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Complete Genome Sequence of the Canine Pathogen *Staphylococcus pseudintermedius*▽

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We report the first whole-genome sequence for a clinical isolate of *Staphylococcus pseudintermedius* (ED99), the major pathogen responsible for canine bacterial pyoderma. *S. pseudintermedius* contains numerous mobile genetic elements and encodes an array of putative virulence factors, including superantigenic, cytolytic, and exfoliative toxins and cell wall-associated surface proteins.

Staphylococcus pseudintermedius is a resident of the skin and mucosal surfaces of most healthy dogs (5). However, disruption of the normal skin flora, damage to the cutaneous barrier by a pruritic condition, immunosuppression, or inherent immunodeficiency can lead to surface, superficial, or deep pyoderma (9). Furthermore, *S. pseudintermedius* occasionally causes severe human zoonotic infections (8), and isolates exhibit various degrees of antimicrobial resistance (6).

Whole-genome sequencing of a representative *S. pseudintermedius* strain (ED99) (1) was carried out with two runs using the Genome Sequencer FLX sequencer, generating a total of 350,290 reads with an average length of 257 bases, corresponding to more than 32.5× genome coverage. Assembly with 454 Newbler software (454 Life Sciences, Branford, CT) resulted in a total of 65 contigs with an N50 value of 85,670 bases. Gaps between contigs were filled by conventional or combinatorial PCR and use of the GPS-1 genome priming system (New England BioLabs), followed by sequencing with an ABI 3730 capillary sequencer. Final assembly, annotation, and genome analysis were carried out as previously described (4). The genome of *S. pseudintermedius* ED99 is composed of a single circular chromosome of 2,572,216 bp and has an average G+C content of 37.6%, which is substantially higher than the 32% average of other staphylococci (2). It contains five ribosomal operons and 58 tRNA loci and encodes 2,401 predicted protein-coding sequences (CDSs). *S. pseudintermedius* ED99 contains numerous predicted mobile genetic elements, including insertion elements, transposons mediating resistance to antibiotics, a remnant of a novel member of the staphylococcal pathogenicity island family (SaPI), a family of reverse transcriptase (RT) group II introns, and a putative integrated plasmid. *S. pseudintermedius* ED99 also contains a type Nmeni CRISPr locus, which includes 23 predicted spacer regions.

S. pseudintermedius encodes a number of predicted toxins, including the superantigen Se-int (3), the bicomponent leukotoxin Luk-I (7), the exfoliative toxin SIET (10), and homologs of hemolysin III and β-hemolysin. In addition, we identified a putative novel exfoliative toxin and numerous exoenzymes, including lipases, a thermonuclease, a thermolysin, and an array of proteases, including a group of eight predicted glutamyl-endopeptidases.

S. pseudintermedius ED99 contains at least 18 genes specific for predicted cell wall-associated proteins and encodes numerous global regulators characteristic of other staphylococcal species, including *agr*, *sar*, *sae*, and *rot*.

Overall, the genome sequence of a strain of *S. pseudintermedius* represents an important framework for investigations into the molecular pathogenesis of canine bacterial pyoderma.

Nucleotide sequence accession number. The complete genome sequence of *S. pseudintermedius* ED99 has been deposited in the GenBank database with the accession number CP002478.

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