

Supplementary materials

Table S1. Results of *S. suis* cps typing with MP PCR.

sites	number of isolates (n=26)	cps type (*)
meningeal swab	2	8, nt
lung	4	8 (2), 13, nt
kidney	4	23, 28, nt (2)
<i>Lnn. cervicales superficiales dexter</i>	1	nt
<i>Lnn. bifurcationis medii</i>	2	24, nt
<i>Lnn. gastrici</i>	5	8, 11, 27, nt (2)
<i>Lnn. jejunaes</i>	1	31
<i>Lnn. colici</i>	2	8 (2)
<i>Lnn. iliaci mediales dexter</i>	3	28, nt (2)
further site ¹	2	3, 8

* Number of isolates with the mentioned capsule type, if >1. nt: non-typable. ¹isolates from heart valve (cps 3) and abscess rip (cps 8).

Table S2. Results of the mismatch amplification mutation assay (MAMA) for distinguishing cps2 and cps1/2.

site	number of iso- lates (n=233)	cps type (*)
meningeal swab	15	1/2 (2), 2 (12), nd
lung	2	1/2 (2)
kidney	2	1/2, 2
<i>Lnn. cervicales superficiales dexter</i>	1	2
<i>Lnn. gastrici</i>	1	1/2
<i>Lnn. inguinales superficiales dexter</i>	1	2
further site ¹	1	1/2

* Number of isolates with the mentioned capsule type, if n>1. nd: not distinguished (isolate can be cps 2 or cps 1/2). ¹inner ear swab.

Table S3. Number of pathotypes of *S. suis* isolates.

pathotype	Number of all detected <i>S. suis</i> isolates	Number of <i>S. suis</i> isolates after correction of multiple counting per herd
<i>cps1 mrp+ sly+ epf+</i>	19	18
<i>cps1 mrp- sly+ epf-</i>	2	2
<i>cps1/2 mrp+ sly+ epf+</i>	31	21
<i>cps1/2 mrp+ sly- epf-</i>	9	7
<i>cps2 mrp+ sly+ epf+</i>	134	75
<i>cps2 mrp+ sly- epf-</i>	9	9
<i>cps2 mrp- sly+ epf+</i>	12	12
<i>cps2 or 1/2 mrp+ sly- epf-</i>	10	10
<i>cps2 or 1/2 mrp- sly+ epf-</i>	1	1
<i>cps3 mrp+ sly- epf-</i>	4	4
<i>cps4 mrp+ sly+ epf-</i>	25	25
<i>cps4 mrp- sly+ epf-</i>	3	3
<i>cps7 mrp+ sly- epf-</i>	32	27

<i>cps8 mrp+ sly+ epf-</i>	1	1
<i>cps8 mrp- sly+ epf+</i>	0	0
<i>cps8 mrp- sly+ epf-</i>	8	7
<i>cps9 mrp+ sly+ epf-</i>	181	126
<i>cps9 mrp- sly+ epf+</i>	6	5
<i>cps9 mrp- sly+ epf-</i>	12	12
<i>cps9 mrp- sly- epf-</i>	4	4
<i>cps11 mrp+ sly+ epf-</i>	1	1
<i>cps13 mrp- sly- epf-</i>	1	1
<i>cps14 mrp+ sly+ epf+</i>	1	1
<i>cps23 mrp+ sly+ epf-</i>	1	1
<i>cps24 mrp- sly- epf-</i>	1	1
<i>cps27 mrp- sly- epf-</i>	2	2
<i>cps28 mrp- sly+ epf-</i>	2	2
<i>cps31 mrp- sly- epf-</i>	1	1
nt <i>mrp+ sly+ epf-</i>	1	1
nt <i>mrp+ sly- epf-</i>	3	3
nt <i>mrp- sly+ epf+</i>	2	2
nt <i>mrp- sly+ epf-</i>	3	3
nt <i>mrp- sly- epf-</i>	7	7
total	529	395

nt: non-typable. Gene detected (+). Gene not detected (-)

Table S4. Number of *cps* types of *S. suis* isolates after correction of multiple counting per herd.

<i>cps</i> type	pathotype	joint swab	meningeal swab	lung	kidney	<i>Ln. cerv. supf.</i>	<i>Ln. bif. m.</i>	<i>Ln. gastricus</i>	<i>Ln. jejunalis</i>	<i>Ln. ileocolicus</i>	<i>Ln. colicus</i>	<i>Ln. iliacus m.</i>	<i>Ln. ing. supf.</i>	further site ¹	total
1	total	5	2	1	2	1	1	1	1	1	0	0	0	5	20
	<i>mrp+ sly+ epf+</i>	4	1	1	2	1	1	1	1	1	0	0	0	5	18
	<i>mrp- sly+ epf -</i>	1	1	0	0	0	0	0	0	0	0	0	0	0	2
1/2	total	0	2	4	3	2	3	3	2	2	1	2	2	2	28
	<i>mrp+ sly+ epf+</i>	0	2	2	2	2	2	2	2	2	1	2	2	0	21
	<i>mrp+ sly- epf -</i>	0	0	2	1	0	1	1	0	0	0	0	0	2	7
2	total	6	12	7	11	11	6	5	5	5	5	7	7	9	96
	<i>mrp+ sly+ epf+</i>	5	10	5	7	9	4	5	4	4	4	5	6	7	75
	<i>mrp+ sly- epf -</i>	0	0	2	2	1	0	0	0	1	0	1	0	2	9
	<i>mrp- sly+ epf+</i>	1	2	0	2	1	2	0	1	0	1	1	1	0	12
2 or 1/2	total	1	1	1	1	1	1	1	0	2	1	0	1	0	11
	<i>mrp+ sly- epf-</i>	1	1	1	1	1	1	1	0	1	1	0	1	0	10
	<i>mrp- sly+ epf+</i>	0	0	0	0	0	0	0	0	1	0	0	0	0	1
3	<i>mrp+ sly- epf-</i>	0	0	0	0	0	1	1	1	0	0	0	0	1	4
4	total	3	2	5	3	1	1	3	1	2	3	1	2	1	28
	<i>mrp+ sly+ epf-</i>	3	2	3	3	1	1	2	1	2	3	1	2	1	25
	<i>mrp- sly+ epf-</i>	0	0	2	0	0	0	1	0	0	0	0	0	0	3
7	<i>mrp+ sly- epf-</i>	2	2	5	3	2	1	1	2	2	1	2	2	2	27
9	total	12	18	11	15	12	10	11	11	9	8	10	11	9	147
	<i>mrp+ sly+ epf-</i>	10	15	8	12	11	9	10	9	8	7	10	9	8	126
	<i>mrp- sly+ epf+</i>	0	2	1	1	0	0	0	1	0	0	0	0	0	5
	<i>mrp- sly+ epf-</i>	1	1	2	1	1	0	1	1	1	1	0	1	1	12
	<i>mrp- sly- epf-</i>	1	0	0	1	0	1	0	0	0	0	0	1	0	4

<i>cps</i> type	pathotype	joint swab	meningeal swab	lung	kidney	<i>Ln. cerv. supf.</i>	<i>Ln. bif. m.</i>	<i>Ln. gastricus</i>	<i>Ln. jejunalis</i>	<i>Ln. ileocolicus</i>	<i>Ln. colicus</i>	<i>Ln. iliacus m.</i>	<i>Ln. ing. supf.</i>	further site ¹	total
11	<i>mrp+ sly+ epf-</i>	0	0	0	0	0	0	1	0	0	0	0	0	0	1
13	<i>mrp- sly- epf-</i>	0	0	1	0	0	0	0	0	0	0	0	0	0	1
14	<i>mrp+ sly+ epf+</i>	1	0	0	0	0	0	0	0	0	0	0	0	0	1
23	<i>mrp+ sly+ ep -</i>	0	0	0	1	0	0	0	0	0	0	0	0	0	1
24	<i>mrp- sly- epf-</i>	0	0	0	0	0	1	0	0	0	0	0	0	0	1
27	<i>mrp- sly- epf-</i>	0	0	0	0	0	0	1	1	0	0	0	0	0	2
28	<i>mrp- sly+ epf-</i>	0	0	0	1	0	0	0	0	0	0	1	0	0	2
31	<i>mrp- sly- epf-</i>	0	0	0	0	0	0	0	1	0	0	0	0	0	1
nt	total	0	1	2	2	1	1	4	2	0	0	3	0	0	16
	<i>mrp+ sly+ epf-</i>	0	0	0	0	0	0	1	0	0	0	0	0	0	1
	<i>mrp+ sly- epf-</i>	0	0	0	1	0	0	1	0	0	0	1	0	0	3
	<i>mrp- sly+ epf+</i>	0	1	1	0	0	0	0	0	0	0	0	0	0	2
	<i>mrp- sly+ epf-</i>	0	0	1	0	0	0	1	1	0	0	0	0	0	3
	<i>mrp- sly- epf-</i>	0	0	0	1	1	1	1	1	0	0	2	0	0	7
total		30	41	39	42	31	26	34	27	23	21	26	25	30	395

Gene detected (+). Gene not detected (-).¹Serosal swab (n=9), bursal swab (n=7), heart valve (n=5), spleen (n=3), and another site (n=6).

Table S5. Number of genotypes of *S. suis* isolates (n=529) divided by age category(*S. suis* isolates from all sites examined).

genotype	age category (number of examined animals)			
	suckling piglet (n=16)	weaning piglet (n=93)	fattening pig (n=15)	total (n=124)
<i>cps1 mrp+ sly+ epf+</i>	5	14	0	19
<i>cps1 mrp - sly+ epf -</i>	2	0	0	2
<i>cps1/2 mrp+ sly+ epf+</i>	0	31	0	31
<i>cps1/2 mrp+ sly - epf -</i>	2	2	5	9
<i>cps2 mrp+ sly+ epf+</i>	0	134	0	134
<i>cps2 mrp+ sly - epf -</i>	0	9	0	9
<i>cps2 mrp - sly+ epf+</i>	0	12	0	12
<i>cps2 or 1/2 mrp+ sly - epf -</i>	0	10	0	10
<i>cps2 or 1/2 mrp - sly+ epf -</i>	0	1	0	1
<i>cps3 mrp+ sly - epf -</i>	0	0	4	4
<i>cps4 mrp+ sly+ epf -</i>	3	21	1	25
<i>cps4 mrp - sly+ epf -</i>	0	3	0	3
<i>cps7 mrp+ sly - epf -</i>	17	12	3	32
<i>cps8 mrp+ sly+ epf -</i>	0	1	0	1
<i>cps8 mrp - sly+ epf -</i>	3	3	2	8
<i>cps9 mrp+ sly+ epf -</i>	0	173	8	181
<i>cps9 mrp - sly+ epf+</i>	0	6	0	6
<i>cps9 mrp - sly+ epf -</i>	0	11	1	12
<i>cps9 mrp - sly - epf -</i>	0	3	1	4
<i>cps11 mrp+ sly+ epf -</i>	0	0	1	1
<i>cps13 mrp - sly - epf -</i>	0	1	0	1
<i>cps14 mrp+ sly+ epf+</i>	0	1	0	1
<i>cps23 mrp+ sly+ epf -</i>	1	0	0	1
<i>cps24 mrp - sly - epf -</i>	0	1	0	1
<i>cps27 mrp - sly - epf -</i>	0	2	0	2
<i>cps28 mrp - sly+ epf -</i>	0	2	0	2
<i>cps31 mrp - sly - epf -</i>	0	1	0	1
<i>nt mrp+ sly+ epf -</i>	0	1	0	1
<i>nt mrp+ sly - epf -</i>	0	0	3	3
<i>nt mrp - sly+ epf+</i>	2	0	0	2
<i>nt mrp - sly+ epf -</i>	0	3	0	3
<i>nt mrp - sly - epf -</i>	0	5	2	7
total	35	463	31	529

nt: non-typable. Gene detected (+). Gene not detected (-).