

Genome Sequence of a Gamma- and UV-Ray-Resistant Strain, *Deinococcus wulumuqiensis* R12

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***Deinococcus wulumuqiensis* R12, isolated from radiation-polluted soil, is a red-pigmented strain of the extremely radioresistant genus *Deinococcus*. It contains a major carotenoid, namely, deinoxanthin. Here, we present a 3.39-Mb assembly of its genome sequence, which might provide various kinds of useful information related to *Deinococcus*, such as about the key enzymes of its radioresistance mechanism and carotenoid biosynthetic pathways.**

Received 20 March 2013 Accepted 27 March 2013 Published 9 May 2013

Citation Xu X, Jiang L, Zhang Z, Shi Y, Huang H. 2013. Genome sequence of a gamma- and UV-ray-resistant strain, *Deinococcus wulumuqiensis* R12. *Genome Announc.* 1(3): e00206-13. doi:10.1128/genomeA.00206-13.

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The genus *Deinococcus* is particularly interesting since a large number of its members are extremely radioresistant (1, 2). *Deinococcus radiodurans* R1 was the first of the deinobacteria to be discovered and was isolated from canned meat that had spoiled following exposure to X rays (3). This strain shows extraordinary resistance to ultraviolet and gamma radiation, desiccation, hydrogen peroxide, and many other DNA-damaging agents (4, 5). For example, the resistance to UV irradiation of *D. radiodurans* is 20 times higher than that of *Escherichia coli*, while the resistance to ionizing radiation is 200 times higher than that of *E. coli* (6).

We recently characterized a new bacterial species, *Deinococcus wulumuqiensis* strain R12, which showed that it warrants recognition as a novel species in the genus *Deinococcus*. It was isolated from the radiation-contaminated soils in the Xinjiang Uigur Autonomous Region of northwest China. Strain R12 is a Gram-positive, reddish orange, non-spore-forming coccus, with gamma radiation resistance to >10 kGy and UV resistance to >700 J m⁻² (7). This strain shows a higher tolerance for gamma radiation and UV light than does *D. radiodurans* R1. R12 is red pigmented because of its carotenoid biosynthetic abilities for cellular protection (8). However, its carotenoid biosynthetic pathways and radioresistance mechanism are not clear. The resistance of R12 and its biosynthetic pathways might be the result of multiple closely coordinated mechanisms involving numerous proteins. Studies that aim to understand these detailed mechanisms are now focused on the analysis and annotation of a complete genome sequence.

Here, we present the draft genome sequence of strain R12, obtained using the Illumina HiSeq 2000 next-generation DNA platform. Sequencing was performed by Shanghai Majorbio Pharm Technology Co., Ltd., with a paired-end library. The reads were trimmed and *de novo* assembled with SOAPdenovo (<http://soap.genomics.org.cn/soapdenovo.html>). Open reading frames (ORFs) were identified by the program Glimmer (<http://www.cbcb.umd.edu/software/glimmer/>). These ORFs were further an-

notated by comparison with the NCBI NR database and BLASTp (BLAST 2.2.24). The rRNAs were predicted by RNAmmer (9), and tRNAs were predicted by tRNAscan (10).

The draft genome sequence of strain R12 comprises 3,391,664 bp, which is assembled into 239 contigs. The N_{50} quality measurement of the contigs is 31,304 bp, with an average contig size of 23 kb, and the largest contig assembled is approximately 133 kb. It has a G+C content of 66.38%. There are 3,160 predicted protein-coding sequences in the genome sequence. The chromosome has 3 rRNA operons and 45 tRNAs as predicted by RNAmmer and tRNAscan, respectively.

The genome sequence of strain R12 serves as a foundation for further investigation of the molecular basis of its resistance to DNA-damaging agents. Further analysis of the genome sequence might also provide other useful information related to R12, such as identifying the genes that are involved in its radioresistance mechanism and carotenoid biosynthetic pathways.

Nucleotide sequence accession numbers. This Whole-Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. [APCS000000000](https://www.ncbi.nlm.nih.gov/nuccore/APCS000000000). The version described in this paper is the first version, accession no. [APCS010000000](https://www.ncbi.nlm.nih.gov/nuccore/APCS010000000).

ACKNOWLEDGMENTS

This work was supported by the National Science Foundation for Distinguished Young Scholars of China (no. 21225626), the National High Technology Research and Development Program of China (2012AA021705, 2012AA022101), and the National Natural Science Foundation of China for Young Scholars (no. 21106064).

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