

**Table S1.** Sources of *S. suis* strains isolated from diseased pigs during 2018-2020.

Provinces	Farms n=14	Strains n=246	Sources of specimens, n (%)								
			Blood n=2	Brain n=20	Joint fluid n=6	Lung n=201	Nasal swab n=11	Pleural effusion n=1	Spleen n=2	Tongue swab n=1	Vaginal swab n=2
			n=105								
Nakhon Pathom	33 (31.4)	84 (34.1)	1 (50.0)	4 (20.0)	-	76 (37.8)	2 (18.2)	-	1 (50.0)	-	-
Ratchaburi	32 (30.5)	77 (31.3)	-	7 (35.0)	4 (66.7)	59 (29.4)	4 (36.4)	1 (100.0)	-	-	2 (100.0)
Chon Buri	13 (12.4)	35 (14.2)	-	-	-	31 (15.4)	3 (27.3)	-	1 (50.0)	-	-
Chachoengsao	6 (5.7)	13 (5.3)	-	2 (10.0)	-	10 (5.0)	-	-	-	1 (100.0)	-
Lopburi	4 (3.8)	17 (6.9)	-	5 (25.0)	1 (16.7)	9 (4.5)	2 (18.2)	-	-	-	-
Prachin Buri	3 (2.9)	4 (1.6)	-	-	-	4 (2.0)	-	-	-	-	-
Kanchanaburi	3 (2.9)	3 (1.2)	-	-	-	3 (1.5)	-	-	-	-	-
Suphan Buri	3 (2.9)	3 (1.2)	-	-	-	3 (1.5)	-	-	-	-	-
Khon Kaen	2 (1.9)	4 (1.6)	-	2 (10.0)	1 (16.7)	1 (0.5)	-	-	-	-	-
Nakhon Ratchasima	2 (1.9)	2 (0.8)	-	-	-	2 (1.0)	-	-	-	-	-
Nakhon Sawan	1 (1.0)	1 (0.4)	-	-	-	1 (0.5)	-	-	-	-	-
Phuket	1 (1.0)	1 (0.4)	-	-	-	1 (0.5)	-	-	-	-	-
Saraburi	1 (1.0)	1 (0.4)	1 (50.0)	-	-	-	-	-	-	-	-
Ubon Ratchathani	1 (1.0)	1 (0.4)	-	-	-	1 (0.5)	-	-	-	-	-

**Table S2.** Distribution of *S. suis* serotypes in different sources of specimens.

Serotypes	Strains	Sources of specimens, n (%)								
		Blood n=246	Brain n=20	Joint fluid n=6	Lung n=201	Nasal swab n=11	Pleural effusion n=1	Spleen n=2	Tongue swab n=1	Vaginal swab n=2
1 or 14	6 (2.4)	-	1 (5.0)	1 (16.7)	4 (2.0)	-	-	-	-	-
2 or ½	63 (25.6)	1 (50.0)	10 (50.0)	3 (50.0)	47 (23.4)	1 (9.1)	-	1 (50.0)	-	-
3	12 (4.9)	-	-	1 (16.7)	11 (5.5)	-	-	-	-	-
4	6 (2.4)	-	2 (10.0)	-	4 (2.0)	-	-	-	-	-
5	8 (3.3)	-	-	-	8 (4.0)	-	-	-	-	-
6	1 (0.4)	-	-	-	1 (0.5)	-	-	-	-	-
7	5 (2.0)	-	-	-	5 (2.5)	-	-	-	-	-
8	19 (7.7)	-	-	-	19 (9.5)	-	-	-	-	-
9	16 (6.5)	-	6 (30.0)	-	9 (4.5)	-	1 (100.0)	-	-	-
10	1 (0.4)	-	-	-	1 (0.5)	-	-	-	-	-
11	1 (0.4)	-	-	-	1 (0.5)	-	-	-	-	-
12	1 (0.4)	-	-	-	1 (0.5)	-	-	-	-	-
15	2 (0.8)	-	-	-	2 (1.0)	-	-	-	-	-
16	9 (3.7)	-	-	-	6 (3.0)	2 (18.2)	-	-	-	1 (50.0)
18	6 (2.4)	-	1 (5.0)	1 (16.7)	4 (2.0)	-	-	-	-	-
21	16 (6.5)	-	-	-	14 (7.0)	2 (18.2)	-	-	-	-
23	1 (0.4)	-	-	-	1 (0.5)	-	-	-	-	-
24	2 (0.8)	-	-	-	2 (1.0)	-	-	-	-	-
25	1 (0.4)	-	-	-	1 (0.5)	-	-	-	-	-
27	4 (1.6)	-	-	-	4 (2.0)	-	-	-	-	-
28	4 (1.6)	-	-	-	2 (1.0)	1 (9.1)	-	-	1 (100.0)	-
29	19 (7.7)	-	-	-	14 (7.0)	5 (45.5)	-	-	-	-
30	1 (0.4)	-	-	-	1 (0.5)	-	-	-	-	-
31	8 (3.3)	-	-	-	7 (3.5)	-	-	-	-	1 (50.0)
Non-typeable	34 (13.8)	1 (50.0)	-	-	32 (15.9)	-	-	1 (50.0)	-	-

**Table S3.** MIC breakpoints and interpretative categories of antimicrobial susceptibility test.

Antibiotic drugs		Interpretive categories and MIC breakpoints, µg/mL <sup>a</sup>			References	
		Susceptibility (S)	Intermediate (I)	Resistance (R)		
Cell-wall synthesis inhibitors	AMC	Amoxicillin/Clavulanicacid	≤ 8/4	16/8	≥ 32/16	Hernandez-Garcia et al., 2017
	AMP	Ampicillin	≤ 0.5	1	≥ 2	CLSI Vet01S, 2020
	CPM	Cefepime	≤ 0.5	-	≥ 1	EUCAST, 2020
	CTX	Cefotaxime	≤ 0.5	-	≥ 1	EUCAST, 2020
	CEF	Ceftiofur	≤ 2	4	≥ 8	CLSI Vet01S, 2020
	CRO	Ceftriaxone	≤ 0.5	-	≥ 1	EUCAST, 2020
	FUR	Cefuroxime	≤ 0.5	-	≥ 1	EUCAST, 2020
	DAN	Danofloxacin	ND	ND	ND	ND
	DAP	Daptomycin	≤ 1	-	≥ 2	CLSI M100, 2020
	ETP	Ertapenem	≤ 0.5	-	≥ 1	EUCAST, 2020
	MEM	Meropenem	≤ 2	-	≥ 4	EUCAST, 2020
Protein synthesis inhibitors	PEN	Penicillin	≤ 0.25	0.5	≥ 1	CLSI Vet01S, 2020
	VAN	Vancomycin	≤ 1	-	≥ 2	CLSI Vet01S, 2020
	AZM	Azithromycin	≤ 0.5	1	≥ 2	CLSI Vet01S, 2020
	CHL	Chloramphenicol	≤ 4	8	≥ 16	CLSI Vet01S, 2020
	CTC	Chlortetracycline	≤ 2	4	≥ 8	Che et al., 2018
	CLI	Clindamycin	≤ 0.5	1-2	≥ 4	CLSI Vet01S, 2020
	ERY	Erythromycin	≤ 0.25	0.5	≥ 1	EUCAST, 2020
	FFC	Florfenicol	≤ 2	4	≥ 8	CLSI Vet01S, 2020
	GEN	Gentamicin	≤ 4	8	≥ 16	Zhang et al., 2020
	LNZ	Linezolid	≤ 2	-	≥ 4	EUCAST 2020
	NEO	Neomycin	≤ 16	-	≥ 32	Gurung et al., 2015
	OXY	Oxytetracycline	≤ 4	-	≥ 8	Gurung et al., 2015
	SPE	Spectinomycin	≤ 64	-	≥ 128	Yu et al, 2018
	TET	Tetracyclin	≤ 0.5	1	≥ 2	CLSI Vet01S, 2020
DNA synthesis inhibitors	TMS	Tiamulin	≤ 16	-	≥ 32	Yu et al., 2018
	TGC	Tigecycline	≤ 0.25	-	≥ 0.5	FDA, 2019
	TMS	Tilmicosin	≤ 16	-	≥ 32	Zhang et al., 2015
	TUL	Tulathromycin	ND	ND	ND	ND
	TYL	Tylosin tartrate	≤ 4	-	≥ 8	Gurung et al, 2015
Antimetabolites	ENO	Enrofloxacin	≤ 0.5	1	≥ 2	CLSI Vet01S, 2020
	LEV	Levofloxacin	≤ 0.01	0.03-2	≥ 4	EUCAST, 2020
	MXF	Moxifloxacin	≤ 0.5	-	≥ 1	EUCAST, 2020
SXT	SDM	Sulphadimethoxine	ND	ND	ND	ND
	SXT	Trimethoprim/sulfamethoxazole	≤ 0.5/9.5	1/19-2/38	≥ 4/76	CLSI Vet01S, 2020

<sup>a</sup> MIC, minimum inhibitory concentration values, are interpreted as susceptible (S), intermediate (I), and resistant (R) using CLSI veterinary breakpoints (Vet01S, 2020), EUCAST (EUCAST, 2020), FDA (FDA, 2019), or previously reported data when available. ND, no data/not determined.







**Table S7.** Oligonucleotide primer sequences (Kerdsin et al., 2014).

Multiplex PCR reaction set	Target genes or serotypes	Nucleotide sequences (5'-3')	Amplicon size (bp)
All	<i>gdh</i>	F: TTCTGCAGCGTATTCTGTCAAACG R: TGTTCCATGGACAGATAAAGATGG	695
1	1 or 14	F: AATCATGGAATAAAGCGGACTACAG B: ACAATTGATACGTCAAAATCCTCAC	550
	2 or ½	F: GATTGTCGGGAGGGTTACTTG B: TAAATAATATGCCACTGTAGCGTCTC	450
	3	F: TGGGAGAACGGCAGAAAGTACGAGA B: ACCCCCAGAACAGAGCGAAGGA	1,273
	7	F: GATGATTTATGGCACCCGAGTAAGC B: AGTCACAATTGCTGGTCTGACACC	150
	9	F: GGGATGATTGCTCGACAGAT B: CCGAAGTATCTGGGCTACTG	300
	11	F: TACAGTGCTTGAGCCCTAC B: CGACTTGTGCTGCCCTGAT	896
	16	F: TGGAGGAGCATCTACAGCTCGGAAT B: TTTGTTGCTGAATCTCAGGCACC	202
2	4	F: ACTTGGAGTTGTCGGACTAGTGC B: ACCCGCATGGATAGGCCGAC	783
	5	F: TGATGGCGGAGTTGGGTCGC B: CGTAACAACCGCCCCAGCCG	166
	8	F: ATGGCGTTGGCGGGAGTT B: TTACGGCCCCCATCACGCTG	320
	12	F: TGTGGCGATAGGACAACAGG B: ACCAAGAAGTTCCGCTGA	209
	18	F: CGGGGCAGTCTTACTCATGG B: ATGACAGCGAACCGGACAGA	432
	19	F: AGCAGGGTTGCGTATGGCGG B: ACAAGCACCAGCAAAGACCGCA	1,024
	24	F: ACCCGGAAAAACCAAGGAGTT B: ACCAATCAATGCCAAGCGAC	500
	25	F: GGAGGAGCTGCCGCTATA B: TGGCCACAACTGGATGCGTT	1211
3	6	F: TACGGTCTCCCTGCGTGA B: AACTCAGCTAGTGCCTCACG	325
	10	F: TTACGAGGGGATTCTGGGGT B: CGGGACAACAGATGGAACCT	153
	13	F: CTGGTGCTGCAATTGCGTT B: GCAGACTAGTCAGTTCCA	1,135
	15	F: GCAAGAAAAGCTCCGGATGGA B: CAAGAGAGTGTGCAACCCCA	274
	17	F: ACTTGGGTTGGAATGGCGAA B: ACCACCGAAACTCAGGTAC	906
	23	F: TGCTCAACAAACGAGCAA B: TGACTGGTACATCTGCAGCC	454
	31	F: GGAGTGCTTATGCCACCTT B: GCATTGCCCTACAGCAAAC	550
4	21	F: GGTGGAAGGAGAGCAAAGT B: ACATGGTAAGCCATTGCTGGA	325
	27	F: CTACGCCAATCGAAGGCCAGA B: CCAGTAAGAACGCTGTCGA	506
	28	F: GGACTTCGGTACCTTAGCGT B: CTCCAGCACATTCCCGTACC	865
	29	F: GTGCGGGCGTTATTTTGGT B: AGCCTTGCAACCCATTCCCT	435