



Draft Genome Sequence of the Gram-Positive Neutrophilic Iron-Precipitating *Kineosporia* sp. Strain A_224

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ABSTRACT We report here the draft genome sequence of the neutrophilic iron-precipitating *Kineosporia* sp. strain A_224. Analysis of the predicted genes may improve our knowledge of its role in ochrous formations in natural and technical water systems. This is the first public genome sequence of a *Kineosporia aurantiaca* strain.

A novel iron-depositing actinobacterial strain of the family *Kineosporiaceae* was isolated from the floodplain area in the Lower Oder Valley National Park, Germany. Based on 16S rRNA gene sequence analysis, the family *Kineosporiaceae* (1) includes the five genera *Angustibacter* (2), *Kineococcus* (3), *Kineosporia* (4), *Pseudokineococcus* (5), and *Quadrisphaera*. The genus *Kineosporia* contains seven species, *K. aurantiaca* (4), *K. babensis* (6), *K. mesophila* (7), *K. mikuniensis*, *K. rhamnosa*, *K. rhizophila*, and *K. succinea* (8). Iron-oxidation ability in the *Actinobacteria* family has been reported for only some acidic actinobacteria, such as members of the *Rubroacteridae* subclass (9), the *Acidimicrobidae* subclass (10, 11), and the TM3 group of uncultured actinobacteria (12).

Kineosporia sp. strain A_224 was obtained from an iron-depositing biofilm of the floodplain area in the Lower Oder Valley National Park, Germany. The strain was isolated by spreading the suspended biofilm on ATA medium (13). Dark, brown-colored colonies that formed on the agar surface were selected after 2 weeks of incubation at room temperature. Iron-deposition ability of the strain was confirmed according to Schmidt et al. (14). Total genomic DNA was extracted using the GeneMATRIX soil DNA purification kit (Roboklon, Berlin, Germany). The paired-end library was prepared by following the Illumina Nextera XT DNA library prep kit protocol. Genome sequencing was done on an Illumina NextSeq 500 sequencer using the NextSeq mid-output kit version 2 with 300-cycle chemistry, generating 25,537,780 raw reads. Demultiplexing was done with bcl2fastq version 2.18.0.12. Quality filtering of the raw reads was performed using Trimmomatic version 0.36 (1). Reads were checked for ambiguous base calls and low complexity with the DUST algorithm (2) and were filtered accordingly with an R script in Microsoft R Open version 3.3.2 (3), followed by preassembly with SPAdes version 3.10.0 (4) using default *k*-mer lengths up to 99 bp. Scaffolds of this preassembly ≥ 500 bp were subject to extension and second-round scaffolding with SSPACE standard version 3.0 (5). Scaffolds $\geq 2,500$ bp were assigned to genome bins by MetaBAT version 0.32.4 (8), and functional annotation of draft genomes was performed with Prokka version 1.12b (9). The shortest scaffold was 2,712 bp, and the longest scaffold was 335,770 bp. The total size of the draft genome was 7,196,381 bp with a GC content of 74%. Annotation resulted in 242 contigs, including 6,546 coding sequences for 6,626 genes, 1 CRISPR repeat unit, 3 rRNAs (5S, 16S, 23S), 63 tRNAs, 1 tmRNA, 13 miscellaneous RNAs, and 530 signal peptide coding sequences. Using the 16S rRNA gene, BLASTn searches (15) revealed a 96% gene sequence similarity to *K. aurantiaca* strain 14067 (NR_041718), and EzBioCloud (16) searches revealed a 96.5% similarity to *K. mesophila* strain YIM 65293 (FJ214362).

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Accession number(s). This genome shotgun project has been deposited in GenBank under the accession number [MWLN00000000](https://www.ncbi.nlm.nih.gov/nuccore/MWLN00000000). The version described in this paper is the first version, MWLN01000000.

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