

^a Keys to Table S1

ST types	MLST of 15 housekeeping genes
Lineage	as figure 1A
Cluster	as figure 1A
<i>opt</i>	<i>opt</i> alleles on plasmid pSFVv_2 and pSFYv_2, <i>optII</i> * indicated the 3 isolates carries a defective <i>optII</i> .

Antibiotics symbol	Name	Breakpoint (mm) for resistance, intermediate and susceptible
AMP	Ampicillin	≥ 17, 14–16, ≤ 13
PIP	Piperacillin	≥ 21, 18–20, ≤ 17
AMC	Amoxicillin-clavulanic acid	≥ 18, 14–17, ≤ 13
SAM	Ampicillin-sulbactam	≥ 15, 12–14, ≤ 11
TIM	Ticarcillin-clavulanic acid	≥ 20, 15–19, ≤ 14
ATM	Aztreonam	≥ 21, 18–20, ≤ 17
CXM	Cefuroxime	≥ 18, 15–17, ≤ 14
CFP	Cefoperazone	≥ 21, 16–20, ≤ 15
FEP	Cefepime	≥ 18, 15–17, ≤ 14
CTX	Cefotaxime	≥ 26, 23–25, ≤ 22
CIP	Ciprofloxacin	≥ 21, 16–20, ≤ 15
NOR	Norfloxacin	≥ 17, 13–16, ≤ 12
OFX	Ofloxacin	≥ 16, 13–15, ≤ 12
LVX	Levofloxacin	≥ 17, 14–16, ≤ 13
NAL	Nalidixic acid	≥ 19, 14–18, ≤ 13
SXT	Trimethoprim-sulfamethoxazole	≥ 16, 11–15, ≤ 10
TMP	Trimethoprim	≥ 16, 11–15, ≤ 10
F	Furazolidone	≥ 17, 15–16, ≤ 14
TET	Tetracycline	≥ 15, 12–14, ≤ 11
DOX	Doxycycline	≥ 14, 11–13, ≤ 10
MIN	Minocycline	≥ 16, 13–15, ≤ 12
KAN	Kanamycin	≥ 18, 14–17, ≤ 13
STR	Streptomycin	≥ 15, 12–14, ≤ 11
GEN	Gentamicin	≥ 15, 13–14, ≤ 12
TOB	Tobramycin	≥ 15, 13–14, ≤ 12
AMK	Amikacin	≥ 17, 15–16, ≤ 14
NET	Netilmicin	≥ 15, 13–14, ≤ 12
CHL	Chloramphenicol	≥ 18, 13–17, ≤ 12
PB	Polymyxin B	≥ 11, –, ≤ 10
IPM	Imipenem	≥ 16, 14–15, ≤ 13

Antibiotic resistance genes	Resistance	Location
<i>aadA2</i>	streptomycin	SRL
<i>oxa-1</i>	ampicillin	SRL
<i>cat</i>	chloramphenicol	SRL
<i>tetR</i>		SRL
<i>tetA</i>	tetracycline	SRL
<i>tetC</i>		SRL
<i>tetD</i>		SRL
<i>dfrA1</i>	trimethoprim	Tn7
<i>sat1</i>	streptothricin	Tn7
<i>aadA1</i>	streptomycin/spectinomycin	Tn7
<i>dfrA5</i>	trimethoprim	X12868.1
<i>blaCTX-M-14</i>	Cephalosporins	NC_019071.1
<i>blaTEM-1</i>	Ampicillin	NC_010558.1
<i>blaCTX-M-3</i>	Ampicillin	NC_019090.1
<i>qnrS</i>	quinolones	NC_010886.1
<i>qepA</i>	quinolones	NC_020278.2
<i>aac(6)-Ib-cr</i>	quinolones	NC_011617.1

Other notes

1. antibiotic susceptibility: R = resistance; S = sensitive; I= intermediate, based on breakpoints listed above.

For *Salmonella* spp. and *Shigella* spp., aminoglycosides, as well as first- and second-generation cephalosporins and cephamycins, may appear active in vitro but are not effective clinically and should not be reported as susceptible.

2. SRL, Tn7, *dfrA5*, *gyrA*, *blaCTX-M-14*, *blaTEM-1*, *blaCTX-M-3*, *qnrS*, *qepA* and *aac(6)-Ib-cr* coverage. The contigs were mapped to the SRL, Tn7 *dfrA5*, *gyrA*, *blaCTX-M-14*, *blaTEM-1*, *blaCTX-M-3*, *qnrS*, *qepA* and *aac(6)-Ib-cr* reference. Percent coverage was calculated based whether any sequence mapped to reference. 0 indicated no or few mapped to reference, "no" indicated no mutation on *gyrA*.

Table S2 Primers SNP genotyping using cluster-specific SNPs

SNPs no.	Upstream Primer	Downstream Primer	Base extension Primer for the SNP
1	ACGTTGGATGTTATCTGTCGGTTTCACCGC	ACGTTGGATGATTACCGGTGATGTCGTGGC	GGATGTCGTGGCACTGGA
3	ACGTTGGATGATTCCCTTCACGACAACCTGC	ACGTTGGATGGGGAATTCCGCATTTCTCAC	TACCCAATTCTGACAGTTA
4	ACGTTGGATGTGTTGAGATTGCCATCAACC	ACGTTGGATGGTAGTCACTTACCTTCACCG	TTCCCCGTTAGCCAAACCTGC
5	ACGTTGGATGAGCTCGTTGTGCTGAATCGG	ACGTTGGATGCTGGATTCATGCGGGTATTC	GGGCCGGTGATCCCGATTCAGGCCTA
6	ACGTTGGATGAAACTGGTGTTCAGGAAGG	ACGTTGGATGGGTGGTCAAAGCATGGTTAC	TGGTTACCAACAATGTTAAT
7	ACGTTGGATGGCATCCGCGATGATTTTCTG	ACGTTGGATGATGAAGGCGGTATTCTCCTG	TTATCCTGTTCGGTCTGATG
9	ACGTTGGATGGCTTCAACAGCAGCACAAAC	ACGTTGGATGACCCATATCTTGACCAGGTG	TTATCACAAACCGGAACCACAA
10	ACGTTGGATGTCGTTGACGTTCAATCCAGC	ACGTTGGATGAGCGCGTTACGCAATAAACC	GATGACCAGTTTCACCC
13	ACGTTGGATGCAGAATCTTAAACAGGCTCG	ACGTTGGATGACTGAAGGTCTTCGGTAAGG	TCGGCAAACTAGTTGAC
14	ACGTTGGATGACAATGGCTTTGAGGTCGGG	ACGTTGGATGATACGTATAGTCCTCTCTGG	GGCGTGATTCTCTGAGTTATATGCT
15	ACGTTGGATGCCGCGACTATTCAGCAAAAAG	ACGTTGGATGCCGTTTTTCGACAATTGCCAC	CCACCGGCATTTTCGC

16	ACGTTGGATGCAACCATCTCGTATATTAACC	ACGTTGGATGCCAGAAAAAATTTCTCGATG	GGTTTCATAACATTATATTTAATTGCTG
17	ACGTTGGATGGGCAATCAGATCTTTCAGGG	ACGTTGGATGGATTTTCGGCGATTCAGGAAG	ATGGTGATGATAGAGATCACT
18	ACGTTGGATGTGTCTGCACTGTGCGAAATG	ACGTTGGATGATATCGCGACCAATCCGTTT	CGTGATGCGGATGAAT
19	ACGTTGGATGATGCAGCATCTACGCATTCC	ACGTTGGATGATAAGATGGGTTTGCTGCGG	CCCGCACCCGCGCTCATTA
20	ACGTTGGATGCAAAACCTGTTGACAGAAAG	ACGTTGGATGAAAAGCGCCATAAGGACTC	GAGGACTCCTTGATTTATTATGTA
21	ACGTTGGATGGCATGACCTTTGCCAACTTC	ACGTTGGATGGTAGTTAAAAGGTGGAGCGG	GCGGAAAGCAAAAAGGCCATTGA
22	ACGTTGGATGTGTAGATCAGCATGGAGCCG	ACGTTGGATGTTTCCTGAAACACAACCCGC	ACCCGCAGAATCCGT
23*	CAGAGTGCAAGCCAATGCTA	CGCGATGTTGACAAGAAGAG	NA
24*	TACCCCGCCTCTCTTCTGACT	TGGTAGCGCAATTGGCAA	NA
25*	CTGGCGATTACAAATCACGA	TGTGACCTGGGTCACGAATTA	NA
26*	TGACGTTGGCCTGAAGTAAGA	ATCACCAGCCTACAGGCTAAA	NA
27*	ACCGCAACCAATCACCGTAT	TGGAGCAACGCAATGGTTAG	NA

*primers for PCR sequencing

Table S3 List of SNPs on pSFXv_2

Chromosome SNP cluster	Lab NO.	no. of isolates	Sero type	SNP on pSFXv_2 ^a																											
				68	69	181	330	362	371	462	798	1368	1396	1628	2226	2459	2987	3007	3124	3126	3315	3318	3304	3604	3787	3972	4000	4535	5606	5745	
2002017			Xv	T	T	G	G	G	G	C	A	C	C	C	A	T	C	C	G	G	C	G	T	A	C	C	A	C	T	A	
Cluster1	Shi06HN347	1	Xv	.	.	C	T	A	A	.	C	
	Shi06HN344	1	X	.	.	C	T	A	A	.	C	
	12 isolates	12	Xv	G	G	C	T	A	A	.	C	
	2002141	1	X	G	G	C	T	A	A	.	C	
Non-clustered	2001044	1	Xv	G	G	C	T	A	A	.	C	
Cluster2	3 isolates	3	Xv	G	G	C	T	A	A	.	C	
	3 isolates	3	Xv	G	G	C	T	A	A	.	C	G	
Cluster3	4 isolates	4	Xv	G	G	C	T	A	A	T	C	T	T	T	.	C	T	A	T	C	.	.	C	C	A	T	.	T	G	.	
Extended cluster3	2005184	1	X	.	.	C	T	A	A	T	C	T	T	T	.	C	T	A	T	C	.	.	C	C	A	T	.	T	G	.	
Non-clustered	Shi06AH091	1	Xv	G	G	C	T	A	A	T	C	T	T	.	G	C	T	A	.	.	A	A	.	C	A	.	.	T	G	C	

^a SNP is named based on base position in the pSFXv_2 plasmid. Dots represent bases identical to the reference bases.

SNP 3972, 4000 and 4535 located on the *opt* gene.

Nature of SNPs are as follows:

- 68 T→G, 69 T→G, resulting in I21→R
- 181 G→C, resulting in V59→L
- 330 G→T, synonymous SNP
- 362 G→A, resulting in C119→Y
- 371 G→A, resulting in R122→H
- 462 C→T, synonymous SNP
- 798 A→C, resulting in L263→F
- 1368 C→T, synonymous SNP
- 1396 C→T, deletion 450Q
- 1628 C→T, resulting in P524→L
- 2226 A→G, synonymous SNP
- 2459 T→C, resulting in L787→P
- 2987 C→T, resulting in S955→F
- 3007 C→A, resulting in Q962→K
- 3124 G→T, 3126 G→C, resulting in E1000→Y
- 3315 C→A, 3318 G→A, synonymous SNPs
- 3304 T→C, resulting in W1059→R
- 3604 A→C, resulting in T1152→P
- 3787 C→A, resulting in Q1210→K
- 3972 C→T, synonymous SNP
- 4000 A→G, resulting in T1280→A
- 4535 C→T, resulting in A1458→V
- 5606 T→G, deletion 1807L
- 5745 A→C, synonymous SNP

			Anhui (1)	
	SG4	65	Henan (9)	A C C C G A A T A G A A C A A C . .
			Gansu (50)	
			Anhui (6)	
Cluster 3	SG5	54	Henan (7)	A C C C A A
			Gansu (2)	
			Anhui (45)	

* see Table 1 for SNP details. Note that SNPs 2, 8, 11 and 12 were excluded. Dots represent bases identical to the reference bases.