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Draft Genome Sequence of a Multiresistant Bovine Isolate of *Staphylococcus lentus* from Tanzania

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We report here the draft genome sequence of a *Staphylococcus lentus* isolate, 050AP, collected in Tanzania from a swab of healthy bovine perineum. The draft genome sequence contained 2.72 Mbp and 2,750 coding sequences with a G+C content of 31.7%.

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Staphylococcus lentus is a member of the *Staphylococcus sciuri* group which also comprises *S. sciuri*, *Staphylococcus vitulinus*, *Staphylococcus fleurettii*, and *Staphylococcus stepanovicii* (1, 2). This group is part of the normal skin and mucosal flora in a wide range of animals, and while not frequently associated with disease, members of the *S. sciuri* group have been isolated from various human and veterinary infections (1, 2). They have furthermore been implicated as a reservoir for virulence and resistance gene exchange with other staphylococci (2). In this study an isolate of *S. lentus*, 050AP, collected from a perineum swab of a healthy Friesian-Jersey mixed breed dairy cow in Nyakato, Tanzania in April 2014 was genome sequenced using an Illumina HiSeq 2000. To our knowledge this is the first veterinary *S. lentus* genome to be reported.

Genome assembly was performed using Velvet software (3), and resulted in an assembly consisting of 37 contigs with a N_{50} of 119,892 bp which was automatically annotated using Prokka (4). The resultant 050AP draft genome was 2,719,515 bp with a G+C content of 31.7% and contained 2,750 predicted protein-coding sequences. The macrolide resistance gene *mph(C)* and tetracycline resistance gene *tet(K)* were identified by ResFinder version 2.1 (5). In the case of *mph(C)* (locus tag: SAMEA3109314_01885) the best full length BLAST match in the nucleotide collection is a 91.9% identify match to *mph(C)* in *Staphylococcus aureus* (CP017097.1). Thus, 050AP appears to encode a novel *mph(C)* variant which may be the same or related to a variant reported as partial coding sequences in *S. lentus* from free-living small mammals in Poland (6). A single nucleotide deletion causes a frameshift mutation in *tet(K)* leading to a predicted protein of at least 419 amino acids versus the typical 296 amino acids. However, with the gene located at the end of a contig the exact size of *tet(K)* in 050AP is uncertain from these sequence data. Phenotypically 050AP was resistant to erythromycin, clindamycin, tetracycline, ciprofloxacin, fusidic acid, oxacillin, and trimethoprim as assessed by Vitek-2 using card AST-P620 (bioMérieux, Basingstoke, United Kingdom) but susceptible to cefoxitin (screen), chloramphenicol, daptomycin, gentamicin, linezolid, mupirocin, penicillin, teicoplanin, tigecycline, and vancomycin. The avail-

ability of this genome for comparative analysis with other staphylococcal genomes will provide insights into the biology of the *S. sciuri* group and their role as commensals and pathogens.

Accession number(s). This whole-genome shotgun project has been deposited in DDBJ/EMBL/GenBank under the accession number [FMRW01000000](https://www.ncbi.nlm.nih.gov/nuccore/FMRW01000000). The version described in this paper is the first version, FMRW01000000.1.

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REFERENCES

1. Becker K, Heilmann C, Peters G. 2014. Coagulase-negative staphylococci. *Clin Microbiol Rev* 27:870–926. <http://dx.doi.org/10.1128/CMR.00109-13>.
2. Nemeghaire S, Argudín MA, Feßler AT, Hauschild T, Schwarz S, Butaye P. 2014. The ecological importance of the *Staphylococcus sciuri* species group as a reservoir for resistance and virulence genes. *Vet Microbiol* 171: 342–356. <http://dx.doi.org/10.1016/j.vetmic.2014.02.005>.
3. Zerbino DR, Birney E. 2008. Velvet: algorithms for *de novo* short read assembly using de Bruijn graphs. *Genome Res* 18:821–829. <http://dx.doi.org/10.1101/gr.074492.107>.
4. Seemann T. 2014. Prokka: rapid prokaryotic genome annotation. *Bioinformatics* 30:2068–2069. <http://dx.doi.org/10.1093/bioinformatics/btu153>.
5. Zankari E, Hasman H, Cosentino S, Vestergaard M, Rasmussen S, Lund O, Aarestrup FM, Larsen MV. 2012. Identification of acquired antimicrobial resistance genes. *J Antimicrob Chemother* 67:2640–2644. <http://dx.doi.org/10.1093/jac/dks261>.
6. Hauschild T, Schwarz S. 2010. Macrolide resistance in *Staphylococcus* spp. from free-living small mammals. *Vet Microbiol* 144:530–531. <http://dx.doi.org/10.1016/j.vetmic.2010.06.017>.