

# Complete Genome Sequence of the Type Strain *Corynebacterium epidermidicanis* DSM 45586, Isolated from the Skin of a Dog Suffering from Pruritus

Christian Rückert,<sup>a,b</sup> Janine Eimer,<sup>b</sup> Anika Winkler,<sup>b</sup> Andreas Tauch<sup>b</sup>

Department of Biology, Massachusetts Institute of Technology, Cambridge, Massachusetts, USA<sup>a</sup>; Institut für Genomforschung und Systembiologie, Centrum für Biotechnologie (CeBiTec), Universität Bielefeld, Bielefeld, Germany<sup>b</sup>

**The complete genome sequence of *Corynebacterium epidermidicanis* DSM 45586 comprises 2,692,072 bp with 58.06% G+C content. The annotation revealed 2,466 protein-coding regions, including genes for surface-anchored proteins with Cna B-type or bacterial Ig-like domains and for an adhesive SpaABC-type pilus with similarity to fimbrial subunits of *Corynebacterium resistens* DSM 45100.**

Received 15 July 2015 Accepted 17 July 2015 Published 20 August 2015

**Citation** Rückert C, Eimer J, Winkler A, Tauch A. 2015. Complete genome sequence of the type strain *Corynebacterium epidermidicanis* DSM 45586, isolated from the skin of a dog suffering from pruritus. *Genome Announc* 3(4):e00959-15. doi:10.1128/genomeA.00959-15.

**Copyright** © 2015 Rückert et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Andreas Tauch, [tauch@cebitec.uni-bielefeld.de](mailto:tauch@cebitec.uni-bielefeld.de).

Currently, the genus *Corynebacterium* comprises 97 species that were isolated from diverse environments (1–7). Some *Corynebacterium* species are used in industrial applications and food production, whereas others are commensals or well-known pathogens of humans and animals, including mammals and birds. A few species originally recovered from animals have been implicated in the transmission of zoonotic infections to humans. These infections occurred in healthy individuals with close contact to wild or companion animals (e.g., by dog bites) (8). *Corynebacterium auriscanis* was isolated from a localized dog bite infection in a previously healthy female (9). Likewise, *Corynebacterium freiburgense* was cultured from a wound swab of a female who had been bitten by her dog in her forearm (10). *Corynebacterium canis* was also isolated from a patient's wound caused by a dog bite (11). A *Corynebacterium* species isolated from the skin of a dog is *Corynebacterium epidermidicanis*, represented by the type strain DSM 45586 (410<sup>T</sup>) (12). Here, we present the complete genome sequence of *C. epidermidicanis* DSM 45586 to provide insights into the gene repertoire of this corynebacterium from a dog with pruritus.

Purified genomic DNA of *C. epidermidicanis* DSM 45586 was obtained from the Leibniz Institute DSMZ (Braunschweig, Germany) and used as input for the construction of two DNA sequencing libraries. A whole-genome shotgun library was generated with the TrueSeq DNA PCR-free library preparation kit (Illumina), and a 7-kb mate pair library was prepared with the Nextera mate pair sample preparation kit according to the gel-plus protocol (Illumina). The whole-genome shotgun library was sequenced in a paired-end run using the MiSeq reagent kit version 3 (600 cycles) and the MiSeq desktop sequencer (Illumina). The shotgun sequencing approach yielded 1,582,565 paired reads and 266,953,870 detected bases. An initial assembly of the paired reads was performed with the Roche GS *De novo* Assembler software (release 2.8) and resulted in 25 scaffolds, including 32 scaffolded contigs. The mate pair library was prepared for DNA sequencing with the MiSeq reagent kit version 3 (600 cycles), generating

692,492 mate pair reads that were added to the initial genome assembly to obtain a single scaffold. Gaps in the genome sequence were closed *in silico* with the Consed version 26 software package (13). Gene prediction was performed with the Prodigal software (14), and the functional annotation of the detected coding regions was carried out by the IMG/ER pipeline (15).

The chromosome of *C. epidermidicanis* DSM 45586 has a size of 2,692,072 bp with a mean G+C content of 58.06%. The fully automated annotation of the complete genome sequence revealed 12 rRNA genes, 52 tRNA genes, 12 other RNA genes, and 2,466 protein-coding regions, including 1,903 protein-coding genes with functional predictions. Cell-cell contact of *C. epidermidicanis* DSM 45586 with the animal host is probably mediated by surface-anchored proteins with Cna B-type or bacterial Ig-like domains (16, 17). A predicted pilus gene cluster consists of the *spaACB* genes with deduced amino acid sequence similarity to the subunits of the SpaABC pilus from *Corynebacterium resistens* DSM 45100 (18, 19).

**Nucleotide sequence accession number.** This genome project has been deposited in the GenBank database under the accession number [CP011541](https://ncbi.nlm.nih.gov/nucl/CP011541).

## ACKNOWLEDGMENT

The *C. epidermidicanis* 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).

## REFERENCES

1. Tauch A, Sandbøte J. 2014. The family *Corynebacteriaceae*, p 239–277. In Rosenberg E, DeLong EF, Lory S, Stackebrandt E, Thompson F (ed), *The prokaryotes: actinobacteria*, 4th ed. Springer, Berlin, Germany.
2. Hoyles L, Ortman K, Cardew S, Foster G, Rogerson F, Falsen E. 2013. *Corynebacterium uterequi* sp. nov., a non-lipophilic bacterium isolated from urogenital samples from horses. *Vet Microbiol* 165:469–474. [http://dx.doi.org/10.1016/j.vetmic.2013.03.025](https://doi.org/10.1016/j.vetmic.2013.03.025).

3. Wiertz R, Schulz SC, Müller U, Kämpfer P, Lipski A. 2013. *Corynebacterium frankenforstense* sp. nov. and *Corynebacterium lactis* sp. nov., isolated from raw cow milk. *Int J Syst Evol Microbiol* 63:4495–4501. <http://dx.doi.org/10.1099/ijs.0.050757-0>.
4. Al-Dilaimi A, Bednarz H, Lömker A, Niehaus K, Kalinowski J, Rückert C. 2015. Revisiting *Corynebacterium glyciniphilum* (ex Kubota et al., 1972) sp. nov., nom. rev., isolated from putrefied banana. *Int J Syst Evol Microbiol* 65:177–182. <http://dx.doi.org/10.1099/ijs.0.065102-0>.
5. Kim PS, Shin NR, Hyun DW, Kim JY, Whon TW, Oh SJ, Bae JW. 2015. *Corynebacterium atrinae* sp. nov., isolated from the gastrointestinal tract of a pen shell, *Atrina pectinata*. *Int J Syst Evol Microbiol* 65:531–536. <http://dx.doi.org/10.1099/ijs.0.067587-0>.
6. Kämpfer P, Jerzak L, Wilharm G, Golke J, Busse HJ, Glaeser SP. 2015. Description of *Corynebacterium trachiae* sp. nov., isolated from a white stork (*Ciconia ciconiae*). *Int J Syst Evol Microbiol* 65:784–788. <http://dx.doi.org/10.1099/ijs.0.000014>.
7. Kämpfer P, Jerzak L, Bochenski M, Kasprzak M, Wilharm G, Golke J, Busse HJ, Glaeser SP. 2015. *Corynebacterium pelargi* sp. nov., isolated from the trachea of white stork nestlings. *Int J Syst Evol Microbiol* 65:1415–1420. <http://dx.doi.org/10.1099/ijs.0.000115>.
8. Talan DA, Citron DM, Abrahamian FM, Moran GJ, Goldstein EJ. 1999. Bacteriologic analysis of infected dog and cat bites. *N Engl J Med* 340:85–92. <http://dx.doi.org/10.1056/NEJM199901143400202>.
9. Bygott JM, Malnick H, Shah JJ, Chattaway MA, Karas JA. 2008. First clinical case of *Corynebacterium auriscanis* isolated from localized dog bite infection. *J Med Microbiol* 57:899–900. <http://dx.doi.org/10.1099/jmm.0.47780-0>.
10. Funke G, Frodl R, Bernard KA, Englert R. 2009. *Corynebacterium freiburgense* sp. nov., isolated from a wound obtained from a dog bite. *Int J Syst Evol Microbiol* 59:2054–2057. <http://dx.doi.org/10.1099/ijs.0.008672-0>.
11. Funke G, Englert R, Frodl R, Bernard KA, Stenger S. 2010. *Corynebacterium canis* sp. nov., isolated from a wound infection caused by a dog bite. *Int J Syst Evol Microbiol* 60:2544–2547. <http://dx.doi.org/10.1099/ijs.0.019927-0>.
12. Frischmann A, Knoll A, Hilbert F, Zasada AA, Kämpfer P, Busse HJ. 2012. *Corynebacterium epidermidicanis* sp. nov., isolated from skin of a dog. *Int J Syst Evol Microbiol* 62:2194–2200. <http://dx.doi.org/10.1099/ijs.0.036061-0>.
13. Gordon D, Green P. 2013. Consed: a graphical editor for next-generation sequencing. *Bioinformatics* 29:2936–2937. <http://dx.doi.org/10.1093/bioinformatics/btt515>.
14. Hyatt D, Chen GL, Locascio PF, Land ML, Larimer FW, Hauser LJ. 2010. Prodigal: prokaryotic gene recognition and translation initiation site identification. *BMC Bioinformatics* 11:119. <http://dx.doi.org/10.1186/1471-2105-11-119>.
15. Markowitz VM, Chen IM, Palaniappan K, Chu K, Szeto E, Pillay M, Ratner A, Huang J, Woyke T, Huntemann M, Anderson I, Billis K, Varghese N, Mavromatis K, Pati A, Ivanova NN, Kyrpides NC. 2014. IMG 4 version of the integrated microbial genomes comparative analysis system. *Nucleic Acids Res* 42:D560–D567. <http://dx.doi.org/10.1093/nar/gkt963>.
16. Finn RD, Bateman A, Clements J, Coghill P, Eberhardt RY, Eddy SR, Heger A, Hetherington K, Holm L, Mistry J, Sonnhammer EL, Tate J, Punta M. 2014. Pfam: the protein families database. *Nucleic Acids Res* 42:D222–D230. <http://dx.doi.org/10.1093/nar/gkt1223>.
17. Foster TJ, Höök M. 1998. Surface protein adhesins of *Staphylococcus aureus*. *Trends Microbiol* 6:484–488. [http://dx.doi.org/10.1016/S0966-842X\(98\)01400-0](http://dx.doi.org/10.1016/S0966-842X(98)01400-0).
18. Schröder J, Maus I, Meyer K, Wördemann S, Blom J, Jaenicke S, Schneider J, Trost E, Tauch A. 2012. Complete genome sequence, lifestyle, and multi-drug resistance of the human pathogen *Corynebacterium resistens* DSM 45100 isolated from blood samples of a leukemia patient. *BMC Genomics* 13:141. <http://dx.doi.org/10.1186/1471-2164-13-141>.
19. Mandlik A, Swierczynski A, Das A, Ton-That H. 2008. Pili in Gram-positive bacteria: assembly, involvement in colonization and biofilm development. *Trends Microbiol* 16:33–40. <http://dx.doi.org/10.1016/j.tim.2007.10.010>.