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Complete Genome Sequence of *Corynebacterium camporealensis* DSM 44610, Isolated from the Milk of a Manchega Sheep with Subclinical Mastitis

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Corynebacterium camporealensis **has been isolated in pure culture from milk samples of dairy sheep affected by subclinical mastitis. The complete genome sequence of the type strain DSM 44610, recovered from milk of a Manchega sheep, comprises 2,451,810 bp with a mean G+C content of 59.41% and 2,249 protein-coding genes.**

Received 27 April 2015 **Accepted** 30 April 2015 **Published** 28 May 2015

Citation Rückert C, Albersmeier A, Winkler A, Tauch A. 2015. Complete genome sequence of *Corynebacterium camporealensis* DSM 44610, isolated from the milk of a Manchega sheep with subclinical mastitis. Genome Announc 3(3):e00572-15. doi:10.1128/genomeA.00572-15.

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Mastitis is a serious health problem in dairy cattle and in other dairy species such as goats and sheep (1). It is also an economically important disease of dairy animals due to the fact that it is associated with reduced milk production and changes in milk composition and milk quality (2). Several *Corynebacterium* species have been linked with cases of clinical and subclinical mastitis in dairy cows and dairy sheep (3, 4). *Corynebacterium bovis*, for instance, was frequently detected in milk samples of dairy cows with infected mammary glands (3, 5) and nonlipophilic corynebacteria were found in the milk of dairy cows suffering from clinical and subclinical mastitis (6). *C. bovis*, *Corynebacterium mastitidis*, *Corynebacteriun pseudodiphtheriticum*, *Corynebacterium pseudotuberculosis*, and *Corynebacterium camporealensis* were isolated from cases of subclinical mastitis in sheep (4, 7, 8). Antimicrobial susceptibility assays with four *C. camporealensis* isolates from ewes with subclinical mastitis revealed low MICs for antimicrobials that are widely used for the treatment and prevention of mastitis (4).

C. camporealensis is a nonlipophilic, facultatively anaerobic *Corynebacterium* species (7). The type strain DSM 44610, originally named CRS-51, was obtained in pure culture from apparently normal milk samples of a Manchega sheep. The milk of sheep of the Manchega breed is used for the production of Manchego cheese (*queso manchego*) in the La Mancha region of Spain. The complete genome sequence of *C. camporealensis* DSM 44610 was determined to provide genetic insights into this economically important pathogen.

Purified genomic DNA of *C. camporealensis* DSM 44610 was obtained from the Leibniz Institute DSMZ. A DNA library was generated with the Nextera DNA sample preparation kit (Illumina) and was sequenced in a 2 × 250-nucleotide paired-end run using the MiSeq reagent kit v2 (500 cycles) and the MiSeq desktop sequencer (Illumina). Sequencing of the *C. camporealensis* DNA resulted in 1,587,464 paired reads and 277,886,417 detected bases. The assembly of the paired reads was conducted with the Roche GS *de novo* Assembler software (release 2.8), resulting in 16 scaffolds and 22 scaffolded contigs. The scaffolds were ordered by synteny analysis with the chromosome of *Corynebacterium vitaeruminis* (9) using the r2cat tool (10). Gaps were bridged by adding 9,325 mate pair reads to the assembly. These reads were derived from DNA sequencing with the MiSeq reagent kit v3 (600 cycles) of a 7-kb mate pair library generated with the Nextera mate pair sample preparation kit according to the gel-plus protocol and including a size selection of 500-bp inserts. The gap closure and finishing steps of this genome project were supported by the Consed finishing package (version 26) (11).

The chromosome of *C. camporealensis* DSM 44610 has a size of 2,451,810 bp with a mean G+C content of 59.41%. Gene recognition was performed with the Prodigal software (12). The subsequent functional annotation of the detected coding regions was supported by IMG/ER (13) and revealed 4 rRNA operons, 51 tRNA genes, and 2,249 protein-coding genes, including 121 genes encoding proteins with signal peptides and 608 genes encoding transmembrane proteins.

Nucleotide sequence accession number. This genome project has been deposited in the GenBank database under the accession number CP011311.

ACKNOWLEDGMENTS

The *C. camporealensis* genome project is part of the "*Corynebacterium* Type Strain Sequencing and Analysis Project." It was supported by the Medical Microbiology and Genomics fund for practical training (eKVV 200937).

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