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GENOME ANNOUNCEMENTS

Complete Genome Sequence of the Veterinary Pathogen *Staphylococcus pseudintermedius* Strain HKU10-03, Isolated in a Case of Canine Pyoderma▽

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***Staphylococcus pseudintermedius* is a member of the coagulase-positive staphylococci and is the commonest cause of canine pyoderma. We report the first genome sequence of *S. pseudintermedius*, which shows the presence of numerous virulence factors akin to those of the related human pathogen *Staphylococcus aureus*.**

Staphylococcus pseudintermedius was first described as a novel *Staphylococcus* species in 2005 and was distinguished from the closely related *Staphylococcus intermedius* and *Staphylococcus delphini* primarily by DNA-DNA hybridization (7). These 3 species together constitute the *S. intermedius* group (SIG), with individual species being considerably difficult to differentiate phenotypically (11). Currently, genotyping by *sodA*, *hsp60*, *nuc*, or *kat* gene sequence is the most useful method in species identification of SIG members (4, 11, 12), while PCR-restriction fragment length polymorphism analyses of the *kat* and *pta* genes have been developed as rapid and affordable alternatives (3, 4). Importantly, epidemiological studies have revealed that *S. pseudintermedius* and not *S. intermedius* is the commonest causative agent of canine pyoderma (2, 6). These findings have led to the realization that many canine isolates previously identified as *S. intermedius* should have been classified as *S. pseudintermedius*.

In addition to pyoderma, *S. pseudintermedius* has been associated with other canine infections, including wound infections, urinary tract infections, and otitis externa. Cases of infections with this agent in humans and other animals have also been reported (14–16). Given the similarities between *S. pseudintermedius* and *Staphylococcus aureus* infections in dogs and humans, respectively, knowledge of host adaptation by *S. pseudintermedius* and the pathogenesis of its infections will potentially have an impact in the areas of public health, infectious diseases, and veterinary medicine.

The genome of *S. pseudintermedius* strain HKU10-03 was sequenced on a GS FLX system (Roche Diagnostics, Basel, Switzerland), which produced approximately 260,000 reads with an approximate 37-fold coverage. This strain was first isolated from the skin swab of a skin lesion swab of a dog suffering from canine pyoderma. Genome assembly was performed using the Newbler assembler and produced 51 large contigs (greater than 500 bp in size). Contig ordering was performed with the assistance of the OSlay software program (10), followed by gap closing and genome finishing by genomic PCR and DNA sequencing of the amplification products on an ABI 3730xl sequencer (Applied Biosystems, California), similar to the strategy employed for our previously sequenced *Staphylococcus lugdunensis* genome (13). The finished genome sequence was validated by genome macrorestriction analysis with the restriction enzymes AscI, AsiSI, NotI, and SbfI. Sequences of all ribosomal operons have been confirmed by additional PCR and DNA sequencing. Protein coding sequences were predicted using the Glimmer3 (5) and Prodigal (8) software programs, and automated annotation of genes and tRNA and rRNA regions was performed on the RAST server (1). Transfer mRNA was predicted using the ARAGORN software program (9).

The circular genome sequence of *S. pseudintermedius* strain HKU10-03 is 2,617,381 bp in length. Genomic G+C content is 37.53 mol%, which is significantly higher than the G+C content of other sequenced staphylococci. No plasmids were present in the sequenced strain. The genome contained 59 tRNA genes, 6 copies of the ribosomal operon, and 2,451 protein coding genes. In addition to housekeeping genes involved in the various major metabolic pathways, numerous putative virulence factors were found, including leukocidins, exotoxins, superantigens, and adherence factors, in keeping with the identity of *S. pseudintermedius* as an animal pathogen. Characterization of these factors and the associated pathogenicity islands would be instrumental in developing more-effective strategies against *S. pseudintermedius* infections.

Nucleotide sequence accession number. The complete genome sequence of *S. pseudintermedius* strain HKU10-03 is available in NCBI GenBank under accession no. CP002439.

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