

Supplemental Table 1. Sequence type and phenotype of parental strains.

Strain	<i>hsdS allele</i>^(1,2)	Transparent vs opaque	Sequence type⁽³⁾	PubMLST id
0556-97	B	Mixed	ST199	38163
3031-06	B	Mixed	ST199	38164

Supplemental Table 2. Primers used in this study

Primer (direction)	Location	Sequence	Purpose (fragment)	Source
5482 (F)	<i>rpsL</i>	CTGGAATTCACCAAAAATAAAA AAACACAGGAG	Transformation into 0556-97 and 3031-06	(4)
3482 (R)	<i>rpsL</i>	CTAGGGCCCCTTTCCTTATGCTT TTGGAC	Transformation into 0556-97 and 3031-06	(4)
5168 (F)	<i>wzx</i>	TTGGTCTGATTATGCACCTC	Creation of <i>wciZ</i> variant constructs (BLS143, 157, 171); Sequencing <i>wciZ</i> region of clinical isolates	This study
3162 (R)	<i>wciZ/JS</i>	CAAACCTTCTAGACTGCATATTA CCTTCTCTCC	Creation of <i>wciZ</i> deletion construct (BLS143); Sequencing <i>wciZ</i> region of clinical isolates	This study
5169 (F)	<i>wciZ/JS</i>	GTAATATGCAGTCTAGAAGTTT GATTTTTAATGG	Creation of <i>wciZ</i> deletion construct (BLS143)	This study
3163 (R)	<i>JS/wchX</i>	GATTTAATCGCGCCCCTTTCCTT ATGCTTTTG	Creation of <i>wciZ</i> deletion construct (BLS143)	This study
5170 (F)	<i>JS/wchX</i>	CATAAGGAAAGGGGCGCGATTA AATCACCTAAAGC	Creation of <i>wciZ</i> deletion construct (BLS143); Sequencing <i>wciZ</i> region of clinical isolates	This study
3164 (R)	<i>wchX</i>	CCCATCATCTCTGAAAGTAG	Creation of <i>wciZ</i> variant constructs (BLS143, 157, 171); Sequencing <i>wciZ</i> region of clinical isolates	This study
3229 (R)	<i>wciZ</i>	CTGCATATTACCTTCTCTCC	BLS171 <i>wciZ</i> construct, 5' fragment	This study
5256 (F)	<i>wciZ</i>	GGAGAGAAGGTAATATGCAG	BLS171 <i>wciZ</i> construct, 3' fragment	This study
5508 (F)	<i>dexB</i>	GCCGTAGTCTATCAAGTCTATC CAA	<i>cps</i> locus deletion construct (BLS147)	This study
3493 (R)	<i>aliA</i>	TGCTTCCAAGGATTGTTTCATAG ATTG	<i>cps</i> locus deletion construct (BLS147)	This study

Supplemental Table 3. *cps* loci differences between a clinical isolate 0556-97 (serotype 15B) used in this study and a reference serotype 15B strain (7904/39 strain) in literature (5)

Nucleotide ^a	7904/39 ^b	BLS141 ^c	Gene	Function	Amino Acid difference ^d
293-1203	<i>aliB</i> , IS1630 tnp	IS1202 tnp			
1204-3382		>90 snps	<i>wzg-wzh</i>	regulatory region	
5743	A	C	<i>wchA</i>	initiating glycosyltransferase	Arg318Arg
5772	G	A	<i>wchA</i>	initiating glycosyltransferase	Gln327Gln
7296	G	A	<i>wzy</i>	polymerase	Met64Ile
7352	G	T	<i>wzy</i>	polymerase	Leu83Phe
10200	A	G	<i>wchM</i>	β -galactosyltransferase	Val298Val
10841	T	C	<i>wchN</i>	α -galactosyltransferase	Val188Ala
12344	A	G	<i>wzx</i>	flippase	Ile385Val
12947	G	A	intergenic	N/A ^e	N/A
14387	C	A	<i>wchX</i>	glycerol phosphotransferase	Gln130Lys
16712	T	C	<i>gtp2</i>	CDP-2-glycerol synthesis	Val162Ala
17156	A	T	<i>gtp3</i>	CDP-2-glycerol synthesis	Val70Val
17393	C	T	<i>gtp3</i>	CDP-2-glycerol synthesis	Arg149Arg
17869-18375		9 snps	IS1381 and IS1671 tnp		

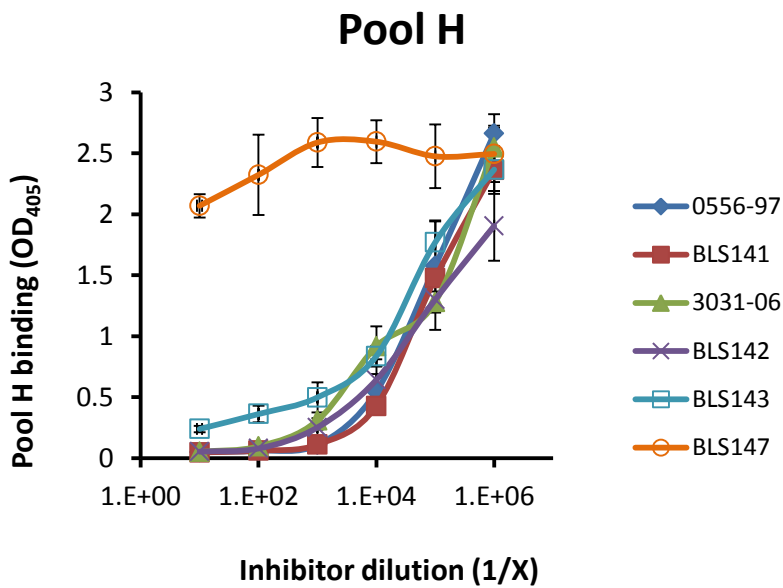
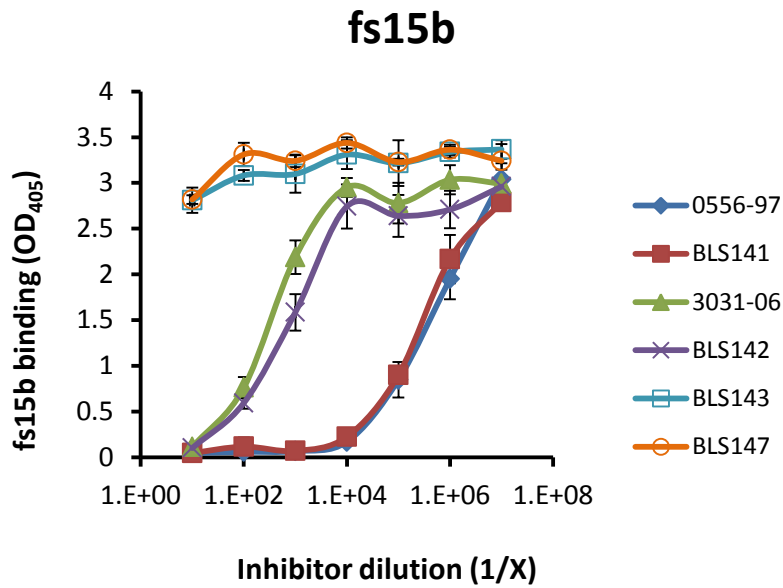
^a Nucleotide number is with respect to the reference sequence (GenBank Accession No. CR931664.1)

^b Accession no. CR931664.1

^c Accession no. KY750633

^d Amino acid sequence differences are with respect to 7904/39. Boldface indicates a missense substitution.

^e N/A means not applicable.



Supplemental Figure 1. Parental clinical isolates (0556-97 and 3031-06) and the transformed reference strains (BLS141 and BLS142, respectively) have equivalent amounts of O-acetylation and capsule based on fs15b and Pool H binding, respectively. Error bars indicate standard deviation of the three intra-assay replicates.

REFERENCES

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