

# Draft Genome Sequence of *Streptococcus equi* subsp. *zoepidemicus* Strain S31A1, Isolated from Equine Infectious Endometritis

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We present the draft genome sequence of *Streptococcus equi* subsp. *zoepidemicus* S31A1, a strain isolated from equine infectious endometritis in Denmark. Comparative analyses of this genome were done with four published reference genomes: *S. zoepidemicus* strains MGCS10565, ATCC 35246, and H70 and *S. equi* subsp. *equi* strain 4047.

Received 31 July 2013 Accepted 12 August 2013 Published 5 September 2013

**Citation** da Piedade I, Skive B, Christensen H, Bojesen AM. 2013. Draft genome sequence of *Streptococcus equi* subsp. *zoepidemicus* strain S31A1, isolated from equine infectious endometritis. *Genome Announc.* 1(5):e00683-13. doi:10.1128/genomeA.00683-13.

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*Streptococcus equi* subsp. *zoepidemicus* is a beta-hemolytic Gram-positive Lancefield group C bacterium found in a wide range of hosts, including farm animals, dogs, and humans (1). *S. equi* subsp. *zoepidemicus* appears to be part of the normal bacterial microflora of the upper respiratory tract and caudal reproductive tract of horses and is also found in healthy bodily systems of other species, such as chickens, pigs, and donkeys (2, 3). However, *S. equi* subsp. *zoepidemicus* is also an opportunistic pathogen associated with a wide variety of diseases, e.g., pneumonia, septicemia, mastitis, placentitis, and endometritis (4–6). Human infections are rare, but severe complications associated with *S. equi* subsp. *zoepidemicus* infection have been reported (7). *S. equi* subsp. *zoepidemicus* is the most frequently isolated pathogen from the uteruses of mares (8, 9). It is hypothesized that gene loss and gain in *S. equi* subsp. *zoepidemicus* have shaped its evolution and enabled it to conquer this niche (10). In support of this, pulsed-field gel electrophoresis (PFGE) and multilocus sequence typing (MLST) have shown that *S. equi* subsp. *zoepidemicus* isolated from infectious endometritis in mares appears to belong to a genetically distinct group (11).

*S. equi* subsp. *zoepidemicus* strain S31A1 was isolated from the uterus of a mare with endometritis in Denmark. The genome sequencing of *S. equi* subsp. *zoepidemicus* S31A1 was achieved using Illumina HiSeq 2000 with paired-end reads. A total of 7,482,442 reads with a length of 98 nucleotides (nt) were assembled *de novo* with the program CLC Genomics Workbench (v4.7.2) with default parameters, resulting in 92 reads with an average size of 21,495 bp and coverage of 374×. The resulting 92 contigs (all >3,000 bp) were ordered by alignment to the reference genomes of *S. equi* subsp. *zoepidemicus* MGCS10565 (12), ATCC 35246 (13), and H70 (10) and *S. equi* subsp. *equi* 4047 (10) using Mauve Contig Mover (14). The total size of the resulting assembly is 1,959,199 bp. The draft genome was annotated using Prokka toolbox v1.5.2 (<http://www.vicbioinformatics.com/software/prokka.shtml>). We identified 1,769 predicted protein-coding sequences and 1,784 gene sequences with average lengths of 304 amino acids and 908 nt, respectively. The G+C content of

the S31A1 genome is 41.5%, a value similar to that of the reference genomes (~41%).

With respect to virulence-associated traits, the S31A1 genome contains M-like proteins, immunoglobulin G-binding proteins (G and H), immunoglobulin A receptor, capsule synthesis proteins, the virulence factor EsxA, T6 antigen, and several toxins, like cholera toxin secretion protein. Antimicrobial resistance factors, like penicillin binding proteins and bacteriophage-associated proteins (phage protein C, bacteriophage scaffolding protein D), have also been identified. Ongoing work is being carried out to compare the genomes of other *S. equi* subsp. *zoepidemicus* isolates in order to identify the genetic loci that are implicated in their pathogenesis.

**Nucleotide sequence accession number.** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. [AUXA00000000](https://www.ncbi.nlm.nih.gov/nuccore/AUXA00000000). The version described in this paper is the first version.

## ACKNOWLEDGMENTS

This work was supported by the Danish Horse Levy Fund and Department of Disease Biology, Faculty of Health and Medical Sciences, University of Copenhagen, Denmark.

## REFERENCES

1. Timoney JF, Gillespie JH, Scott FW, Barlough JE. 1998. The genus *Streptococcus*, p 181–196. In Timoney JF (ed), Hagan and Bruner's microbiology and infectious diseases of domestic animals, 8th ed. Comstock, Ithaca, NY.
2. Roy K, Bisgaard M, Kyvsgaard NC, Christensen JP, Nielsen OL, Biswas PK, Pors SE, Bojesen AM. 2013. Pathogenicity of wild-type and small-colony variants of *Streptococcus equi* subsp. *zoepidemicus* in layer chickens. *Avian Pathol.* 42:316–322.
3. Anzai T, Walker JA, Blair MB, Chambers TM, Timoney JF. 2000. Comparison of the phenotypes of *Streptococcus zoepidemicus* isolated from tonsils of healthy horses and specimens obtained from foals and donkeys with pneumonia. *Am. J. Vet. Res.* 61:162–166.
4. Priestnall S, Erles K. 2011. *Streptococcus zoepidemicus*: an emerging canine pathogen. *Vet. J.* 188:142–148.
5. Bisgaard M, Bojesen AM, Petersen MR, Christensen H. 2012. A major

- outbreak of *Streptococcus equi* subsp. *zooepidemicus* infections in free-range chickens is linked to horses. *Avian Dis.* 56:561–566.
6. Timoney JF. 2004. The pathogenic equine streptococci. *Vet. Res.* 35: 397–409.
  7. Poulin MF, Boivin G. 2009. A case of disseminated infection caused by *Streptococcus equi* subspecies *zooepidemicus*. *Can. J. Infect. Dis. Med. Microbiol.* 20:59–61.
  8. Petersen MR, Nielsen JM, Lehn-Jensen H, Bojesen AM. 2009. *Streptococcus equi* subspecies *zooepidemicus* resides deep in the endometrium of the chronically infected mare. *Clin. Theriogenol.* 1:161–167.
  9. Ricketts SW. 2011. Uterine and clitoral cultures, p 1963–1978. In McKinnon AO, Squires EL, Vaala WE, Varner DD (ed), *Equine reproduction*, vol 2, 2nd ed. Wiley-Blackwell, Chichester, United Kingdom.
  10. Holden MT, Heather Z, Paillot R, Steward KF, Webb K, Ainslie F, Jourdan T, Bason NC, Holroyd NE, Mungall K, Quail MA, Sanders M, Simmonds M, Willey D, Brooks K, Aanensen DM, Spratt BG, Jolley KA, Maiden MC, Kehoe M, Chanter N, Bentley SD, Robinson C, Maskell DJ, Parkhill J, Waller AS. 2009. Genomic evidence for the evolution of *Streptococcus equi*: host restriction, increased virulence, and genetic exchange with human pathogens. *PLOS Pathog.* 5:e1000346. doi: [10.1371/journal.ppat.1000346](https://doi.org/10.1371/journal.ppat.1000346).
  11. Rasmussen CD, Haugaard MM, Petersen MR, Nielsen JM, Pedersen HG, Bojesen AM. 2013. *Streptococcus equi* subsp. *zooepidemicus* isolates from equine infectious endometritis belong to a distinct genetic group. *Vet. Res.* 44:26. doi: [10.1186/1297-9716-44-26](https://doi.org/10.1186/1297-9716-44-26).
  12. Beres SB, Sesso R, Pinto SW, Hoe NP, Porcella SF, Deleo FR, Musser JM. 2008. Genome sequence of a Lancefield group C *Streptococcus zooepidemicus* strain causing epidemic nephritis: new information about an old disease. *PLOS One* 3:e3026. doi: [10.1371/journal.pone.003026](https://doi.org/10.1371/journal.pone.003026).
  13. Ma Z, Geng J, Zhang H, Yu H, Yi L, Lei M, Lu CP, Fan HJ, Hu S. 2011. Complete genome sequence of *Streptococcus equi* subsp. *zooepidemicus* strain ATCC 35246. *J. Bacteriol.* 193:5583–5584.
  14. Rissman AI, Mau B, Biehl BS, Darling AE, Glasner JD, Perna NT. 2009. Reordering contigs of draft genomes using the Mauve aligner. *Bioinformatics* 25:2071–2073.