Draft Genome Sequence of *Kroppenstedtia sanguinis* X0209\(^T\), a Clinical Isolate Recovered from Human Blood

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**ABSTRACT** *Kroppenstedtia sanguinis* X0209\(^T\), a thermoactinomycete, was isolated from the blood of a patient in Sweden. We report on the draft genome sequence obtained with an Illumina MiSeq instrument. The assembled genome totaled 3.73 Mb and encoded 3,583 proteins. Putative genes for virulence, transposons, and biosynthetic gene clusters have been identified.

The genus *Kroppenstedtia* was established by von Jan et al. (1) and presently comprises four species, *Kroppenstedtia eburnea* (1), *Kroppenstedtia guangzhouensis* (2), *Kroppenstedtia pulmonis* (3), and *Kroppenstedtia sanguinis* (3). Strains of the genus *Kroppenstedtia* are characterized as chemoorganotrophic Gram-positive non-acid-fast nonmotile aerobic bacteria capable of producing a substrate mycelium with the ability to form heat-resistant endospores (1–3). *K. sanguinis* X0209\(^T\) was isolated from a blood culture from a patient in Sweden (3). The *K. sanguinis* X0209\(^T\) genome was selected for sequencing due to its isolation from a human clinical specimen and its potential source of secondary metabolites (4).

A single colony was grown in Trypticase soy broth at 35°C for 5 days. Genomic DNA was purified using the MasterPure DNA purification kit (Epicentre, Madison, WI). DNA fragments averaging 500 bp in length were obtained by shearing purified DNA on a Covaris M220 focused ultrasonicator (Covaris, Inc., Woburn, MA). Libraries were created using the NEBNext Ultra II DNA kit (New England BioLabs, Ipswich, MA), and fragments were quantified using a Qubit v1.0 instrument (Thermo Fisher Scientific, Waltham, MA). Paired-end sequencing (2 \(\times\) 250 bp) was performed using a MiSeq v2 500-cycle reagent kit (Illumina, San Diego, CA). Illumina sequencing produced a total of 2,352,322 paired reads. Reads were imported into CLC Genomics Workbench v11.0.1. Reads were then trimmed to remove adapters and low-quality sequences using default parameters, resulting in 2,332,279 high-quality reads with an average length of 197.4 bp. Removal of low-coverage contigs (<5X) and de novo assembly resulted in 27 contigs with a median coverage of 127X and an \(N_{50}\) contig length of 260,037 bp. The assembled genome was annotated through NCBI’s Prokaryotic Genome Annotation Pipeline (PGAP) (5). The *Kroppenstedtia sanguinis* X0209\(^T\) genome has the GenBank accession number QWDJ00000000 and contains 3.73 Mbp with a G+C content of 68.8%, 3,583 protein-coding sequences (CDSs), 1 rRNA operon, 45 tRNAs, and no plasmids.

BLAST+ was used to probe the *Kroppenstedtia sanguinis* genome for virulence factors by aligning the genome to the Virulence Factor Database (VFDB) (6, 7). A total of 98 potential genes associated with virulence factors were identified (7). One Tn\(10\) family transposase was discovered, as well as 3 putative transposases and 3 putative OrfB transposases. One clustered regularly interspaced short palindromic repeat (CRISPR) array was identified in the genome.

AntiSMASH v4.0 Web version was utilized with all features enabled to search for biosynthetic gene clusters (BGCs) in the *Kroppenstedtia sanguinis* genome, and 38 BGCs
were identified (8); 27 putative BGCs (of unknown function) were identified, along with 3 nonribosomal polyketide synthases (NRPSs), 2 terpenes, 1 bacteriocin, 1 putative fatty acid, 1 putative fatty acid with ectoine, 1 linaridin, 1 other unclassified BGC, and 1 siderophore type 1 NRPS. The high percentage of BGCs with unknown functions suggests that this species has significant potential as a source of novel secondary metabolites.

Data availability. The whole-genome sequence of *Kroppenstedtia sanguinis* X0209T (BioSample number SAMN09906766) has been deposited at DDBJ/ENA/GenBank under the accession number QWDJ00000000. The version described in this paper is version QWDJ02000000. The Illumina raw reads have been submitted to the SRA under number SRX4636631.

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