



Draft Genome Sequence of the Radioresistant Bacterium *Deinococcus aerius* TR0125, Isolated from the High Atmosphere above Japan

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ABSTRACT *Deinococcus aerius* strain TR0125 is a bacterium isolated from the high atmosphere above Japan that shows strong resistance to desiccation, UV-C, and gamma radiation. Here, we report the draft genome sequence of *D. aerius* (4.5 Mb), which may provide useful genetic information supporting its biochemical features.

Members of the genus *Deinococcus* are best known as radioresistant bacteria, and about 70 *Deinococcus* species have been isolated from various environments over 60 years (<http://www.bacterio.net/deinococcus.html>) since the first isolation of *Deinococcus radiodurans* (1). Recently, the whole-genome sequences of some *Deinococcus* bacteria were determined. These provide important information to elucidate the unique features of *Deinococcus* bacteria. *Deinococcus aerius* strain TR0125 was initially isolated as an orange-pigmented, nonmotile, desiccation-tolerant, UV- and gamma-resistant, and coccoid bacterium from the upper troposphere in Japan (2–4).

The draft genome sequence of *D. aerius* strain TR0125 had a total length of 4,524,446 bp, with 50-fold average coverage and an average G+C content of 68.0%, and it comprised 43 large contigs (>500 bp). The sequences obtained with the Roche GS FLX+ and GS Junior+ systems were assembled using the GS *De Novo* Assembler version 3.0. Automatic annotation was performed using the Microbial Genome Annotation Pipeline (5), which predicted a total of 4,446 protein-coding sequences (CDSs). Moreover, all CDSs were manually validated. The tRNA and rRNA operon (5S/16S/23S) detection was performed using the tRNAscan software version 1.23 (6) and RNAmmer software version 1.2 (7), which predicted a total of 52 tRNAs and 1 rRNA operon, respectively.

Since *D. aerius* strain TR0125 was negative for nitrate reduction, urease, arginine hydrolase, and ornithine decarboxylase activities and was unable to use some carbon sources (3), the genes regarding these biochemical features were searched. The annotation of the draft genome sequence indicates that strain TR0125 does not possess some genes (*narB*, *ureAB*, *ureC*, *arcA*, *nosA*, *nylA*, *speC*, *speF*, *gpmA*, and *betB*) involved in nitrogen, arginine, ornithine, and carbohydrate metabolism. Strain TR0125 exhibited much slower growth than some *Deinococcus* species (e.g., *D. radiodurans*, *D. grandis*, and *D. geothermalis*) (4). This feature might be related to the fact that the strain TR0125 genome possesses only one rRNA operon as an important component for protein synthesis, although many *Deinococcus* bacteria possess multiple rRNA operons (8, 9).

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The relationship between the number of rRNA operons and the cell growth rate in other bacteria, such as *Bacillus subtilis* and *Escherichia coli*, has also been reported (10, 11). Like some *Deinococcus* species (e.g., *D. deserti*, *D. gobiensis*, and *D. maricopensis*, but excluding *D. radiodurans*, *D. grandis*, and *D. geothermalis*), the strain TR0125 genome encodes a DNA photolyase involved in UV resistance. Naturally, strain TR0125 possesses genes (including *pprI*, *pprA*, *recA*, *ddrA*, and *ddrO*) regarding the radiation/desiccation response system (12), which is the best-known unique feature of *Deinococcus* bacteria. In the future, the draft genome sequence of *D. aerius* strain TR0125 will be useful to elucidate the common principles of its radioresistance based on the highly efficient DNA repair mechanisms in *Deinococcus* bacteria by the comparative analysis of genomic sequences.

Accession number(s). The draft genome sequence of *D. aerius* strain TR0125 was deposited at DDBJ/EMBL/GenBank under the accession number [BFAG00000000](https://www.ncbi.nlm.nih.gov/nuccore/BFAG00000000). The version described in this paper is the first version, BFAG01000000.

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