

Complete Genome Sequence of *Corynebacterium falsenii* DSM 44353 To Study the Evolution of *Corynebacterium* Cluster 3 Species

Alina Glaub, Christina Bomholt, Kerstin Gravermann, Karina Brinkrolf, Andreas Albersmeier, Christian Rückert, Andreas Tauch

Institut für Genomforschung und Systembiologie, Centrum für Biotechnologie, Universität Bielefeld, Bielefeld, Germany

***Corynebacterium falsenii* is a member of the natural microflora of wild and domesticated birds and is rarely detected in human clinical specimens. The chromosomal sequence of the type strain *C. falsenii* DSM 44353 comprises 2,677,607 bp and provides detailed insights into the evolution of *Corynebacterium* species assigned to the highly diverse cluster 3.**

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Address correspondence to Andreas Tauch, tauch@cebitec.uni-bielefeld.de.

Corynebacterium falsenii was first described by Sjöden et al. (1) in a polyphasic taxonomic study of four coryneform strains that were isolated from human blood cultures and a cerebrospinal fluid sample between 1991 and 1995. Based on the alignments of *rpoB* gene sequences, *C. falsenii* was grouped into the cluster 3 of the genus *Corynebacterium*, with *Corynebacterium jeikeium* being the closest phylogenetic relative (2). The species *C. falsenii* is represented by the type strain DSM 44353, which was isolated in 1994 from a blood culture of a 4-year-old boy suffering from acute lymphatic leukemia (1). However, the clinical significance of *C. falsenii* remains largely unknown, as it has since been recovered very rarely from human clinical material (3, 4). On the other hand, *C. falsenii* was isolated from the respiratory tracts of eagles and black storks (5, 6) and from bioaerosols sampled in duck houses (7). *C. falsenii* was also detected by 16S rRNA gene sequencing in the cloacal microbial community of black-winged stilts (8). Hence, *C. falsenii* may represent a member of the natural microflora of wild and domesticated birds.

To get insights into the genetic organization of this rarely recovered corynebacterium, we sequenced the genome of the *C. falsenii* type strain (1). *C. falsenii* DSM 44353 (BL 8171, CCUG 33651) was obtained from the Leibniz Institute DSMZ (Braunschweig) and grown in brain heart infusion broth-yeast extract at 37°C (9). Genomic DNA was purified with the Genomic-tip 500/G system and the Genomic DNA buffer set (Qiagen), and it was used as starting material to prepare a standard sequencing library according to the workflow of the Nextera DNA sample preparation kit (Illumina). The genomic library was sequenced in a 2 × 250 nucleotide (nt) paired-end run using the MiSeq reagent kit version 2 and the MiSeq desktop sequencer (Illumina), resulting in 1,077,270 reads and an 81-fold genome coverage. The reads were preprocessed by quality trimming in such a way that the terminal five nucleotides had a Phred quality value of ≥30 (10). Preprocessed reads were assembled with the GS *de novo* assembler software (release 2.8) to yield 44 contigs in 12 scaffolds. The software r2cat (11) supported the ordering of the scaffolds according to alignments with the chromosomal sequence of *C. jeikeium*

K411 (12). The remaining gaps in the genome sequence were closed *in silico* with the Consed software (version 24) (13).

The genome sequence of *C. falsenii* DSM 44353 includes a circular chromosome of 2,677,607 bp (63.18% G+C content) and the circular coryneophage ΦCFAL8171I genome of 42,009 bp (61.74% G+C content). An identical linear copy of ΦCFAL8171I is present in the chromosome as a prophage, suggesting that this coryneophage had entered a lytic cycle in a subpopulation of the culture used to prepare the genomic DNA. The automatic annotation of the genome sequence with the NCBI Prokaryotic Genome Annotation Pipeline and the GeneMarkS+ software (version 2.3) revealed 2,248 protein-coding regions, 35 pseudogenes, 50 tRNA genes, 1 noncoding RNA (ncRNA) gene, and 3 rRNA operons in the chromosome of *C. falsenii* DSM 44353 and 58 protein-coding regions in the circular genome of ΦCFAL8171I.

Nucleotide sequence accession numbers. This genome project has been deposited in the GenBank database under accession no. CP007156 (chromosome) and CP007157 (ΦCFAL8171I).

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