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Draft Genome Sequence of *Kocuria rhizophila* P7-4[▽]

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We report the draft genome sequence of *Kocuria rhizophila* P7-4, which was isolated from the intestine of *Siganus doliatus* caught in the Pacific Ocean. The 2.83-Mb genome sequence consists of 75 large contigs (>100 bp in size) and contains 2,462 predicted protein-coding genes.

Kocuria rhizophila is a coccoid, Gram-positive, spherical, saprotrophic bacterium that belongs to the suborder *Micrococcineae* (9–11). *Kocuria* species are highly adapted to their ecological niches, and *K. rhizophila* in particular has important industrial applications, exhibiting tolerance of organic solvents, making it useful for developing bacterial bioconversion systems (5). The type strain of *K. rhizophila* P7-4 was isolated from the intestine of a pencil-streaked rabbitfish (*Siganus doliatus*) caught in the Pacific Ocean. This bacterium is resistant to low water potentials and can tolerate desiccation as well as salt concentrations up to 10% NaCl in growth medium (6, 7). Genomic DNA was extracted from the cultured bacteria using the alkaline lysis method, with slight modifications (3).

In this report, we present the draft genome sequence of the *K. rhizophila* strain, which consisted of 75 contigs. The whole-genome shotgun strategy using a Roche-454 Titanium pyrosequencing system (337,868 reads totaling ~138 Mb; ~51.4-fold coverage of the genome) was applied using Roche software according to the manufacturer's instructions. Quality filtered reads were assembled *in silico* using the 454 Newbler 2.3 assembler, giving 75 contigs (~2.83 Mb) >100 bp in size and 23 contigs (2.80 Mb) >2,000 bp in size. Open reading frames (ORFs) were predicted using the Glimmer version 3.02 modeling software package (4) and RNAmmer version 1.2 (8) and searched using the Clusters of Orthologous Groups (COGs) databases (12). The draft genome sequence was also uploaded to the Rapid Annotation Using Subsystem Technology (RAST) server to check the annotated sequences and screen for noncoding rRNAs and tRNAs.

The percentage of GC content in all contigs was 70.4%. The predicted proteins were annotated using Basic Local Alignment Search Tool (BLAST) (1) and the RAST server (2). Overall, 38.6% ($n = 29$) of the ORFs were annotatable with known proteins. The genome contained 2,462 protein-coding genes, 2 copies of the 5S rRNA gene, 49 tRNA genes, 4 copies of LSU-SSU ribosomal proteins, and 55 copies of RNA genes. There were 2,462 possible ORFs in 29 contigs, with a size range between 15 and 6,192 bp. There were only 159 ORFs with lengths >2,000 bp, and the average ORF was 989.7 bp.

The genome contains putative genes for membrane transport of the major facilitator superfamily, 76 transcriptional regulators, 27 integral membrane proteins, and 16 glycosyl transferases. There are 232 subsystems represented in the genome, and we used this information to reconstruct the metabolic network. Interestingly, many of the amino acid derivatives and the signal transduction profile included genes involved in fatty acid biosynthesis FASII, biotin biosynthesis, arginine biosynthesis, isoleucine degradation, methionine biosynthesis, and molybdenum cofactor biosynthesis. Genes not yet conclusively identified in the inventory include those that likely belong to carbohydrate and amino acid derivative subsystems. These may be identified upon finalization of the genome.

Nucleotide sequence accession number. The draft genome sequence of *Kocuria rhizophila* P7-4 is available in GenBank under the accession number AFID00000000.

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