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PROKARYOTES

Draft Genome Sequence of *Cystobacter ferrugineus* Strain Cbfe23

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ABSTRACT In an effort to explore myxobacterial natural product biosynthetic pathways, the draft genome sequence of *Cystobacter ferrugineus* strain Cbfe23 has been obtained. Analysis of the genome using antiSMASH suggests a multitude of unique natural product biosynthetic pathways. This genome will contribute to the investigation of secondary metabolism in other myxobacterial species.

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Myxobacteria are a prolific source of natural products with members of the genus *Cystobacter* producing a variety of structurally diverse antibiotics (1–6). Isolated from a soil sample in China collected in 1982, *Cystobacter ferrugineus* strain Cbfe23, DSM 52764, was recently reported to produce the novel diterpene cystodienoic acid (7). Here, we report a draft genome sequence for *C. ferrugineus* strain Cbfe23 collected in an effort to explore myxobacterial natural products.

C. ferrugineus was acquired from the German Collection of Microorganisms (DSM) in Braunschweig (DSM 52764) and cultivated using the suggested medias and conditions. Genomic DNA was isolated using a GeneJET genomic DNA purification kit (ThermoFisher). Sequencing was performed at MR DNA (Shallowater, TX) using an Illumina HiSeq system. The libraries were prepared using a Nextera DNA sample preparation kit (Illumina) following the manufacturer's user guide. Following the library preparation, the final concentration of the library (13.0 ng/μL) was measured using the Qubit dsDNA HS assay kit (Life Technologies), and the average library size (845 bp) was determined using the Agilent 2100 Bioanalyzer (Agilent Technologies). The libraries were pooled and diluted (to 10.0 pM) and sequenced paired end for 500 cycles with an average coverage of 50×. An initial annotation was completed using the Rapid Annotations using Subsystems Technology (RAST) server (8) with further annotation requested by the NCBI Prokaryotic Genome Annotation Pipeline (9, 10). The draft genome contains 12,051,756 bp with 74 identified RNAs, 9,992 coding sequences, and a 68.5% G+C content across 42 contigs containing protein-encoding genes.

Using antiSMASH version 3.0.5, 44 unique secondary metabolite biosynthetic pathways were identified including pathways for 10 terpenes, eight nonribosomal peptides, seven bacteriocins, four lantipeptides, four polyketides, three hybrid nonribosomal peptide-polyketides, and three microcins (11). Sequence homology between the identified pathways and reported myxobacterial biosynthetic pathways suggests that *C. ferrugineus* may produce metabolites structurally similar to tubulysin, myxochelin, and cystobactamid natural products (3, 12, 13). We believe the draft genome sequence will help facilitate characterization of myxobacterial secondary metabolism.

Accession number(s). This whole-genome shotgun project has been deposited in DDBJ/ENA/GenBank under the accession number MPIN00000000. The version described in this paper is the first version, MPIN00000000.1.

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