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Genome Sequence of the Facultative Anaerobe *Oerskovia enterophila* DFA-19 (DSM 43852^T)

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Here, we report the draft genome sequence of *Oerskovia enterophila* DFA-19 (DSM 43852^T), a facultative anaerobe soil bacterium, which was originally isolated from millipede feces and first described as *Promicromonospora enterophila*. The genome consists of a circular chromosome comprising approximately 4.65 Mb and 4,044 predicted protein-encoding genes.

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The genus *Oerskovia* was first characterized in 1970 by Prauser et al. (1), and members are described as Gram-positive bacteria that show extensively branching vegetative hyphae, growing on and into the agar. In addition, a very variable cell shape was observed (1). The species *O. enterophila* was first described as *Promicromonospora enterophila* due to microscopic structures erroneously identified as spores and the supposed close relationship to the type strain *Promicromonospora citrae* (2). Subsequent phylogenetic analysis revealed *P. enterophila* as a member of the genus *Oerskovia*. Moreover, the type strain of *O. turbata* shows 99.6% 16S rRNA gene sequence similarity with the type strain of *P. enterophila*, and thus both are close phylogenetic neighbors (3).

For genome sequencing of *O. enterophila* DFA-19, the strain was received from the Deutsche Sammlung von Mikroorganismen und Zellkulturen (DSMZ) and was inoculated in 5 ml trypticase soy-yeast extract medium (medium 92; DSMZ) and incubated overnight at 30°C. Whole-genomic DNA was isolated using the MasterPure Gram-positive DNA purification kit (Epicentre, Madison, WI, USA). Isolated DNA was used to generate Illumina shotgun sequencing libraries. Sequencing was performed by employing a MiSeq system using a MiSeq reagent kit version 3 (600 cycles), as recommended by the manufacturer (Illumina, San Diego, CA, USA). Sequencing resulted in 2,498,636 paired-end reads that were trimmed using Trimmomatic version 0.32 (4). *De novo* assembly performed with the SPAdes genome assembler software version 3.8.0 (5) yielded 114 contigs (>500 bp) with an average coverage of 90.5-fold. The genome of *O. enterophila* DFA-19 (DSM 43852^T) consists of a circular chromosome of 4.65 Mb with an overall G+C content of 72.28%. Gene prediction and annotation were performed using the Prokka rapid prokaryotic genome annotation tool (6). The genome harbored three rRNA genes, 58 tRNA genes, 2,820 protein-encoding genes with predicted functions, and 1,224 genes coding for hypothetical proteins.

Analysis of the genome revealed that *O. enterophila* DFA-19 has several genes encoding enzymes involved in the degradation of plant polymers that are ubiquitously available in soils, such as cellulose, starch, or chitin (7–9). Accordingly, *O. enterophila* DFA-19 was first isolated from millipede feces and described as a soil bacterium (2). Potential genes encoding two endoglucanases and one cellulose 1,4-beta-cellobiosidase are present in the *O. enterophila* DFA-19 genome. Furthermore, putative genes encoding amylases for the conversion of starch or glycogen to dextrin were identified. Additionally, genes encoding chitinases, chitin-binding proteins, and a chitobiose phosphorylase were also present in the genome.

Accession number(s). This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number MAQA00000000. The version described in this paper is the first version, MAQA01000000.

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