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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.

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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_2 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.

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. Raw sequence reads are deposited at DDBJ/EMBL/GenBank under accession number SRR5364302.

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