

Table S1: Genome quality statistics for all the assembled genomes

Isolate no.	No. of contigs	Largest contig	Size(bp)	GC (%)	N50	L50	Genome fraction (%)
S44	40	517772	5482928	57.27	308712	7	92.224
S54	46	1082409	5691332	57.15	435362	4	98.04
S55	79	1010433	5752447	56.75	345690	6	92.898calc
S56	86	992865	5708668	57.05	226397	5	90.508
S57	101	605472	5718919	56.86	233432	9	90.207
S58	104	584373	5839331	56.58	306551	8	91.983
S59	70	698263	5769731	56.77	350190	6	93.125
S60	72	851986	5714482	56.83	286886	6	93.1
S61	34	512126	5352578	57.8	363661	7	33.733
S62	2947	86358	7457857	56.15	4818	346	92.984
S63	2187	71415	7190142	56.28	11256	176	93.917
S65	83	698263	5745130	56.78	287340	7	93.105
S66	335	357715	6494540	56.07	95700	19	93.42
S67	115	504304	6062433	56.53	200969	11	93.098

Table S2: Sequence types of isolates based on MLST scheme

Isolate	Chr_ST	gapA	infB	mdh	pgi	phoE	rpoB	tonB
S44	ST86	9	4	2	1	1	1	27
S54	ST23	2	1	1	1	9	4	12
S55	ST2096	1	6	1	1	1	46	1
S56	ST147	3	4	6	1	7	4	38
S57	ST43	2	6	1	5	11	1	15
S58	ST231	2	6	1	3	26	1	77
S59	ST2096	1	6	1	1	1	46	1
S60	ST2096	1	6	1	1	1	46	1
S61	ST3857	18	23	56	260	25	92	548
S62	ST147-1LV	3	4	6	1	-	4	38
S63	ST336-1LV	2	1	1	1	72	4	-
S65	ST2096	1	6	1	1	1	46	1
S66	ST15	1	1	1	1	1	1	1
S67	ST15-1LV	1	1	1	1	1*	1	1

Data Availability:

The genome sequenced files are submitted to NCBI SRA under the accession number SRR17640814, SRR17640813, SRR17640812, SRR17640811, SRR17640810, SRR17640809, SRR17640808, SRR17640807, SRR17640806, SRR17640805, SRR17640804, SRR17640803, SRR17640802, SRR17640801

Table S3: List of highly mutated genes with their respective functions (as found in UniProt and NCBI)

Gene Names	Function
<i>KP1_0403</i>	Putative secretion ATPase
KP1_4102	hypothetical protein
<i>fimD</i>	Putative fimbrial usher protein
<i>mobB</i>	Mobilization protein, GTP binding
<i>wzi</i>	Surface assembly of capsule
<i>wzc</i>	ATP Binding and protein tyrosine kinase activity
KP1_0410	Fimbrial biogenesis outer membrane usher protein
<i>ardC</i>	Single-stranded DNA binding
<i>wza</i>	Polysaccharide transmembrane transporter activity
KP1_4970	AsmA2 domain-containing protein YhdP
<i>RmpA</i>	DNA binding
<i>WcaJ</i>	Transferase activity
<i>entA</i>	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase activity
<i>entD</i>	holo-[acyl-carrier-protein] synthase activity, magnesium ion binding
<i>entC</i>	isochorismate synthase activity

