>	P-value for overall associations <sup>3</sup>	P-values for significant associations with specific phylogenetic clades <sup>4,5,6</sup>
<b>Association between phylogenetic clades and virulence factors</b>		
PI-PLC Activity	P < 0.001	I: P < 0.001
Hemolysis	P = 0.720	ND
Growth at 6°C	P < 0.001	III: P = 0.043 IV: P = 0.002 VI: P < 0.001
<i>hblCDA</i> gene presence	P < 0.001	III: P < 0.001 VI: P = 0.047
<i>nheABC</i> gene presence	P = 0.032	VII: P = 0.019
<i>entFM</i> gene presence	P < 0.001	I: P < 0.001
<i>cytK</i> gene presence	P < 0.001	I: P = 0.025 IV: P < 0.001 VI: P < 0.001
Hbl-L2 Immunoassay Detection	P < 0.001	IV: P < 0.001 VI: P = 0.005
NheB Immunoassay Detection	P < 0.001	I: P < 0.001 IV: P = 0.043
Cytotoxicity	P < 0.001	I: P = 0.001 VI: P = 0.002
<b>Cytotoxicity versus presence/absence of selected genes</b>		
<i>hblCDA</i>	P = 1.000	NA
<i>cytK</i>	P = 0.316	NA
<i>nheABC</i>	P = 0.422	NA
<b>Cytotoxicity versus immunoassay detection of Hbl-L2 and NheB</b>		
Hbl-L2	P = 0.098	NA
NheB	P = 0.140	NA

<sup>1</sup> Includes both *cytK-1* and *cytK-2*.

<sup>2</sup> Considered *hblCDA* or *nheABC* positive if at least one gene in the toxin gene operon was detected via PCR.

<sup>3</sup> P-values from Fisher's exact tests, corrected using False Discovery Rate for multiple comparisons.

<sup>4</sup> P-values from Fisher's exact tests, uncorrected.

<sup>5</sup> ND = not determined (i.e. analysis not performed).

<sup>6</sup> NA = not applicable.

**Table S3.** Number and proportion of PCR-positive results for toxin genes.

Clade	Gene <sup>1</sup>							
	<i>hblA</i>	<i>hblC</i>	<i>hblD</i>	<i>nheA</i>	<i>nheB</i>	<i>nheC</i>	<i>cytK</i>	<i>entFM</i>
I	6 (1.00)	5 (0.83)	6 (1.00)	0 (0.00)	0 (0.00)	6 (1.00)	0 (0.00)	1 (0.17)
II	2 (0.40)	3 (0.60)	3 (0.60)	5 (1.00)	5 (1.00)	5 (1.00)	2 (0.40)	5 (1.00)
III	2 (0.22)	2 (0.22)	2 (0.22)	9 (1.00)	9 (1.00)	9 (1.00)	7 (0.78)	9 (1.00)
IV	14 (0.93)	13 (0.87)	14 (0.93)	15 (1.00)	15 (1.00)	15 (1.00)	14 (0.93)	15 (1.00)
V	3 (1.00)	3 (1.00)	3 (1.00)	3 (1.00)	3 (1.00)	3 (1.00)	0 (0.00)	3 (1.00)
VI	12 (0.92)	13 (1.00)	13 (1.00)	9 (0.69)	13 (1.00)	13 (1.00)	0 (0.00)	13 (1.00)
VII	0 (0.00)	0 (0.00)	0 (0.00)	0 (0.00)	0 (0.00)	0 (0.00)	1 (1.00)	1 (1.00)
Total	39 (0.75)	39 (0.75)	41 (0.79)	41 (0.79)	45 (0.87)	51 (0.98)	24 (0.46)	47 (0.90)

<sup>1</sup>Number and proportion (in parentheses) of isolates in a given clade that were PCR-positive for gene

**Table S4.** Number of isolates with positive results for toxin genes using WGS data, within each clade.

Clade	Gene <sup>1</sup>															
	<i>hblA</i>		<i>hblC</i>		<i>hblD</i>		<i>nheA</i>		<i>nheB</i>		<i>nheC</i>		<i>cytK</i>		<i>entFM</i>	
I	6	(1.00)	5	(0.83)	4	(0.67)	0	(0.00)	3	(0.50)	4	(0.67)	0	(0.00)	0	(0.00)
II	2	(0.40)	3	(0.60)	3	(0.60)	5	(1.00)	5	(1.00)	5	(1.00)	2	(0.40)	5	(1.00)
III	2	(0.22)	2	(0.22)	2	(0.22)	9	(1.00)	9	(1.00)	9	(1.00)	7	(0.78)	9	(1.00)
IV	14	(0.93)	14	(0.93)	13	(0.87)	15	(1.00)	15	(1.00)	15	(1.00)	14	(0.93)	14	(0.93)
V	3	(1.00)	3	(1.00)	3	(1.00)	3	(1.00)	3	(1.00)	3	(1.00)	0	(0.00)	3	(1.00)
VI	13	(1.00)	10	(0.77)	13	(1.00)	13	(1.00)	13	(1.00)	13	(1.00)	0	(0.00)	13	(1.00)
VII	0	(0.00)	0	(0.00)	0	(0.00)	0	(0.00)	0	(0.00)	0	(0.00)	1	(1.00)	1	(1.00)
Total	40	(0.77)	37	(0.71)	38	(0.73)	45	(0.87)	48	(0.92)	49	(0.94)	24	(0.46)	45	(0.87)

<sup>1</sup> Proportion of isolates in a given clade that were PCR-positive for gene