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## Draft Genome Sequence of Staphylococcus epidermidis (Winslow and Winslow) Evans (ATCC 14990)

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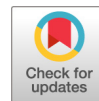


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# Draft Genome Sequence of *Staphylococcus epidermidis* (Winslow and Winslow) Evans (ATCC 14990)

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**ABSTRACT** Here, we report the draft genome sequence for the type strain *Staphylococcus epidermidis* (Winslow and Winslow) Evans (ATCC 14990). The assembly consisted of 2,457,519 bp with an observed G+C content of 32.04%. Thirty-seven contigs were produced, including two putative plasmids, with a 296.8× coverage and an  $N_{50}$  of 180,848 bp.

As part of an attempt to generate complete genomes for a subset of type strains in the ATCC collection, we report here the genome sequence and annotation of *Staphylococcus epidermidis* (Winslow and Winslow) Evans (ATCC 14990) isolated from the nose.

The purchased culture isolate was grown on 5% sheep blood agar (BD BBL prepared plated media) under 5% CO<sub>2</sub> at 35°C for 48 h. To extract genomic DNA, cells were resuspended in 0.5 mL DNA extraction buffer (20 mM Tris-Cl, 2 mM EDTA, 1.2% Triton X-100, pH 8), followed by the addition of 50 μL of lysozyme (20 mg/mL), 30 μL of mutanolysin, and 5 μL of RNase (10 mg/mL). After incubation at 37°C for 1 h, 80 μL of 10% SDS and 20 μL of proteinase K were added and incubated at 55°C for 2 h. Then, 210 μL of 6M NaCl and 700 μL of phenol-chloroform were added and incubated with rotation for 30 min, followed by a 10-min centrifugation at 13,500 rpm. The aqueous phase was extracted, and an equivalent volume of isopropanol was added. The solution was centrifuged at 13,500 rpm for 10 min after a 10-min incubation. The supernatant was decanted, and the DNA pellet was precipitated using 600 μL of 70% ethanol. Following ethanol evaporation, the DNA pellet was resuspended in Tris-EDTA and stored at -20°C.

The extracted genomic DNA was diluted in water to a concentration of 0.2 ng/μL, as measured by a fluorometric-based method (Life Technologies, Inc.). Library preparation of 1 ng (5 μL) of input DNA was performed using the Nextera XT DNA library preparation kit. The library was sequenced on the MiSeq sequencer (Illumina) using the MiSeq version 2 reagent kit (500 cycles) producing 1,689,436 paired-end reads in total. Reads were first processed, removing adapter sequences and phiX contaminants, using BBDuk from the BBMap package (<http://sourceforge.net/projects/bbmap>). The resulting trimmed reads were assembled using SPAdes version 3.5 (1), followed by scaffolding with SSPACE (2). In total, 37 contigs, varying in size from 504 bp to 749,904 bp ( $N_{50}$  = 180,848 bp), were produced with an average coverage of 296.8×. Two of these contigs (13,346 bp and 4,566 bp in length) correspond to individual plasmids within the strain. Confirmed via BLAST (BLASTn) to the GenBank NR/NT nucleotide database, these two plasmid sequences exhibit homology to *S. epidermidis* ATCC 12228 plasmid pSE-12228-04 (GenBank no. AE015933) and *S. aureus* plasmid SAP093A (GenBank no.

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GQ900441), respectively. Annotations were generated using the software tool Peasant (3). Nine rRNAs, 59 tRNAs, and 2,274 protein-coding sequences were identified. Furthermore, one possible clustered regularly interspaced short palindromic repeat (CRISPR) array was found (4). The final genome size for the *S. epidermidis* strain Evans (ATCC 14990) was 2,457,519 bp with an observed G+C content of 32.04%.

**Accession number(s).** The draft whole-genome project for *S. epidermidis* strain Evans (ATCC 14990) has been deposited at DDBJ/EMBL/GenBank under accession number [NARC00000000](https://ncbi.nlm.nih.gov/submit/submit.cgi?tbl=Accession). Raw sequence reads are deposited at DDBJ/EMBL/GenBank under accession number [SRR5364302](https://ncbi.nlm.nih.gov/submit/submit.cgi?tbl=Accession).

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