AMERICAN SOCIETY FOR MICROBIOLOGY | Microbiology Resource Announcements

GENOME SEQUENCES

Draft Genome Sequence of a *Streptococcus suis* Isolate from a Case of Cattle Meningitis

Ogi Okwumabua,[a,b] Charles H. D. Williamson,[c] Talima R. Pearson,[c] Jason W. Sahl[c]

[a]Department of Pathology and Population Medicine, College of Veterinary Medicine, Midwestern University, Glendale, Arizona, USA
[b]Department of Pathobiological Sciences, School of Veterinary Medicine, University of Wisconsin, Madison, Wisconsin, USA
[c]Pathogen and Microbiome Institute, Northern Arizona University, Flagstaff, Arizona, USA

ABSTRACT *Streptococcus suis* is primarily a pig pathogen and a zoonotic agent. Recently, the isolation of *S. suis* strain 10-36905 from a case of meningitis in cattle was reported. The draft genome sequence of this isolate demonstrates its divergent relationship with other *S. suis* strains.

Streptococcus suis is a Gram-positive bacterium that primarily causes diseases in swine, such as meningitis, endocarditis, septicemia, and arthritis, and sudden death (1). *S. suis* is also a zoonotic agent. Human infections are often due to occupational exposure to pigs or consumption of undercooked pork (2, 3). Isolation of *S. suis* from dogs, cats, ruminants, and horses has been reported (1, 4–6), but whole-genome data are limited, hindering understanding of its taxonomy, biology, evolution, and host adaptability. Recently, *S. suis* strain 10-36905 was isolated from the brain of a calf (cattle) with meningitis that subsequently died in Wisconsin (7). In this study, we announce a draft genome assembly of 10-36905.

Genomic DNA was extracted after culture (8) and sequenced at the University of Wisconsin Biotechnology Center using a MiSeq sequencer and a MiSeq 500-bp (v2) sequencing cartridge, with paired read lengths of 250 bp after library preparation using the TruSeq Nano DNA low-throughput (LT) library prep kit (Illumina). Images were analyzed using the standard Illumina pipeline (v1.8.2). Default parameters were used for all software unless otherwise specified.

Reads were processed with Skewer (-k, 15; -l, 25) (v0.1.126) (9), and short reads (<250 nucleotides [nt]) were removed with BBTools (reformat.sh; min length, 250) (v38.61b; https://sourceforge.net/projects/bbmap/). The genome sequence was assembled from 692,810 read pairs with SPAdes (–careful –cov-cutoff auto) (v3.10.1) (10) and annotated with PGAP (11). The final genome assembly was 2,148,541 bp, distributed in 36 contigs (N_{50}, 119,199 bp), with an average G+C content of 39.78%. Genome analysis revealed 2,049 coding genes. The isolate was assigned a new multilocus sequence type for *S. suis* (12), namely, sequence type 1289 (ST1289) (https://pubmlst.org/ssuis/) (13).

A comparison of the genome assembly of 10-36905 to publicly available *Streptococcus* genomes (n = 622) with Mash (k = 21, s = 1,000,000) (v2.2) (14) distances followed by clustering with the UPGMA within QIIME (v1.9.1) (15) (subset of 77 genomes; Fig. 1A) showed that it clustered with *S. suis*. Proteins common to a set of 73 *S. suis* and 1 *S. parasuis* genomes were identified with the LS-BSR tool (16) (v1.0.3) (TBLASTN [17] alignment option), extracted from genome assemblies with TBLASTN, and aligned with MUSCLE (v3.8.31) (18) using the extract_core_genome.py tool within LS-BSR. A maximum likelihood phylogeny was generated with IQ-TREE (v1.6.10) (-m MFP) (19) on the alignment of 185,775 amino acids using the best-fit model identified by Modelfinder (20) (Fig. 1B). Results demonstrate that the isolate is most closely related to other *S. suis* genomes but falls outside the large clade of complete *S. suis*

Citation Okwumabua O, Williamson CHD, Pearson TR, Sahl JW. 2020. Draft genome sequence of a *Streptococcus suis* isolate from a case of cattle meningitis. Microbiol Resour Announc 9:e00153-20. https://doi.org/10.1128/MRA.00153-20.

Editor David A. Baltrus, University of Arizona

Address correspondence to Ogi Okwumabua, ookwum@midwestern.edu.

Received 18 February 2020
Accepted 15 April 2020
Published 7 May 2020

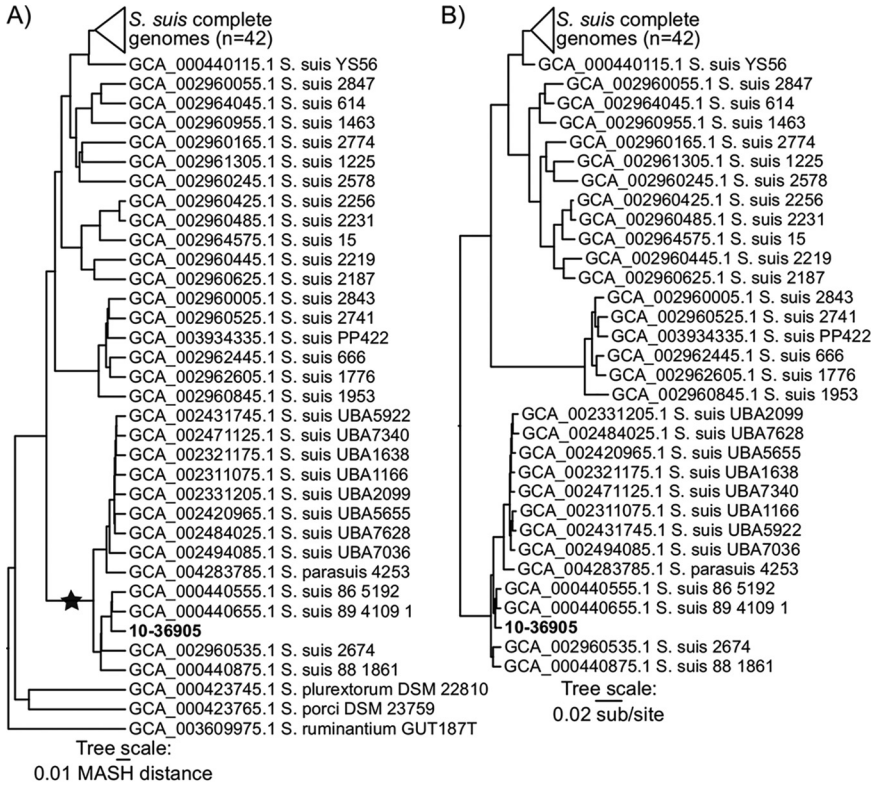

FIG 1 Clustering of *Streptococcus* genomes based on Mash distances (A) and a concatenated core protein phylogeny of *S. suis* and *S. parasuis* genomes (B). The newly sequenced genome is in bold type. The clade labeled with a star in panel A includes divergent *S. suis* genomes to which 10-36905 was compared with Mash; the average MASH distance between 10-36905 and other genomes within this clade is 0.042.

genomes (average Mash distance, 0.107; $n = 42$) and with other more divergent *S. suis* genomes (average Mash distance, 0.042; $n = 13$), including a recently sequenced *S. parasuis* genome (ENA accession no. GCA_004283785.1). The previously identified extracellular protein factor, muramidase-released protein, and suilysin (21–23) in swine *S. suis* were not identified in this strain. The availability of this assembly opens possibilities for genetic studies of *S. suis* of cattle origin, particularly pathogenicity analysis, molecular evolution, host adaptability, and therapeutic and vaccine development.

Data availability. Data are available from NCBI under BioProject PRJNA590796. The whole-genome shotgun project was deposited at DDBJ/ENA/GenBank under accession no. WNXH00000000. The version described here is the first version, WNXH01000000.

ACKNOWLEDGMENTS

This research was supported by the USDA National Institute of Food and Agriculture, Animal Health and Disease Extension Program, project NI18AHDRXXXXG021, and, in part, by miscellaneous funds from the University of Wisconsin—Madison. The funders of the work did not influence the study design, data collection and analysis, decision to publish, or preparation of the manuscript.

We thank Zenan Tao, Adel Talaat, and Hensen Chungyi for technical assistance.

REFERENCES

1. Staats J, Feder I, Okwumabua O, Chengappa M. 1997. Streptococcus suis: past and present. Vet Res Commun 21:381–407. https://doi.org/10.1023/a:1005870317757.
2. Yu H, Jing H, Chen Z, Zheng H, Zhu X, Wang H, Wang S, Liu L, Zu R, Luo L, Xiang N, Liu H, Liu X, Shu Y, Lee SS, Chuang SK, Wang Y, Xu J, Yang W; Streptococcus suis Study Groups. 2006. Human Streptococcus suis outbreak, Sichuan, China. Emerg Infect Dis 12:914–920. https://doi.org/10.3201/eid1206.051194.
3. Ho DTN, Le TPT, Wolbers M, Cao QT, Nguyen VMH, Tran VTN, Le TPT, Nguyen HP, Tran THC, Dinh XS, To SD, Hoang TTH, Hoang T, Campbell

J, Nguyen VVC, Nguyen TC, Nguyen VD, Ngo TH, Spratt BG, Tran TH, Farrar J, Schultsz C. 2011. Risk factors of Streptococcus suis infection in Vietnam. A case-control study. PLoS One 6:e17604. https://doi.org/10.1371/journal.pone.0017604.
4. Muckle A, Giles J, Lund L, Stewart T, Gottschalk M. 2010. Isolation of Streptococcus suis from the urine of a clinically ill dog. Can Vet J 51:773–774.
5. Muckle A, Lopez A, Gottschalk M, López-Méndez C, Giles J, Lund L, Saab M. 2014. Isolation of Streptococcus suis from 2 lambs with a history of lameness. Can Vet J 55:946–949.
6. Sánchez del Rey V, Fernández-Garayzábal JF, Briones V, Iriso A, Domínguez L, Gottschalk M, Vela AI. 2013. Genetic analysis of Streptococcus suis isolates from wild rabbits. Vet Microbiol 165:483–486. https://doi.org/10.1016/j.vetmic.2013.04.025.
7. Okwumabua O, Peterson H, Hsu H-M, Bochsler P, Behr M. 2017. Isolation and partial characterization of Streptococcus suis from clinical cases in cattle. J Vet Diagn Invest 29:160–168. https://doi.org/10.1177/1040638717690014.
8. Okwumabua O, Staats J, Chengappa M. 1995. Detection of genomic heterogeneity in Streptococcus suis isolates by DNA restriction fragment length polymorphisms of rRNA genes (ribotyping). J Clin Microbiol 33:968–972. https://doi.org/10.1128/JCM.33.4.968-972.1995.
9. Jiang H, Lei R, Ding S-W, Zhu S. 2014. Skewer: a fast and accurate adapter trimmer for next-generation sequencing paired-end reads. BMC Bioinformatics 15:182. https://doi.org/10.1186/1471-2105-15-182.
10. Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol 19:455–477. https://doi.org/10.1089/cmb.2012.0021.
11. Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Nawrocki EP, Zaslavsky L, Lomsadze A, Pruitt KD, Borodovsky M, Ostell J. 2016. NCBI Prokaryotic Genome Annotation Pipeline. Nucleic Acids Res 44:6614–6624. https://doi.org/10.1093/nar/gkw569.
12. King SJ, Leigh JA, Heath PJ, Luque I, Tarradas C, Dowson CG, Whatmore AM. 2002. Development of a multilocus sequence typing scheme for the pig pathogen Streptococcus suis: identification of virulent clones and potential capsular serotype exchange. J Clin Microbiol 40:3671–3680. https://doi.org/10.1128/jcm.40.10.3671-3680.2002.
13. Jolley KA, Bray JE, Maiden MC. 2018. Open-access bacterial population genomics: BIGSdb software, the PubMLST.org website and their applications. Wellcome Open Res 3:124. https://doi.org/10.12688/wellcomeopenres.14826.1.
14. Ondov BD, Treangen TJ, Melsted P, Mallonee AB, Bergman NH, Koren S, Phillippy AM. 2016. Mash: fast genome and metagenome distance estimation using MinHash. Genome Biol 17:132. https://doi.org/10.1186/s13059-016-0997-x.
15. Caporaso JG, Kuczynski J, Stombaugh J, Bittinger K, Bushman FD, Costello EK, Fierer N, Peña AG, Goodrich JK, Gordon JI, Huttley GA, Kelley ST, Knights D, Koenig JE, Ley RE, Lozupone CA, McDonald D, Muegge BD, Pirrung M, Reeder J, Sevinsky JR, Turnbaugh PJ, Walters WA, Widmann J, Yatsunenko T, Zaneveld J, Knight R. 2010. QIIME allows analysis of high-throughput community sequencing data. Nat Methods 7:335–336. https://doi.org/10.1038/nmeth.f.303.
16. Sahl JW, Caporaso JG, Rasko DA, Keim P. 2014. The large-scale blast score ratio (LS-BSR) pipeline: a method to rapidly compare genetic content between bacterial genomes. PeerJ 2:e332. https://doi.org/10.7717/peerj.332.
17. Altschul SF, Madden TL, Schäffer AA, Zhang J, Zhang Z, Miller W, Lipman DJ. 1997. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res 25:3389–3402. https://doi.org/10.1093/nar/25.17.3389.
18. Edgar RC. 2004. MUSCLE: multiple sequence alignment with high accuracy and high throughput. Nucleic Acids Res 32:1792–1797. https://doi.org/10.1093/nar/gkh340.
19. Nguyen L-T, Schmidt HA, von Haeseler A, Minh BQ. 2015. IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. Mol Biol Evol 32:268–274. https://doi.org/10.1093/molbev/msu300.
20. Kalyaanamoorthy S, Minh BQ, Wong TK, von Haeseler A, Jermiin LS. 2017. ModelFinder: fast model selection for accurate phylogenetic estimates. Nat Methods 14:587–589. https://doi.org/10.1038/nmeth.4285.
21. Berthelot-Hérault F, Morvan H, Kéribin A-M, Gottschalk M, Kobisch M. 2000. Production of muraminidase-released protein (MRP), extracellular factor (EF) and suilysin by field isolates of Streptococcus suis capsular types 2, 1/2, 9, 7 and 3 isolated from swine in France. Vet Res 31:473–479. https://doi.org/10.1051/vetres:2000133.
22. Jacobs A, Loeffen P, Van Den Berg A, Storm PK. 1994. Identification, purification, and characterization of a thiol-activated hemolysin (suilysin) of Streptococcus suis. Infect Immun 62:1742–1748. https://doi.org/10.1128/IAI.62.5.1742-1748.1994.
23. Vecht U, Wisselink HJ, Jellema ML, Smith H. 1991. Identification of two proteins associated with virulence of Streptococcus suis type 2. Infect Immun 59:3156–3162. https://doi.org/10.1128/IAI.59.9.3156-3162.1991.