



Genome Sequences of *Streptococcus suis* Isolates Obtained from Pigs in the United States between 2015 and 2017

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ABSTRACT *Streptococcus suis* is a zoonotic swine pathogen responsible for substantial health and economic burdens to the swine industry worldwide. Here, we report the draft genome sequences of 106 *S. suis* isolates obtained within the United States between 2015 and 2017.

The Gram-positive bacterium *Streptococcus suis* causes a spectrum of clinical disease outcomes in pigs, including pneumonia, endocarditis, septicemia, and meningitis (1–4). *S. suis* is also a zoonotic pathogen capable of causing diseases in humans (5–8). Here, we report the draft genome sequences of 106 *S. suis* isolates obtained from swine samples collected within the United States and submitted to the University of Minnesota Veterinary Diagnostic Laboratory between 2015 and 2017.

Frozen stocks (–80°C in 30% glycerol) of *S. suis* isolates (Table 1) were streaked onto tryptic soy agar containing 5% sheep blood (Becton, Dickinson and Co., Franklin Lakes, NJ) and grown overnight at 37°C with 5% CO₂. Single colonies were used to inoculate Todd-Hewitt broth (Thermo Fisher Scientific Inc., Waltham, MA) supplemented with 0.2% yeast extract (MilliporeSigma, St. Louis, MO) and 5% filtered heat-inactivated horse serum (MilliporeSigma). The broth cultures were grown at 37°C overnight in a shaking incubator (250 rpm). Genomic DNA was extracted using a MasterPure Gram-positive DNA purification kit (Lucigen Corporation, Middleton, WI) with the following modifications to the manufacturer's instructions to prevent degradation: 1 mL of the overnight broth cultures was pelleted by centrifugation (5,000 × *g*, 5 min), the supernatant was removed, and the pelleted cells were resuspended in 300 μL lysis buffer consisting of 2% sodium dodecyl sulfate (SDS) (Thermo Fisher Scientific Inc.), 0.25 M EDTA (Thermo Fisher Scientific Inc.), and 30% proteinase K (Roche, Mannheim, Germany). The suspension was incubated for 3 h at 55°C. An aliquot (300 μL) of the Gram-positive lysis solution from the MasterPure Gram-positive DNA purification kit was added, and the suspension was incubated for 30 min at 70°C. The samples were then placed on ice for 5 min, 350 μL of MPC protein precipitation reagent from the MasterPure Gram-positive DNA purification kit was added, and the DNA precipitation instructions provided in the manufacturer's protocol were followed. The DNA was quantified using a Qubit fluorometer (Thermo Fisher Scientific), and the integrity was further checked using 1% agarose gel electrophoresis.

Illumina HiSeq data were obtained from libraries created using the Illumina DNA PCR-free library prep kit (Illumina, San Diego, CA) for each isolate and sequenced on a HiSeq 3000 instrument, generating 2 × 150-bp paired-end reads. The sequenced reads were assessed for quality using FastQC (<https://www.bioinformatics.babraham.ac.uk/projects/fastqc/>) (9). The reads were randomly subsampled using seqtk (<https://github.com/lh3/seqtk>) to a target genome coverage of 150×, based on an average expected genome length of 2.1 Mbp. The sequence data were assembled using MIRA v. 4.9.6 (<http://mira-assembler.sourceforge.net/docs/DefinitiveGuideToMIRA.html>). The average coverage obtained for each isolate is listed in Table 1. To be retained in an assembly, contigs were required to be >1,500 bp long and have a coverage of >66% of the average coverage for the genome. The assembly tool

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TABLE 1 Sequencing metrics for the isolates in this study

Isolate name	State	Yr of isolation	No. of contigs	Total length (bp)	Total no. of read pairs	Coverage (x)	N ₅₀ (bp)	GC content (%)	BioSample accession no.	GenBank accession no.	SRA accession no.
29862	IN	2015	48	2,251,716	7,343,325	133.03	83,031	41.07	SAMN13975617	JAASEC0000000000	SRRI16467350
29878	IN	2015	48	2,284,132	7,506,691	127.58	84,529	41.24	SAMN13975615	JAASED0000000000	SRRI16467349
29885	MO	2015	49	2,173,352	9,205,343	134.07	91,617	41.22	SAMN13975614	JAASEE0000000000	SRRI16467406
29898	IA	2015	47	2,178,444	5,341,767	129.02	93,430	41.09	SAMN13975610	JAASEI0000000000	SRRI16467395
29932	IL	2015	63	2,314,599	8,040,797	126.82	75,849	40.85	SAMN13975609	JAASEJ0000000000	SRRI16467378
29992	SD	2015	50	2,195,598	4,814,995	136.08	68,886	41.10	SAMN13975608	JAASEK0000000000	SRRI16467367
29995	IA	2015	76	2,374,783	4,873,380	111.13	59,114	41.37	SAMN13975607	JAASEL0000000000	SRRI16467356
30040	TX	2015	42	2,116,594	6,639,957	141.65	76,373	41.02	SAMN13975606	JAASEM0000000000	SRRI16467341
30068	MO	2015	42	2,204,627	6,393,204	135.25	90,716	40.98	SAMN13975605	JAASEN0000000000	SRRI16467330
30076	NE	2015	79	2,663,032	6,180,797	105.89	56,292	40.18	SAMN13975604	JAASEO0000000000	SRRI16467319
30087	OK	2015	42	2,083,159	6,055,340	146.98	91,389	41.22	SAMN13975603	JAASEP0000000000	SRRI16467348
30114	OK	2015	47	2,157,124	6,483,145	135.11	67,655	41.06	SAMN13975602	JAASEQ0000000000	SRRI16467415
30118	AR	2015	46	2,205,635	7,863,850	133.91	84,153	40.98	SAMN13975601	JAASER0000000000	SRRI16467414
30183	IL	2015	32	2,331,858	6,169,523	130.85	148,269	40.68	SAMN13975599	JAASES0000000000	SRRI16467413
30184	IL	2015	22	2,073,234	5,419,998	154.5	163,892	41.34	SAMN13975599	JAASET0000000000	SRRI16467412
30192	KS	2015	44	2,120,940	10,243,684	137.81	76,223	41.01	SAMN13975598	JAASEU0000000000	SRRI16467411
30212	IA	2015	43	2,143,433	8,005,203	138.25	81,447	41.11	SAMN13975597	JAASEV0000000000	SRRI16467410
30413	CO	2015	50	2,129,844	5,588,291	137.53	78,835	41.10	SAMN13975596	JAASEW0000000000	SRRI16467409
30428	OK	2015	42	2,300,026	6,856,178	125.62	140,153	40.87	SAMN13975595	JAASEX0000000000	SRRI16467408
30807	MO	2015	18	2,082,444	5,539,269	133.61	187,681	41.20	SAMN13975594	JAASEY0000000000	SRRI16467407
30815	MN	2015	50	2,130,068	6,365,728	137.6	66,423	41.08	SAMN13975593	JAASEZ0000000000	SRRI16467405
30831	NE	2015	24	2,146,626	6,095,723	135.76	169,618	41.27	SAMN13975592	JAASFA0000000000	SRRI16467404
31869	CO	2015	40	2,142,339	7,140,956	137.86	71,875	41.05	SAMN13975591	JAASFB0000000000	SRRI16467403
31872	KS	2015	63	2,208,236	5,497,746	131.95	74,622	40.95	SAMN13975590	JAASFC0000000000	SRRI16467402
31877	TX	2015	44	2,117,457	8,895,490	137.34	83,135	41.01	SAMN13975589	JAASFD0000000000	SRRI16467401
32052	MN	2015	25	2,141,393	5,800,493	141.92	139,547	41.27	SAMN13975589	JAASBG0000000000	SRRI16467400
34114	IA	2016	34	2,169,107	8,314,053	141.74	123,258	41.00	SAMN13975589	JAASBI0000000000	SRRI16467399
34195	TN	2016	50	2,181,371	4,857,380	137.04	70,271	41.10	SAMN13975588	JAASAZ0000000000	SRRI16467398
34638	AR	2016	52	2,175,052	9,595,574	133.25	68,343	41.08	SAMN13975587	JAASBF0000000000	SRRI16467397
37889	MI	2016	28	2,308,889	7,097,826	128.7	172,853	40.93	SAMN13975587	JAASBK0000000000	SRRI16467396
37904	MI	2016	45	2,286,927	7,850,659	130.41	105,186	40.83	SAMN13975586	JAASBD0000000000	SRRI16467394
37910	KS	2016	45	2,107,225	4,997,859	123.2	81,101	41.39	SAMN13975586	JAASBH0000000000	SRRI16467393
38529	IA	2016	54	2,182,770	5,528,362	137.03	69,212	41.08	SAMN13975588	JAASBJ0000000000	SRRI16467392
38728	SD	2016	50	2,274,090	5,022,620	136.46	98,834	40.89	SAMN13975586	JAASBB0000000000	SRRI16467391
38807	IN	2016	27	2,277,563	4,759,958	130.07	242,095	40.90	SAMN13975587	JAASBA0000000000	SRRI16467390
39556	OH	2016	44	2,204,997	6,035,463	134.33	74,903	40.98	SAMN13975586	JAASBC0000000000	SRRI16467389
39631	IL	2016	23	2,079,145	6,900,887	146.91	138,113	41.24	SAMN13975586	JAASBE0000000000	SRRI16467388
40417	AR	2017	53	2,148,113	4,228,522	138.89	68,719	41.09	SAMN13975586	JAASBL0000000000	SRRI16467381
40418	AR	2017	41	2,306,970	6,740,289	128.62	131,307	40.90	SAMN13975585	JAASBM0000000000	SRRI16467380
40419	AR	2017	49	2,176,688	7,207,730	136.36	76,099	41.09	SAMN13975584	JAASBN0000000000	SRRI16467379
40420	AR	2017	51	2,255,802	1,613,264	124.28	98,901	40.90	SAMN13975584	JAASBO0000000000	SRRI16467377
40421	IA	2017	68	2,095,324	1,606,342	120.38	61,498	41.16	SAMN13975582	JAASBP0000000000	SRRI16467376
40422	IA	2017	75	2,370,354	5,816,415	114.84	47,632	41.17	SAMN13975581	JAASBQ0000000000	SRRI16467375
40423	IN	2016	62	2,190,897	7,249,835	134.35	63,211	41.09	SAMN13975580	JAASBR0000000000	SRRI16467374
40424	IN	2016	22	2,078,417	5,780,647	148.53	171,399	41.22	SAMN13975579	JAASBS0000000000	SRRI16467373
40425	KS	2017	61	2,358,396	8,589,599	115.85	61,517	41.07	SAMN13975578	JAASBT0000000000	SRRI16467372
40426	KS	2017	123	2,485,447	8,083,961	116.17	35,027	41.15	SAMN13975577	JAASBU0000000000	SRRI16467371
40427	MI	2017	54	2,186,242	8,932,314	133.98	68,802	41.09	SAMN13975576	JAASBV0000000000	SRRI16467370
40428	KS	2016	47	2,117,783	5,108,657	142.17	69,531	41.01	SAMN13975575	JAASBW0000000000	SRRI16467369
40429	KS	2016	22	2,199,038	5,086,341	139.56	178,779	41.05	SAMN13975574	JAASBX0000000000	SRRI16467368
40430	MN	2017	53	2,124,110	6,472,196	128.24	62,482	42.53	SAMN13975573	JAASBY0000000000	SRRI16467366
40431	MN	2017	37	2,129,965	5,887,999	141.39	104,103	41.11	SAMN13975572	JAASBZ0000000000	SRRI16467365
40432	MI	2016	24	2,332,219	3,974,596	131.82	234,337	40.71	SAMN13975571	JAASCA0000000000	SRRI16467364
40433	MO	2017	38	2,222,567	7,400,367	137.52	126,219	40.93	SAMN13975570	JAASCB0000000000	SRRI16467363
40435	MN	2016	46	2,116,976	8,704,879	140.52	90,437	41.16	SAMN13975569	JAASCC0000000000	SRRI16467362
40436	MN	2016	47	2,173,971	7,259,883	130.25	81,119	40.93	SAMN13975568	JAASCD0000000000	SRRI16467361
40437	MO	2017	32	2,156,302	7,453,015	144.22	149,312	41.06	SAMN13975567	JAASCE0000000000	SRRI16467360
40438	ND	2017	52	2,184,961	7,109,893	136.06	68,284	41.09	SAMN13975566	JAASCF0000000000	SRRI16467359
40439	NE	2017	30	2,173,266	7,105,642	132.01	201,770	41.05	SAMN13975565	JAASCG0000000000	SRRI16467358
40440	NE	2016	37	2,227,263	5,725,440	130.36	167,646	40.83	SAMN13975564	JAASCH0000000000	SRRI16467357
40441	OH	2017	32	2,212,985	6,100,423	134.96	171,780	40.93	SAMN13975563	JAASCI0000000000	SRRI16467355
40442	NE	2016	51	2,154,434	6,444,197	135.71	76,210	41.08	SAMN13975562	JAASCK0000000000	SRRI16467354
40443	OH	2017	59	2,066,469	4,328,005	133.38	85,384	41.11	SAMN13975561	JAASCK0000000000	SRRI16467353
40444	NE	2016	28	2,253,557	4,924,036	135.56	171,848	40.88	SAMN13975560	JAASCL0000000000	SRRI16467352
40445	OH	2016	56	2,675,782	7,295,687	89.66	115,022	41.11	SAMN13975559	JAASCM0000000000	SRRI16467351
40446	OH	2017	49	2,266,939	7,076,766	133.94	98,348	40.86	SAMN13975558	JAASCN0000000000	SRRI16467346
40447	OH	2016	51	2,231,024	7,840,230	133.17	112,038	40.96	SAMN13975557	JAASCO0000000000	SRRI16467345
40449	OK	2017	51	2,144,015	6,252,232	138.27	73,534	41.09	SAMN13975556	JAASCP0000000000	SRRI16467344
40450	OK	2017	43	2,084,894	8,236,021	146.97	91,548	41.22	SAMN13975555	JAASCQ0000000000	SRRI16467343
40451	SD	2017	48	2,252,669	5,381,670	129.11	69,956	40.99	SAMN13975554	JAASCR0000000000	SRRI16467342
40452	TN	2017	41	2,134,069	7,242,591	141.52	102,064	41.15	SAMN13975553	JAASCs0000000000	SRRI16467340
40453	TX	2016	20	2,246,713	9,975,492	135.86	188,943	41.03	SAMN13975552	JAASCT0000000000	SRRI16467339
40454	IA	2016	17	2,195,938	5,388,008	125.9	381,150	42.04	SAMN13975551	JAASCU0000000000	SRRI16467338
40455	KY	2016	38	2,033,844	4,483,777	150.63	98,746	41.38	SAMN13975550	JAASCV0000000000	SRRI16467337
40456	MA	2016	58	2,346,852	3,815,706	119.35	72,602	40.72	SAMN13975549	JAASCW0000000000	SRRI16467336
40457	MI	2016	29	2,287,488	6,160,054	131.1	153,160	40.69	SAMN13975548	JAASCX0000000000	SRRI16467335
40458	MN	2016	36	2,153,410	5,415,384	135.3	109,234	41.13	SAMN13975547	JAASCY0000000000	SRRI16467334
40459	NE	2016	51	2,228,781	5,498,705	131.59	137,030	40.95	SAMN13975546	JAASCZ0000000000	SRRI16467333
40460	NE	2016	49	2,210,789	7,291,456	134.7	72,648	40.99	SAMN13975545	JAASDA0000000000	SRRI16467332
40461	TN	2016	51	2,187,845	7,495,870	136.84	68,736	41.10	SAMN13975544	JAASDB0000000000	SRRI16467331
40462	AR	2017	38	2,073,317	4,694,386	147.21	115,971	41.16	SAMN13975543	JAASDC0000000000	SRRI16467329
40463	HI	2017	192	2,452,326	3,844,469	104.91	21,210	40.99	SAMN13975542	JAASDD0000000000	SRRI16467328
40464	IL	2017	57	2,188,004	4,423,125	134.29	63,599	41.06	SAMN13975541	JAASDE0000000000	SRRI16467327
40465	IL	2017	43	2,198,528	6,430,415	137.					

TABLE 1 (Continued)

Isolate name	State	Yr of isolation	No. of contigs	Total length (bp)	Total no. of read pairs	Coverage (x)	N ₅₀ (bp)	GC content (%)	BioSample accession no.	GenBank accession no.	SRA accession no.
40471	OH	2017	53	2,217,221	6,858,449	129.25	74,997	41.08	SAMN13975634	JAASDL000000000	SRR16467320
40472	OK	2017	49	2,153,617	7,238,515	139.44	86,165	40.96	SAMN13975633	JAASDM000000000	SRR16467318
40473	MN	2017	43	2,139,676	5,521,983	148.24	84,215	41.10	SAMN13975632	JAASDN000000000	SRR16467317
40521	KS	2017	33	2,092,795	5,244,664	144.58	130,991	41.32	SAMN13975631	JAASDO000000000	SRR16467316
40522	TN	2017	51	2,187,477	6,212,488	132.44	68,834	41.10	SAMN13975630	JAASDP000000000	SRR16467315
40523	MN	2017	51	2,145,018	6,801,896	135.45	68,576	41.10	SAMN13975629	JAASDQ000000000	SRR16467388
40524	MN	2017	46	2,129,884	6,759,167	141.74	85,022	41.11	SAMN13975628	JAASDR000000000	SRR16467387
40525	IL	2016	40	2,146,250	6,041,284	135.56	81,429	41.07	SAMN13975627	JAASDS000000000	SRR16467386
40526	AR	2016	52	2,189,260	5,074,989	134.43	68,431	41.10	SAMN13975626	JAASDT000000000	SRR16467385
40527	MI	2016	51	2,168,915	5,658,625	136.55	70,483	41.10	SAMN13975625	JAASDU000000000	SRR16467384
40529	SD	2016	16	2,205,574	4,894,541	134.73	347,320	41.10	SAMN13975624	JAASDV000000000	SRR16467383
40530	MO	2016	50	2,194,886	5,771,525	135.98	70,620	41.07	SAMN13975623	JAASDW000000000	SRR16467347
40531	OH	2016	54	2,151,164	4,822,958	135.29	79,625	41.10	SAMN13975622	JAASDX000000000	SRR16467420
40532	MO	2016	52	2,144,763	6,367,791	138.91	66,423	41.10	SAMN13975621	JAASDY000000000	SRR16467419
40533	IL	2017	20	2,068,081	6,466,665	148.84	234,947	41.06	SAMN13975620	JAASDZ000000000	SRR16467418
40534	IL	2017	31	2,292,622	4,086,827	132.73	139,654	40.95	SAMN13975619	JAASEA000000000	SRR16467417
40535	SD	2017	46	2,264,821	8,023,664	128.61	117,716	40.98	SAMN13975618	JAASEB000000000	SRR16467416

identified repetitive elements, which were required to have a contig length of >2,000 bp to remain in the assembly. Unless specified otherwise, default parameters were used for all software. The final annotations were completed using NCBI's Prokaryotic Genome Annotation Pipeline (PGAP) v. 4.11 (10). The accession numbers and genome statistics are summarized in Table 1.

Data availability. This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the BioProject accession number [PRJNA604583](#) and Sequence Read Archive (SRA) study number [SRP341913](#). Detailed information is provided in Table 1, including the BioSample, GenBank, and SRA accession numbers.

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