Complete Genome Sequences of Three Important Methicillin-Resistant Clinical Isolates of *Staphylococcus pseudintermedius*

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We report the first complete genome sequences of three predominant clones (ST68, ST71, and ST84) of methicillin-resistant *Staphylococcus pseudintermedius* in North America. All strains were isolated from canine infections and have different SCCmec elements and antibiotic resistance gene patterns.

*Staphylococcus pseudintermedius* is a Gram-positive opportunistic pathogen (1) that primarily causes infections in canines but is also relevant to human medicine (2–4), particularly with the worldwide expansion of methicillin-resistant clonal lineages (5–8). While a complete genome is publicly available for a European methicillin-resistant *S. pseudintermedius* (MRSP) isolate (9), no complete MRSP genomes from dominant clonal lineages in North America are available. Here, we present the complete circular chromosomes of MRSP strains NA45, 081661, and 063228, which were isolated from canine infections in 2006 and 2008 and represent three dominant sequence types (ST) in North America, namely, ST84, ST71, and ST68, respectively (10).

All isolates were sequenced using Roche/454 (Roche Diagnostics, Switzerland), Illumina MiSeq (Illumina, Inc., USA), and Ion Torrent technologies (Thermo, Fisher Scientific, USA); isolates NA45 and 063228 were additionally sequenced using PacBio single-molecule real-time sequencing technology (Pacific Biosciences, USA). All genomes were mapped using the Argus Whole Genome Mapping System (Opgen, Inc., USA). De novo assemblies were individually produced and merged using Geneious version 9.1.3 (11) and CLC Genomics Workbench version 9.0 (https://www.qiagenbioinformatics.com). PacBio reads and whole-genome maps were used for scaffolding and genome closure (12). Automated annotation for strain 063228 was performed using the RAST server (http://rast.nmpdr.org), while the NCBI Prokaryote Genome Annotation Pipeline (http://www.ncbi.nlm.nih.gov/genome/annotation_prok) was used for NA45 and 081661.

The total number of high-quality reads for strain NA45 were 29,463 (PacBio), 583,182 (Illumina), 279,674 (Roche), and 4,660,374 (Ion Torrent), resulting in >250-fold overall coverage. The NA45 genome is 2,841,212 bp with a 37.3% GC content, 2,665 predicted coding sequences, and 78 predicted RNAs. High-quality reads for strain 081661 were 456,358 (Illumina), 113,288 (Roche), and 3,864,512 (Ion Torrent), resulting in >250-fold overall coverage. The genome 081661 is 2,766,566 bp with a 37.4% GC content, 2,734 predicted coding sequences, and 77 predicted RNAs.

High-quality reads for strain 063228 were 24,585 (PacBio), 15,886,636 (Illumina), 113,288 (Roche), and 3,864,512 (Ion Torrent), resulting in >250-fold overall coverage. The genome 063228 is 2,731,109 bp with a 37.5% GC content, 2,610 predicted coding sequences, and 87 predicted RNAs.

The versions described in this paper are the first versions, CP016072.1, and CP015626.1. The versions deposited in DDBJ/ENA/GenBank under the accession numbers CP016072, CP016073, and CP015626. The versions described in this paper are the first versions, CP016072.1, CP016073.1, and CP015626.1.

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