DATA NOTE

Genome sequence of a pathogenic Corynebacterium ulcerans strain isolated from a wild boar with necrotizing lymphadenitis

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Abstract

Objectives: Corynebacterium ulcerans can colonize a wide variety of animals and also humans are infected, typically by zoonotic transmission. Symptoms range from skin ulcers or systemic infections to diphtheria-like illness. In contrast, Corynebacterium pseudotuberculosis is widely distributed among herds of sheep, goats and other farm animals, where it causes high economic losses due to caseous lymphadenitis. Here we describe the genome sequence of an atypical C. ulcerans strain isolated from a wild boar with necrotizing lymphadenitis. This strain has similarities to C. pseudotuberculosis.

Data description: Genome sequence data of C. ulcerans isolate W25 were generated, analyzed and taxonomical relationship to other Corynebacterium species as well as growth properties of the isolate were characterized. The genome of C. ulcerans W25 comprises 2,550,924 bp with a G+C content of 54.41% and a total of 2376 genes.

Keywords: Emerging pathogen, Genomics, Toxigenic corynebacteria, Zoonotic transmission

Objective

The genus Corynebacterium (C.) comprises more than one hundred species with about half of these isolated from human and animal material [1, 2]. While most species are only rarely causing disease, others are connected to severe infections. This is especially true for the group of toxigenic corynebacteria [3], i.e. C. diphtheriae, C. ulcerans and C. pseudotuberculosis. C. diphtheriae is almost exclusively restricted to humans and is the etiological agent of diphtheria. In contrast, C. ulcerans can colonize a wide variety of animals and also humans are infected, typically by zoonotic transmission. In the case of human infections, skin ulcers and diphtheria-like illnesses are most common, besides cases of systemic infections. C. pseudotuberculosis is widely distributed among herds of sheep, goats and other farm animals, where it causes high economic losses due to caseous lymphadenitis. Human infections with this species are extremely rare and restricted to persons with close animal contact.

Here, we describe the genome sequence of an atypical C. ulcerans strain isolated from a wild boar with necrotizing lymphadenitis. Sequence data of C. ulcerans isolate W25 were generated and assembled and taxonomical relationship to other Corynebacterium species was characterized. Since only a very limited number of C. ulcerans whole genome sequences are available, the data may be valuable for taxonomical investigations and the prediction of pathogenicity based on genome mining approaches [4–7].

Data description

The data represent genome sequence information of C. ulcerans strain W25, isolated from a hunted wild boar (Sus scrofa). The chromosomal DNA of C. ulcerans W25 was sequenced using Illumina MiSeq and deposited at DDBJ/ENA/GenBank under the accession VFEM00000000 (Table 1), which is also the version described in this paper. The genome assembly consisted of 13 contigs with an estimated total size of 2,550,924 bp.
and a G+C content of 54.41%. A 50-fold coverage of the genome sequence was obtained with an N50 of 328,900 bp. A total of 2376 genes with 2013 coding genes, 304 pseudogenes, and 59 RNA genes were identified. Compared to five published genome sequences [8, 9] no significant variations in respect to sequence length, the number of coding sequences and RNA genes was found. In contrast, the G+C content of the genomic DNA of the W25 strain is with 54.4%, 1.0% to 1.1% higher than in other C. ulcerans strains (see Data set 2, Table 1).

The data set provided includes a PDF file (Data set 1) containing two images of the growth behavior of the isolate as well as a phylogenetic tree of corynebacteria reflecting an atypical phenotype of C. ulcerans W25 by its close taxonomical relationship to C. pseudotuberculosis (Table 1).

Table 1 Overview of data files/data sets

| Label | Name of data file/data set | File types (file extension) | Data repository and identifier (DOI or accession number) |
|-------|-----------------------------|-----------------------------|----------------------------------------------------------|
| The whole-genome shotgun sequencing project | The whole-genome shotgun sequencing project | No file type | https://www.ncbi.nlm.nih.gov/nucleotide/VFEM0000000.1/ [15] |
| Sequence read archive | SRX6047294: Genome sequence of a pathogenic Corynebacterium ulcerans strain isolated from a wild boar with necrotizing lymphadenitis | 1 ILLUMINA (Illumina MiSeq) run: 700,493 spots, 333.3 M bases, 194.7 Mb downloads | https://www.ncbi.nlm.nih.gov/sra/SRX6047294/ [15] |
| Assembly data | ASM637053v1 | fasta | https://www.ncbi.nlm.nih.gov/assembly/GCA_006370535.1 [15] |
| BioSample | Corynebacterium ulcerans strain W25 | No file type | SAMN12027930: https://www.ncbi.nlm.nih.gov/biosample/SAMN12027930/ [15] |
| BioProject | Corynebacterium ulcerans strain W25 | No file type | PRJNA548458: https://www.ncbi.nlm.nih.gov/bioproject/548458 [15] |
| Supplemental material W25 | Supplemental material W25 (Data_set_1_supplemental_material_W25) | Pdf | https://doi.org/10.6084/m9.figshare.8397245 |
| Table S1 | Table S1 (Data_set_2_table_S1) | Pdf | https://doi.org/10.6084/m9.figshare.8397320 |

Methodology

Growth of bacteria

Corynebacterium ulcerans isolate W25 was isolated from a hunted wild boar and propagated as a pure culture on Columbia Blood Agar (CBA) plates. On this solid medium, the bacteria had a waxy appearance and showed no hemolysis (Data set 1, Table 1). For subsequent experiments, C. ulcerans strains were grown in Brain Heart Infusion (BHI) containing 10% fetal bovine serum (FBS) and 0.05% Tween 80.

Genome sequencing

After 72 h of cultivation in BHI DNA was prepared using QIAGEN Genomic-tips 20/G and a QIAGEN Genomic DNA Buffer Set (Qiagen, Hilden, Germany). The DNA quality was examined by using a Qubit 2.0 fluorometer (Life Technologies, Darmstadt, Germany) and by agarose gel electrophoresis. Nextera XT Library Preparation Kit library according to the manufacturer’s instruction. Sequencing was done with an Illumina MiSeq run 2 × 300 bp. Quality was assessed and assembled with SPAdes v. 3.11.1 (with the additional command-careful) [10] was used and for annotation the Prokka annotation pipeline 1.12-beta in standard settings [11] as described before [12]. The mean coverage was 236 reads with a standard deviation of 71 reads. Mapped to the Corynebacterium ulcerans BR-AD22 77.4% was covered with a mean coverage of 57 reads.

Data analysis

To assess the phylogenetic classification of assorted Corynebacterium species PhyloPhlAn was used with the annotation files resulting from Prokka. The analysis was performed with standard-setting on all samples and visualized with Dendroscope as described before [12–14].

Limitations

The data represent the first characterization of genome sequence data of a newly isolated C. ulcerans strain. For further analyses, it may be necessary to close existing gaps and improve and cure the current annotation. For example, long-read sequencing (PacBio or MinIon) could generate in a hybrid assembly a more conclusive picture of the genome structure and possibly regulative aspects of protein expression.
Abbreviations
BHI: brain heart infusion; CBA: Columbia Blood Agar; FBS: fetal bovine serum; bp: base pair(s).

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Authors’ contributions
ABus sequenced and analyzed the genome and was responsible for data storage; conceptualization, supervision of experiments and administration was carried out by HH. JM was involved in the growth and data analysis and writing of the draft. The manuscript was written by ABur and finalized by ABus. All authors read and approved the final manuscript.

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Availability of data materials
The data described in this Data note can be freely and openly accessed on DDBJ/ENA/GenBank under the accession https://www.ncbi.nlm.nih.gov/nuccore/VFEM00000000.1/. Please see Table 1 and Reference list for details and links to the data.

Ethics approval and consent to participate
Not applicable.

Consent for publication
Not applicable.

Competing interests
The authors declare that they have no competing interests.

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