

Draft Genome Sequences of 11 *Staphylococcus epidermidis* Strains Isolated from Wild Mouse Species

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We report here the draft genome sequences of 11 strains of *Staphylococcus epidermidis*, a common bacterium inhabiting the skin of humans and other animals. These isolates, obtained from five mouse species, provide valuable information on the native *Staphylococcus* spp. of this important model organism and form a basis for studying host-bacterial interactions in their natural environment.

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The genus *Staphylococcus* contains important members of the human skin microbiome (1). The major members are commensal under normal circumstances but can also be pathogenic. *Staphylococcus aureus* is so far the main species of interest, as it is a major source of nosocomial infections and can afflict numerous organs (2). Other examples include *Staphylococcus haemolyticus* (causing infective endocarditis [3]) and *Staphylococcus saprophyticus* (causing urinary tract infections [4]). *Staphylococcus epidermidis*, on the other hand, is of critical importance, as it is the most common source of medical device-associated infections (5), but at the same time, it is capable of inhibiting *S. aureus* colonization in human nasal cavities (6). Given this important clinical relevance, infection models are established in mice but are so far limited to human *S. aureus* isolates (7). Understanding the interaction and coevolutionary history between mice and their native bacterial species has attracted recent attention (8), although native *Staphylococcus* strains remain unexplored. Furthermore, we recently discovered *Staphylococcus* to contain important members of the native mouse skin microbiota influencing susceptibility to autoimmune skin blistering (9).

In order to provide insight into the native species of *Staphylococcus* inhabiting mice, we isolated *Staphylococcus* spp. from 11 wild mice representing five species and subspecies (*Mus musculus musculus*, *M. musculus domesticus*, *M. musculus castaneus*, *M. musculus spicilegus*, and *Apodemus uralensis*), which were captured from the wild and maintained in conventional animal facilities at the Max Planck Institute for Evolutionary Biology, Plön, Germany. The majority of isolates belonged to *S. epidermidis*, and we subsequently selected 11 strains for genome sequencing. The sequencing libraries were prepared using the Illumina Nextera XT kit and run on the MiSeq platform with paired-end reads of 250 bp, with a minimum coverage of 31× and a maximum of 61×. The reads were assembled *de novo* using Velvet (10) with parameters optimized by VelvetOptimiser (<http://www.vicbioinformatics.com/software.velvetoptimiser.shtml>). The contigs were annotated by the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) version 2.0 (11).

For the 11 strains, we obtained a minimum of 91 and maximum of 277 contigs, and the total number of assembled nucleotides ranged from 2,458,755 to 2,762,809 per strain. The average G+C contents ranged from 31.7% to 32.0%, which is close to those of the available reference strains (32.1% for *S. epidermidis* ATCC 12228 and 32.2% for *S. epidermidis* RP62A). A range of 2,259 to 2,541 proteins were predicted and annotated using the NCBI PGAP, with 83.6% to 92.2% of the proteins having homologs in the *S. epidermidis* ATCC 12228 (NCBI accession no. NC_004461) (12) and/or RP62A genomes (NCBI accession no. NC_002976) (13) (BLASTp [14] with an *E* value of 1E-20 and similarity threshold of 0.8). Thirteen to 70 tRNA genes and 3 to 24 rRNA genes are predicted for each strain. Further analyses of the genomic content may reveal important aspects of the interaction and coevolution of *S. epidermidis* and mouse hosts.

Nucleotide sequence accession numbers. The draft genome sequences are deposited in GenBank under accession no. [ATCU00000000](https://www.ncbi.nlm.nih.gov/nuclink/ATCU00000000), [ATCV00000000](https://www.ncbi.nlm.nih.gov/nuclink/ATCV00000000), [ATCW00000000](https://www.ncbi.nlm.nih.gov/nuclink/ATCW00000000), [ATCX00000000](https://www.ncbi.nlm.nih.gov/nuclink/ATCX00000000), [ATCY00000000](https://www.ncbi.nlm.nih.gov/nuclink/ATCY00000000), [ATDA00000000](https://www.ncbi.nlm.nih.gov/nuclink/ATDA00000000), [ATDC00000000](https://www.ncbi.nlm.nih.gov/nuclink/ATDC00000000), [ATDE00000000](https://www.ncbi.nlm.nih.gov/nuclink/ATDE00000000), [ATDF00000000](https://www.ncbi.nlm.nih.gov/nuclink/ATDF00000000), [ATDG00000000](https://www.ncbi.nlm.nih.gov/nuclink/ATDG00000000), and [ATDH00000000](https://www.ncbi.nlm.nih.gov/nuclink/ATDH00000000). The second versions are described in this paper: [ATCU02000000](https://www.ncbi.nlm.nih.gov/nuclink/ATCU02000000), [ATCV02000000](https://www.ncbi.nlm.nih.gov/nuclink/ATCV02000000), [ATCW02000000](https://www.ncbi.nlm.nih.gov/nuclink/ATCW02000000), [ATCX02000000](https://www.ncbi.nlm.nih.gov/nuclink/ATCX02000000), [ATCY02000000](https://www.ncbi.nlm.nih.gov/nuclink/ATCY02000000), [ATDA02000000](https://www.ncbi.nlm.nih.gov/nuclink/ATDA02000000), [ATDC02000000](https://www.ncbi.nlm.nih.gov/nuclink/ATDC02000000), [ATDE02000000](https://www.ncbi.nlm.nih.gov/nuclink/ATDE02000000), [ATDF02000000](https://www.ncbi.nlm.nih.gov/nuclink/ATDF02000000), [ATDG02000000](https://www.ncbi.nlm.nih.gov/nuclink/ATDG02000000), and [ATDH02000000](https://www.ncbi.nlm.nih.gov/nuclink/ATDH02000000).

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