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Draft Genome Sequence of the Radioresistant Bacterium *Deinococcus grandis*, Isolated from Freshwater Fish in Japan

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***Deinococcus grandis* is a radioresistant bacterium isolated from freshwater fish in Japan. Here we reported the draft genome sequence of *D. grandis* (4.1 Mb), which will be useful for elucidating the common principles of radioresistance in *Deinococcus* species through the comparative analysis of genomic sequences.**

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Although the radioresistance of organisms varies greatly among species, there is a group of bacteria that shows extraordinary resistance to radiation. Members of the genus *Deinococcus* are the best known as radioresistant bacteria, and more than 50 *Deinococcus* species have been isolated from various environments (http://www.bacterio.net/deinococcus.html). Radioresistance in *Deinococcus* species is attributed to their highly proficient DNA repair capacity (1–4). *Deinococcus grandis* was initially isolated as a Gram-negative, red-pigmented, radioresistant, rod-shaped bacterium from freshwater fish and named *Deinobacter grandis* (5). Later, on the basis of 16S rRNA gene sequence analysis, *Deinobacter grandis* was transferred to the genus *Deinococcus* as *Deinococcus grandis* (6).

The draft genome sequence of *D. grandis* ATCC 43672 was 4,092,497 bp, with an average G+C content of 67.5%, and comprised 4 circular contigs (3,250,361 bp, 389,340 bp, 91,291 bp, and 8,055 bp) and 3 linear contigs (98,058 bp, 108,779 bp, and 146,613 bp). The linear contigs composed a single circular contig. This suggests that the genome structure of *D. grandis* is made up of multiple circular DNAs, as is the case in other *Deinococcus* species (*D. radiodurans*, *D. geothermalis*, *D. deserti*, *D. maricopensis*, *D. proteolyticus*, *D. gobiensis*, and *D. peraridilitoris*) (7). The sequences were obtained with the Roche GS Junior and Applied Biosystems 3500 genetic analyzers and assembled using the GS DeNovo assembler ver. 3.0 and DNASTAR SeqMan Pro ver. 12.2.0. Automatic annotation was performed using the Microbial Genome Annotation Pipeline (8), which predicted a total of 4,043 protein-coding sequences (CDSs). Moreover, all CDSs were manually validated. The tRNA and rRNA operon (5S/16S/23S) detections were performed using the tRNA scan software ver. 1.23 (9) and RNAmmer software ver. 1.2 (10), which predicted a total of 51 tRNAs and 4 rRNA operons, respectively.

The annotation of the draft genome sequence indicates that *D. grandis* possesses a DNA damage response regulator (encoded by a *pprI* homolog) and radiation-desiccation response (RDR) regulons (*recA*, *ddrA*, *ddrO*, *pprA*, and *gyrA* homologs, etc.), which are involved in the unique radiation/desiccation response system in *D. radiodurans* (4). *D. grandis* seems to employ the same radioresistance mechanisms as *D. radiodurans*. In future, the draft genome sequence of *D. grandis* will be useful for elucidating the common principles of radioresistance based on the extremely efficient DNA repair mechanisms in *Deinococcus* species through comparative analysis of genomic sequences. Furthermore, as the *D. grandis* host vector systems have already been developed (11), this genomic information will also be helpful for improvement of the host toward the efficient expression of endogenous and foreign genes.

Nucleotide sequence accession numbers. The draft genome sequence of *D. grandis* was deposited at DDBJ/EMBL/Genbank under the accession number BCMS00000000. The version described in this paper is the first version: BCMS00000000.1.

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REFERENCES

1. **Cox MM, Battista JR**. 2005. *Deinococcus radiodurans*—the consummate survivor. Nat Rev Microbiol **3**:882–892. http://dx.doi.org/10.1038/nrmicro1264.
2. **Blasius M, Sommer S, Hübscher U**. 2008. *Deinococcus radiodurans*: what belongs to the survival kit? Crit Rev Biochem Mol Biol **43**:221–238. http://dx.doi.org/10.1080/10409230802122274.
3. **Misra HS, Rajpurohit YS, Kota S**. 2013. Physiological and molecular basis of extreme radioresistance in *Deinococcus radiodurans*. Curr Sci **104**: 194–205.

4. **Ishino Y, Narumi I**. 2015. DNA repair in hyperthermophilic and hyperradioresistant microorganisms. Curr Opin Microbiol **25:**103–112. http://dx.doi.org/10.1016/j.mib.2015.05.010.
5. **Oyaizu H, Stackebrandt E, Schleifer KH, Ludwig W, Pohla H, Ito H, Hirata A, Oyaizu Y, Komagata K**. 1987. A radiation-resistant rod-shaped bacterium, *Deinobacter grandis* gen. nov., sp. nov., with peptidoglycan containing ornithine. Intl J Sys Bact **37:**62–67. http://dx.doi.org/10.1099/00207713-37-1-62.
6. **Rainey FA, Nobre MF, Schumann P, Stackebrandt E, da Costa MS**. 1997. Phylogenetic diversity of the deinococci as determined by 16S ribosomal DNA sequence comparison. Int J Syst Bacteriol **47:**510–514. http://dx.doi.org/10.1099/00207713-47-2-510.
7. **Yuan M, Chen M, Zhang W, Lu W, Wang J, Yang M, Zhao P, Tang R, Li X, Hao Y, Zhou Z, Zhan Y, Yu H, Teng C, Yan Y, Ping S, Wang Y, Lin M**. 2012. Genome sequence and transcriptome analysis of the radioresistant bacterium *Deinococcus gobiensis*: insights into the extreme environmental adaptations. PLoS One **7:**e34458. http://dx.doi.org/10.1371/journal.pone.0034458.
8. **Sugawara H, Ohyama A, Mori H, Kurokawa K**. 2009. Microbial genome annotation pipeline (MiGAP) for diverse users, abstr S-001, pp 1–2. Abstr. 20th Int Conf Genome Informatics, Kanagawa, Japan.
9. **Schattner P, Brooks AN, Lowe TM**. 2005. The tRNAscan-SE, snoscan and snoGPS web servers for thse detection of tRNAs and snoRNAs. Nucleic Acids Res **33:**W686–W689. http://dx.doi.org/10.1093/nar/gki366.
10. **Lagesen K, Hallin P, Rødland EA, Staerfeldt H-H, Rognes T, Ussery DW**. 2007. RNAmmer: consistent and rapid annotation of ribosomal RNA genes. Nucleic Acids Res **35:**3100–3108. http://dx.doi.org/10.1093/nar/gkm160.
11. **Satoh K, Tu Z, Ohba H, Narumi I**. 2009. Development of versatile shuttle vectors for *Deinococcus grandis*. Plasmid **62:**1–9. http://dx.doi.org/10.1016/j.plasmid.2009.01.005.