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

Citation: Ruckert, Christian, Janine Eimer, Anika Winkler, and Andreas Tauch. “Complete Genome Sequence of the Type Strain Corynebacterium Epidermidicanis DSM 45586, Isolated from the Skin of a Dog Suffering from Pruritus.” Genome Announc. 3, no. 4 (August 20, 2015): e00959–15.

As Published: http://dx.doi.org/10.1128/genomeA.00959-15

Publisher: American Society for Microbiology

Persistent URL: http://hdl.handle.net/1721.1/99637

Version: Final published version: final published article, as it appeared in a journal, conference proceedings, or other formally published context

Terms of use: Creative Commons Attribution
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.

**REFERENCES**

1. Tauch A, Sandbote 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. Hoyle I, Orman T, 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 163:469–474. [http://dx.doi.org/10.1016/j.vetmic.2013.03.025](http://dx.doi.org/10.1016/j.vetmic.2013.03.025).

**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 project number CP011541).
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. 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.

9. 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.

10. Frischmann A, Knoll A, Hilbert F, Zasada AA, Kämpfer P, Busse HJ. 2012. Corynebacterium epidermidis 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.

11. Gordon D, Green P. 2013. Consed: a graphical editor for next-generation sequencing. Bioinformatics 29:2936–2937. http://dx.doi.org/10.1093/bioinformatics/bts155.

12. 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.

13. 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, Puglisi 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.

14. Finn RD, Bateman A, Clements J, Coggill 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–D229. http://dx.doi.org/10.1093/nar/gkt1223.

15. Foster TJ, Hooke M. 1998. Surface protein adhesins of Staphylococcus aureus. Trends Microbiol 6:484–488. http://dx.doi.org/10.1016/S0966-842X(98)01400-0.

16. 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 resistent DSM 45100 isolated from blood samples of a leukemia patient. BMC Genomics 13:141. http://dx.doi.org/10.1186/1471-2164-13-141.

17. Mandlik A, Świerczynski 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.