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GENOME SEQUENCES

Draft Genome Sequence of *Erysipelothrix rhusiopathiae*, Isolated from a Canine Case of Diskospondylitis

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ABSTRACT This is the draft genome of an *Erysipelothrix rhusiopathiae* strain isolated from the blood of a canine. Initial 16S ribosomal DNA amplification identified the isolate as belonging to the *Erysipelothrix* genus but could not elucidate the species due to previous misidentification of *E. rhusiopathiae* and *E. tonsillarum*. The species identification was confirmed by whole-genome sequencing.

Erysipelothrix species are Gram-positive coccobacilli. The most common species is *E. rhusiopathiae*, which causes septicemia, joint infection, and skin lesions in a variety of animal species, primarily in pigs (1). In dogs, there are a few case reports that document bacteremia, septic polyarthritis, endocarditis, and infection of the aortic valve (2–11). Previous work has suggested that some isolates from dogs with endocarditis are *E. tonsillarum* rather than *E. rhusiopathiae* (12).

Here, we present the draft genome of *Erysipelothrix rhusiopathiae* strain 268691, isolated from a 2.5-year-old male Great Dane canine that presented for lumbar pain and was diagnosed with diskospondylitis. Amplification of the 16S ribosomal DNA as previously described (13) identified the bacterium as belonging to the *Erysipelothrix* genus but could not identify the species.

Three independent blood samples were collected and cultured by inoculating the blood into a commercial blood culture system (Bactec Plus aerobic/F culture vials; BD Franklin Lakes, NJ). Subcultures were plated at 24 h, 48 h, and 7 days onto Trypticase soy agar supplemented with 5% sheep's blood (BAP). The isolates were stored at −80°C in brucella broth supplemented with 10% glycerol and revived for sequencing by inoculating an aliquot of the frozen bacteria onto a BAP. An isolated colony was used to inoculate a 5-ml culture of Trypticase soy broth, which was incubated overnight. A 1-ml aliquot of this culture was used for DNA isolation. All cultures were incubated at 35°C ± 2°C in an atmosphere supplemented with 5% CO_2.

For the subsequent procedures, default parameters and manufacturer's protocols were used unless stated otherwise. Genomic DNA was extracted from 1-ml aliquots of each isolate that were pelleted and subsequently lysed in a Qiagen TissueLyser using Macherey-Nagel bead tubes (type B) and lysis buffer from the NucleoMag tissue DNA kit. DNA was isolated using a commercial kit following the manufacturer's protocol (Macherey-Nagel). Prior to sequencing, the DNA quality was verified using a genomic DNA TapeStation run (Agilent). Illumina libraries were prepared using the Illumina Nextera DNA Flex library preparation kit. An Illumina MiSeq v2 2 × 250-bp kit was used for sequencing. The sequencing data were uploaded onto Illumina's BaseSpace for run monitoring, FASTQ generation, demultiplexing, and adapter trimming.

Sequencing resulted in 2,853,326 paired-end reads of 251 bp, which is approximately 400× coverage, with an N_{50} value of 303,535 bp. These reads were assembled using SPAdes v3.13.0 with the "careful" parameter (14). The resultant assembly was 1,697,258 bp long and had 77 contigs and a GC content of 37.41%. Annotation

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was completed using PGAP using the default parameters during submission to the NCBI Genome Submission Portal. The genome was analyzed for completeness using BUSCO (*Firmicutes* database) with a resultant score of 84.9%—potentially a lower score due to this species having one of the smallest genomes in the phylum *Firmicutes* (~1,700,000 bp) and missing many typical orthologs for cell wall genes, fatty acid biosynthesis pathways, and amino acid biosynthesis genes (15). Species identification was confirmed using ribosomal multilocus sequence typing (rMLST) (16), with 100% support from the database, which included comparison to *E. tonsillarum*, as well as NCBI's average nucleotide identity analysis (17).

Data availability. This whole-genome shotgun sequencing project has been deposited at DDBJ/ENA/GenBank under the accession number JAAAMP000000000; the raw MiSeq reads are available under SRA accession number SRR10850371. This announcement represents the first version of the genome.

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REFERENCES

1. Wang Q, Chang BJ, Riley TV. 2010. *Erysipelothrix rhusiopathiae*. Vet Microbiol 140:405–417. https://doi.org/10.1016/j.vetmic.2009.08.012.
2. Bibler MR. 1988. *Erysipelothrix rhusiopathiae* endocarditis. Rev Infect Dis 10:1062–1063. https://doi.org/10.1093/clinids/10.5.1062.
3. Foster JD, Hartmann FA, Moriello KA. 2012. A case of apparent canine erysipeloid associated with *Erysipelothrix rhusiopathiae* bacteraemia. Vet Dermatol 23:528-e108. https://doi.org/10.1111/j.1365-3164.2012.01115.x.
4. Golini L, Morgan JP, Glaus T, Steffen F. 2012. Successful medical treatment of *Erysipelothrix rhusiopathiae*-induced lumbosacral diskospondylitis in a dog. Vet Rec 170:543. https://doi.org/10.1136/vr.100657.
5. Goudswaard J, Hartman EG, Janmaat A, Huisman GH. 1973. *Erysipelothrix rhusiopathiae* strain 7, a causative agent of endocarditis and arthritis in the dog. Tijdschr Diergeneeskd 98:416–423.
6. Hoenig M, Gillette DM. 1980. Endocarditis caused by *Erysipelothrix rhusiopathiae* in a dog. J Am Vet Med Assoc 176:326–327.
7. Houlton JEF. 2010. A commendation on "Septic polyarthritis caused by *Erysipelothrix rhusiopathiae* in a dog. Vet Comp Orthop Traumatol 23:223. https://doi.org/10.3415/VCOT-10-03-0029.
8. Houlton JEF, Jefferies AR. 1989. Infective polyarthritis and multiple discospondylitis in a dog due to Erysipelothrix rhusiopathiae. J Small Anim Pract 30:35–38. https://doi.org/10.1111/j.1748-5827.1989.tb01459.x.
9. Marshall KR, Walton SA, Boyd M, Bishop B, Wellehan J, Craft W, Santoro D. 2019. Erysipeloid lesions caused by *Erysipelothrix rhusiopathiae* in a dog: clinical and histopathological findings, molecular diagnosis and treatment. Vet Dermatol 30:434-e134. https://doi.org/10.1111/vde.12773.
10. Seelig U, Klopfleisch R, Weingart C, Walther B, Luebke-Becker A, Brunnberg L. 2010. Septic polyarthritis caused by *Erysipelothrix rhusiopathiae* in a dog. Vet Comp Orthop Traumatol 23:71–73. https://doi.org/10.3415/VCOT-09-05-0058.
11. Sisson D, Thomas WP. 1984. Endocarditis of the aortic valve in the dog. J Am Vet Med Assoc 184:570–577.
12. Takahasi T, Fujisawa T, Yamamoto K, Kijima M, Takahashi T. 2000. Taxonomic evidence that serovar 7 of *Erysipelothrix* strains isolated from dogs with endocarditis are *Erysipelothrix tonsillarum*. J Vet Med B Infect Dis Vet Public Health 47:311–313. https://doi.org/10.1046/j.1439-0450.2000.00344.x.
13. Nikkari S, Lopez FA, Lepp PW, Cieslak PR, Ladd-Wilson S, Passaro D, Danila R, Relman DA. 2002. Broad-range bacterial detection and the analysis of unexplained death and critical illness. Emerg Infect Dis 8:188–194.
14. Nurk S, Bankevich A, Antipov D, Gurevich AA, Korobeynikov A, Lapidus A, Prjibelski AD, Pyshkin A, Sirotkin A, Sirotkin Y, Stepanauskas R, Clingenpeel SR, Woyke T, McLean JS, Lasken R, Tesler G, Alekseyev MA, Pevzner PA. 2013. Assembling single-cell genomes and mini-metagenomes from chimeric MDA products. J Comput Biol 20:714–737. https://doi.org/10.1089/cmb.2013.0084.
15. Ogawa Y, Ooka T, Shi F, Ogura Y, Nakayama K, Hayashi T, Shimoji Y. 2011. The genome of *Erysipelothrix rhusiopathiae*, the causative agent of swine erysipelas, reveals new insights into the evolution of *Firmicutes* and the organism's intracellular adaptations. J Bacteriol 193:2959–2971. https://doi.org/10.1128/JB.01500-10.
16. Jolley KA, Bliss CM, Bennett JS, Bratcher HB, Brehony C, Colles FM, Wimalarathna H, Harrison OB, Sheppard SK, Cody AJ, Maiden MCJ. 2012. Ribosomal multilocus sequence typing: universal characterization of bacteria from domain to strain. Microbiology 158:1005–1015. https://doi.org/10.1099/mic.0.055459-0.
17. Ciufo S, Kannan S, Sharma S, Badretdin A, Clark K, Turner S, Brover S, Schoch CL, Kimchi A, DiCuccio M. 2018. Using average nucleotide identity to improve taxonomic assignments in prokaryotic genomes at the NCBI. Int J Syst Evol Microbiol 68:2386–2392. https://doi.org/10.1099/ijsem.0.002809.