

Table S1. Primers used in this study

oligo	
FBO752	5'-GCTTGTA AATTCTATCATAATTG-3'
FBO753	5'-AGGGAATCATTGAAGGTTGG-3'
FBO1339	5'-ATGGATAACGAACAACCTCAA-3'
FBO1340	5'-AAAGTGTCGTTGTCT CTC AAC-3'
FBO1566	5'-AAATTCATTGATCGCCACTCC-3'
FBO1567	5'-CGACAGTGAAGTCTTGATC-3'
FBO1568	5'-CTGATCTGTATCTTTTCGACC-3'
FBO1569	5'-GCAATGTCCGCAATTGTTTC-3'
FBO1570	5'-TTGATGAGCTGTATGATGTGC-3'
FBO1571	5'-CGTCTGCAACCATGACATTC-3'
FBO1572	5'-CGAGTATAATGCAAAGGAGG-3'
FBO1573	5'-GTCTCTAAAAGAGCGGTCAC-3'
<i>bacA-F</i>	5'-GCGTATGACGGCATTAAAGCA-3'
<i>bacA-R</i>	5'-GGGTGGGATACGATGACAGT-3'
<i>bacB-F</i>	5'-GTCCGTCAGAGGAGATACGG-3'
<i>bacB-R</i>	5'-GATGCGGTTCCACGTTTGTA-3'
<i>bacC-F</i>	5'-GTGTATCCACCGTCTGCG-3'
<i>bacC-R</i>	5'-CTCGGCAAGCCTGAAGAA-3'
<i>bacD-F</i>	5'-GTTGGTCGTAATGGCGTCAA-3'
<i>bacD-R</i>	5'-TACTCGGTCGCGGTCATAAA-3'
<i>bacE-F</i>	5'-CCTCACCGTATTCCATTGCG-3'
<i>bacE-R</i>	5'-GACGTTCTGTATCGGCTTCG-3'
<i>bacF-F</i>	5'-GGTTCGGGACTAAGGCGATA-3'
<i>bacF-R</i>	5'-GAAAGAAGCCATCGCGGAAT-3'
<i>bacG-F</i>	5'-CGGCGCCAATATGTTTACCA-3'
<i>bacG-R</i>	5'-AACCCGGGATTACAGACAGTT-3'
<i>gyrA-F</i>	5'-CTAACCCGCCGCCCTTAT-3'
<i>gyrA-R</i>	5'-CTGCGAATGATTTCCAAC-3'

Table S2. Protein sequence alignment for *sprT* product and SprT s in some other species

Species	Identities %	Positives %	Gaps %
<i>Bacillus velezensis</i> DSM 23117	100	100	0
<i>Bacillus subtilis</i> 168	83	89	0
<i>Bacillus licheniformis</i>	74	84	0
<i>Bacillus pumilus</i>	67	80	2
<i>Bacillus salaceticus</i>	65	81	0
<i>Bacillus cereus</i>	59	78	0
<i>Bacillus siamensis</i>	97	98	0
<i>Bacillus thuringiensis</i> subsp. <i>konkukian</i>	59	79	0

<i>Bacillus nakamurai</i>	91	93	0
<i>Bacillus spizizenii</i>	83	89	0
<i>Bacillus intestinalis</i>	83	89	0
<i>Bacillus sp. EKM208B</i>	96	97	0
<i>Jeotgalibacillus campisalis</i>	66	81	2
<i>Aeribacillus pallidus</i>	63	81	0
<i>Priestia koreensis</i>	62	81	0
<i>Escherichia coli</i>	25	48	2
<i>Haemophilus influenzae</i> 86-028NP	26	43	6
<i>Klebsiella pneumoniae</i>	25	42	6
<i>Pseudomonas ogarae</i>	22	41	8
<i>Actinobacillus pleuropneumoniae</i>	24	43	10
<i>Enterobacter hormaechei</i>	24	44	6
<i>Vibrio parahaemolyticus</i>	29	43	8
<i>Pectobacterium brasiliense</i>	25	42	10
<i>Streptococcus equi</i>	43	66	2
<i>Shewanella xiamenensis</i>	24	41	17

Note: Identities stands for protein sequence identity, Positives stands for protein sequence similarity, and Gaps stands for protein sequence gaps that failed to match.