Research Square

Preprints are preliminary reports that have not undergone peer review.
They should not be considered conclusive, used to inform clinical practice,
or referenced by the media as validated information.

Comparative genome and protein analysis of Deinococcus radiodurans on heavy metal and radiation resistance

Minde Hailu

mindhailu@gmail.com

Debark University

Seid Mohammed

Adama Science and Technology University

Systematic Review

Keywords: D. radiodurans, Genome, Proteome, phylogenetic

Posted Date: October 7th, 2026

DOI: https://doi.org/10.21203/rs.3.rs-8121068/v1

License: This work is licensed under a Creative Commons Attribution 4.0 International License.
Read Full License

Additional Declarations: No competing interests reported.

Abstract

D.radiodurans is robust bacteria that carry an extraordinary DNA repair system. The presence of multiple components distributed on the chromosomes and megaplasmid enables them to survive in a variety of environments under conditions of starvation, oxidative stress, and high amounts of DNA damage. Although recent developments in genes and genomic sequencing have significantly increased our knowledge of microbes, studies on the D. radiodurans R1 DSM 20539T using an integrated comparative genomics approach are scarce. So the study aims to analyze the genome and proteome of the D. radiodurans R1 DSM 20539T for heavy metal and radiation resistance by applying the integrated comparative genomics approach, such as phylogenic analysis and average nucleotide identity (ANI). The Study was conducted by extracting the 16S rRNA sequencing of organisms, and reannotation was done to identify noble genes that encode heavy metal resistance proteins. The phylogenetic tree with the maximum likelihood method showed that D. radiodurans DSM 20539T formed clades with D. wulumuqiensis R12T. The ANI value also indicated that the OrthoANI values of D. wulumuqiensis R12T were highest with strain D. radiodurans R1 DSM 20539T (85.60%). Generally, based on analysis of 16S rRNA gene sequence and OrthANI values, D. radiodurans R1 DSM 20539T is phylogenetically very closely related to D. wulumuqiensis R12T, where the OrthANI value is 85.56%, which is higher than all values.

1. Introduction

Deinococcus spp. are robust bacteria that carry an extraordinary DNA repair system that enables them to endure in a variety of environments, including hot springs, radiation-contaminated areas, Antarctic soils, deserts, etc. They also exhibit some of the highest levels of ionizing radiation resistance known in nature. The highly effective radiation protection mechanisms of *Deinococcus* rely on a combination of passive and active defense mechanisms, such as DNA damage repair by self-repair, effective cellular damage clearance mechanisms (hydrolysis of damaged proteins, overexpression of repair proteins, etc.), and efficient clearance of reactive oxygen species (ROS). These methods help *Deinococcus* cells withstand oxidation, radiation, and desiccation to a high degree (Jin *et al.,* 2019).

The model *Deinococcus* species, *D. radiodurans,* is most recognized for its extreme resistance to the lethal effects of ionizing radiation (Liu *et al.,* 2003). The first of the Deinobacteria to be identified was the gram-positive aerobic bacterium *Deinococcus radiodurans* strain R, which was found in Oregon in 1956. *Deinococcus radiodurans* R1 has an extraordinary resistance to gamma radiation and a wide range of other DNA-damaging conditions, including desiccation and oxidizing agents. The other, a second strain of *D. radiodurans* (SARK), was discovered as an air contaminant in a hospital in Ontario. Then, six closely related radiation-resistant species have been identified: *Deinococcus radiopugnans* from haddock tissue; *Deinococcus radiophilus* from Bombay duck; *Deinococcus proteolyticus* from the feces of Lama glama; the rod-shaped *Deinococcus grandis* from elephant feces; and the two thermophilic species *Deinococcus geothermalis* and *Deinococcus murrayi* from hot springs in Portugal and Italy, respectively (Makarova *et al.,* 2001).

Similar to other bacteria, *Deinococcus* spp. also exhibit a RecA-dependent DNA repair mechanism several hours after irradiation; however, a RecA-independent mechanism is activated in *D. radiodurans* during the first 1.5 hours after irradiation. They were also able to reconstruct an intact genome in a few hours from several hundred DNA fragments. Furthermore, numerous genes are overexpressed after exposure to radiation, and two proteins, namely, DdrO and IrrE, play a major role in regulating the expression of approximately twenty genes. The transcriptional repressor DdrO blocks the expression of these genes under normal growth conditions. After exposure to genotoxic agents, the IrrE metalloprotease cleaves DdrO and relieves gene repression (Eugénie *et al.,* 2021).

In *Deinococcus*, the main response pathway to genotoxic conditions is regulated by the constitutively expressed metalloprotease IrrE and the transcriptional repressor DdrO. Once cells are exposed to genotoxic stress conditions, IrrE cleaves the C-terminal region of DdrO, abolishing its DNA binding properties and leading to the expression of the genes repressed by DdrO. Transcriptome analyses of *D. radiodurans* after exposure to gamma radiation showed induced expression of many genes, including several required for DNA repair (e.g., *recA*). Several highly induced novel genes were also identified (e.g., *ddrA*, *ddrP*, *pprA, etc.*). The expression of *recA* and other DNA repair genes is controlled by LexA, the repressor of the well-known SOS response, but LexA is irrelevant to *recA* induction in *D. radiodurans* (Blanchard *et al.,* 2017).

The complete genome sequence of the radiation-resistant bacterium *D. radiodurans* R1 is composed of two chromosomes, chromosomes 1 and 2, and two plasmids: a megaplasmid (pMP1) and a small plasmid (pCP1). The presence of multiple components distributed on the chromosomes and megaplasmid enables *D. radiodurans* to survive under conditions of starvation, oxidative stress, and high amounts of DNA damage. *D. radiodurans* represents an organism in which all systems for DNA repair, DNA damage export, desiccation and starvation recovery, and genetic redundancy are present in one cell (White *et al.,* 1999).

Recent developments in genes and genomic sequencing have significantly increased our knowledge of microbes. Nowadays, an integrated comparative genomics approach that includes phylogeny analysis, average amino acid identity (AAI), average nucleotide identity (ANI), core and pan-genome analysis, and DNA-DNA hybridization (DDH) is increasingly influencing our understanding of microbes (Gupta *et al.,* 2023). To date, studies on comparative genome and proteome analysis of heavy metal and radiation-resistant *D. radiodurans* strains using an integrated comparative genomics approach are scarce. Therefore, this study aims to analyze the genome and proteome of *D. radiodurans* strains on heavy metal and radiation resistance by applying the integrated comparative genomics approach, such as phylogenic analysis and average nucleotide identity (ANI).

2. Objectives

2.1. General objective

To compare the genome and protein analysis of *D. radiodurans* strain on heavy metal and radiation resistance.

2.2. Specific objectives

- To identify heavy metal and radiation resistance-related genomes and proteomes of *D. radiodurans*
- To predict the phylogenetic history of heavy metal and radiation resistance in *D. radiodurans*

3. Materials and methods

3.1. 16 S rRNA phylogeny

Acomplete genome of *D. radiodurans* R1 DSM 20539^T and the other five (such as *D. aquaticus* strain PB-314 ^{T}, *D. deserti* VCD115 ^{T}, *D. gobiensis* I-0 ^{T}, *D. grandis* ATCC 43672 ^{T}, and *D. wulumuqiensis* R12^T) were retrieved from the NCBI database (https://www.ncbi.nlm.nih.gov), and the 16S rRNA sequences of these organisms were extracted from the EZbiocloud database(https://www.ezbiocloud) using the ContESt 16S algorithmby utilizing the retrieved sequence of these organisms (Lee *et al.,* 2017). A phylogenetic relationship was drawn using the Maximum Likelihood Tree method and Tamura-Nei model by aligning the 16S rRNA gene sequences extracted from this database using ClustalW by MEGA 11 software with a bootstrap of 1000 replicates.

3.2. Genome-based comparisons

For genomic comparison of *D. radiodurans* strain R1 DSM 20539^T, the available genomes of five strains with best hits, including, D. *aquaticus* strain PB-314 ^{T}, *D. deserti* VCD115 ^{T}, *D. gobiensis* I-0 ^{T}, *D. grandis* ATCC 43672 ^{T}, and *D. wulumuqiensis* R12 ^{T} were selected. For each selected genome, OrthoANI values (%) and the Genome-to-Genome Distance Calculator (GGDC) were calculated by utilizing OrthoANI tools (OAT).

3.3. Annotation

Genome reannotation of *D. radiodurans* strain R1 DSM 20539^T was done by utilizing Rapid Annotation Subsystems Technology (RAST). By doing so, these specific heavy metal genes (which encode tellurite resistance proteins) were identified and utilized to construct a phylogenic tree to depict the relationship between these genes. Additionally, the SEED Web site (SEED viewer) was used to compare the genomic neighborhood of a given gene across genomes.

3.4. Three-dimensional structure generation

The 3D structure of the desiccation and radiation resistance proteins of *D. radiodurans* R1 DSM 20539^{T}was predicted by online tools, specifically by SWISS-MODEL (https://swissmodel.expasy.org/interactive/2SmbLC/models). Modelling was done by uploading the target protein sequence to SWISS-MODEL, and then the modelling process was started by searching for a template with an identified and known three-dimensional structure.

4. Results

4.1. Genomic features of *D. radiodurans* R1 DSM 20539^{T} from annotation

The genome of strain *D. radiodurans* R1 DSM 20539^{T} has a total length of 3, 279, 598 bp and a GC content of 66.7 %. The reannotation bacterial genome predicted a total of 3220 coding sequences (CDS), 57 RNA genes and 255 numbers of subsystems (Table 1). Furthermore, the reannotation undertaken by using rapid annotation subsystem technology (RAST) revealed that notable gene contents for stress response (23 genes) and other such as RNA metabolism, DNA metabolism (38 genes), and metabolism of aromatic compounds (15 genes) as depicted on Figure 1.

Table 1: Genome statistics from annotation

Features	Value
Genome size(pb)	3, 279, 598
GC content	66.7
N50	2, 644, 543
L50	1
Number of Contigs	4
Number of subsystems	255
Number of coding sequence	3, 220
Number of RNAs	57

4.2. Genome based comparison of six *Deinococcus* species

The general features of the six *Deinococcus* species genomes are summarized in Table 2. The whole genome sequences of *D. radiodurans* R1 DSM 20539^{T} were composed of 3279598 bp with 66.7 GC content. The genome size and GC content of *D. radiodurans* R1 DSM 20539^{T} are more related to *D. wulumuqiensis* R12 ^{T} than the other, while the number of their Contigs shows variation. The genome size

of *D. wulumuqiensis* R12 was 3505947 bp with 66.0 GC content. The number of Contigs in *D. radiodurans* R1 DSM 20539^T is equal to that in *D. deserti* VCD115 ^{T} (Table 2).

The length of the 16S rRNA gene sequence of *D. radiodurans R1* DSM 20539^T is 1,502 bp. This sequence was compared with other five strains of *Deinococcus species,* and the result indicates that *D. radiodurans* R1 DSM 20539^T shared high 16S rRNA gene sequence similarities with *D. deserti* VCD115 (100.0% 16S rRNA gene similarity), *D. wulumuqiensis* R12 ^{T} (99.6%), *D. grandis* ATCC 43672 ^{T} (99.4%), *D. aquaticus* PB-314 ^{T} (98.3%), and D. *gobiensis* I-0 ^{T} (98.0%) (Table 2).

Table 2: Genome based comparison of *Deinococcus* type strains

Species	Genome size (bP)	No. of Contigs	GC content	Length of rRNA	Similarity
D. aquaticus strain PB-314^T	3, 874, 407	5	68.8	1, 427	98.3%
D. deserti VCD115^T	3, 855, 329	4	63.0	1, 428	100.0%
D. gobiensis I-0^T	4, 406, 036	7	69.2	1, 428	98.0%
D. grandis ATCC 43672^T	4, 092, 497	7	69.9	1, 425	99.4%
D. radiodurans R1 DSM 20539^T	3, 279, 598	4	66.7	1, 502	-
D. wulumuqiensis R12^T	3, 505, 947	5	66.0	1, 424	99.6%

4.3. ANI analyses

A genome-based comparison between *D. radiodurans* R1 DSM 20539^T and other five *Deinococcus* species was calculated with OrthoANI program (Lee *et al.,* 2015) and the resulting ANI values and the phylogenomic tree obtained were given below (Figure 2).

Heatmap shows the average nucleotide percentage similarity by (OrthoANI) between *D. radiodurans* strains R1 DSM 20539^T and the other five (*D. aquaticus* strain PB-314 ^{T}, *D. deserti* VCD115 ^{T}, *D. gobiensis* I-0 ^{T}, *D. grandis* ATCC 43672 ^{T}, *D. radiodurans* DSM 20539 ^{T} and *D. wulumuqiensis* R12 ^{T}) strains. The OrthoANI similarity between *D. radiodurans* R1 DSM 20539^T and all the other strains were in the range of 74.43%–85.60%. At the same time, OrthoANI values of strain *D. wulumuqiensis* R12 ^{T} were highest with the *D. radiodurans* R1 DSM 20539^T (85.60 %). According to these value, it confirmed that these strains aren't belongs to the strains of the same species.

4.4. Phylogenetic tree analysis

With a bootstrap value of 1000, a phylogenetic tree constructed using the maximum likelihood technique demonstrated that *D. radiodurans* R1 DSM 20539^T forms clades with *D. wulumuqiensis* R12 ^{T} (Figure 3). According to comparative 16S rRNA gene sequencing results, D. radiodurans R1 DSM 20539^T is also closely related to *D. gobiensis* I-0 ^{T} and *D. aquaticus* PB-314 ^{T}.

4.6. Phylogenetic analysis of genes

The identified tellurite resistance genes were utilized to construct a phylogenetic tree that is used to depict the relationship between these genes (Figure 4). A total of four copies of the tellurium resistance protein *TerD* were identified by reannotation of the whole genome sequence of *D. radiodurans* R1 DSM 20539T using RAST, which are different in the length of the amino acid sequence. The organization of tellurite resistance genes (including, *Ter P, Ter D, Ter B,* and *Ter A*) was shown by their order (Figure 5).

4.7. Three dimensional model generation

In homology modelling, structural templates that have the highest sequence homology with the target protein (desiccation and radiation resistance protein) are used to predict the three-dimensional structure. The sequence alignment search of desiccation and radiation resistance proteins was carried out against the three-dimensional structures deposited in the Protein Data Bank (PDB). The sequence alignment search generated a total of 50 templates, and three models were identified. Desiccation and radiation resistance protein (*DR_1769*) from *Deinococcus radiodurans* strain ATCC 13939/DSM 20539^T was found to be the best alignment with 100% sequence identity (Figure 6).

5. Discussion

In this study, genomic features and the phylogenetic relationships between six type strains of *Deinococcus,* including *D. radiodurans* R1 DSM 20539^T, were investigated. The whole-genome sequence of *D. radiodurans* R1 DSM 20539^T has been deposited at NCBI under the accession number NZ_CP038663.1. The whole-genome sequence was composed of 3279598 bp with 66.7% GC content (Table 1). It is composed of four Contigs. The genome has 3220 protein-coding genes, 57 RNAs, and 255 subsystems. Among the protein-coding genes, many of them were functionally annotated, while some weren't. This finding indicates that a considerable portion of the genes still need to be further discovered to reveal their functions.

Furthermore, the genome size of *D. radiodurans* R1 DSM 20539^T is the smallest among the genomes that are currently studied, while *D. gobiensis* I-0^T has the largest (Table 2). Their number of Contigs and GC

content also show great variation; these**findings suggest that the two strains are distantly related to each other,** as supported by the ANI value of 77.35% compared to *D. wulumuqiensis* R12^{T8} (85.6%).

The ANI value between the genomes of *D. radiodurans* R1 DSM 20539^{T} and *D. wulumuqiensis* R12^{T} was 85.60%, as analyzed by the software OAT, which was higher than all type strains. This indicates that *D. radiodurans* R1 DSM 20539^{T} is more related to *D. wulumuqiensis* R12^{T}; the result is supported by the 16S rRNA sequence as both strains form a clade. In contrast to this, the similarity of rRNA between these type strains indicates that the similarity between *D. radiodurans* R1 DSM 20539^{T} and *D. wulumuqiensis* R12^{T} was 99.6%, while a higher similarity is seen with *D. deserti* VCD115^{T}. Phylogenetic analysis shows that *D. radiodurans* R1 DSM 20539^{T} and *D. deserti* VCD115^{T} are not particularly close and form a clade. Nevertheless, their rRNA has 100% similarity. Average nucleotide identity analysis based on whole genome sequence is an accurate and effective method for identification of bacteria and depicts the similarity (Zhou *et al.,* 2022).

The length of the 16S rRNA gene sequence of *D. radiodurans R1* DSM 20539^{T} is 1,502 bp. This sequence was compared with other five strains of *Deinococcus species,* and the result indicates that *D. radiodurans* R1 DSM 20539^{T} shared high 16S rRNA gene sequence similarities with *D. deserti* VCD115 (100.0% 16S rRNA gene similarity), *D. wulumuqiensis* R12 ^{T} (99.6%), *D. grandis* ATCC 43672 ^{T} (99.4%), *D. aquaticus* PB-314 ^{T} (98.3%), and D. *gobiensis* I-0 ^{T} (98.0%).

The heatmap (Figure 2) shows the average nucleotide percentage similarity between *D. radiodurans* R1 DSM 20539^{T} and other type strains, and similarity between *D. radiodurans* R1 DSM 20539^{T} and all other type strains was in the range of 74.43%–85.60%, which indicates the ANI value between genomes of all strains was more than 70%, which is the ANI cut-off value frequently used for species demarcation (Goris *et al.,* 2007). At the same time, OrthoANI values of *D. radiodurans* R1 DSM 20539^{T} were highest with *D. wulumuqiensis* R12 (85.60%) and smallest with *D. deserti* VCD115 ^{T} (74.43%), but both values are lower than the threshold cut-off value (96%) used for strain demarcation. Values larger than 96% indicate that strains belong to the same species (Lee *et al*. 2015). According to these values, it was confirmed that these strains don't belong to the same species. At the same time, ANI value analysis suggested that all the strains from this study belong to the same genus (*Deinococcus*) as their values are higher than 70%.

Phylogenetic analysis of tellurium resistance genes indicated that a total of four copies of the tellurium resistance protein TerD were identified by reannotation of the whole genome sequence of *D. radiodurans* R1 DSM 20539T using RAST, which are different in the length of the amino acid sequence. The result suggested that the presence of*many copies of the same gene that encodes tellurium resistance proteins may make them more resistant to heavy metals*.

6. Conclusion

The genome of *D. radiodurans* R1 DSM 20539^T has a total length of 3, 279, 598 bp and a GC content of 66.7 %. The reannotation bacterial genome predicted a total of 3220 coding sequences (CDS), 57 RNA genes and 255 numbers of subsystems. The length of the 16S rRNA gene sequence is 1,502 bp. Generally, the following points are extrapolated based on this study: *On the basis of the analysis of 16S rRNA gene sequence and OrthANI value, D. radiodurans R1 is phylogenetically very closely related to D. wulumuqiensis R12* ^{T}*, where the OrthANI value for the strain is 85.56%. The D. radiodurans* R1 DSM 20539^T *has many copies of the same gene that encodes tellurium resistance proteins; this may make them more resistant to heavy metals.*

Abbreviations

ANI *Average nucleotide identity*

CDS *Coding sequences*

GGDC *Genome-to-Genome Distance Calculator*

NCBI *National Center for Biotechnology Information*

OAT *OrthoANI tools*

RAST *Rapid annotation subsystem technology*

Declarations

Ethics approval and consent to participate: Not applicable.

Consent for publication: Not applicable.

Data availability: The data used in this study are available through the links provided in the body of the manuscript.

Competing interest:

The authors declare that there is no conflict of interest regarding the publication of this paper. The research was conducted without any personal, financial, or professional affiliations that could be perceived as influencing the results or interpretations presented.

Funding

The research conducted in this study did not receive any specific grant from funding agencies in the public, commercial, or not-for-profit sectors. All expenses related to the research were self-funded or supported by institutional resources.

Author Contribution: As the corresponding author of this paper, Minde Hailu wrote the entire document, which was subsequently revised and edited by Dr. Seid Mohammed.

Acknowledgements: Not applicable.

References

1. Blanchard L, Guérin P, Roche D, Cruveiller S, Pignol D, Vallenet D, Armengaud J, De Groot A. Conservation and diversity of the IrrE/DdrO-controlled radiation response in radiation-resistant *Deinococcus* bacteria. Microbiologyopen. 2017 Aug;6(4):e00477.
2. Eugénie N, Zivanovic Y, Lelandais G, Coste G, Bouthier de la Tour C, Bentchikou E, Servant P, Confalonieri F. Characterization of the radiation desiccation response regulon of the radioresistant bacterium *Deinococcus radiodurans* by integrative genomic analyses. Cells. 2021 Sep 25;10(10):2536.
3. Felsenstein J. Confidence limits on phylogenies: an approach using the bootstrap. evolution. 1985 Jul 1;39(4):783-91.
4. Goris J, Konstantinidis KT, Klappenbach JA, Coenye T, Vandamme P, Tiedje JM. DNA–DNA hybridization values and their relationship to whole-genome sequence similarities. International journal of systematic and evolutionary microbiology. 2007 Jan;57(1):81-91.
5. Gupta RK, Singh AK, Bajaj A, Khardenavis AA, Purohit HJ. Phylogenomic analysis of *Citrobacter* sp. strain AAK_AS5 and its metabolic capabilities to support nitrogen removal behavior. Journal of Basic Microbiology. 2023 Mar;63(3-4):359-76.
6. Jin M, Xiao A, Zhu L, Zhang Z, Huang H, Jiang L. The diversity and commonalities of the radiation-resistance mechanisms of *Deinococcus* and its up-to-date applications. AMB express. 2019 Sep 3;9(1):138.
7. Kimura M. A simple method for estimating evolutionary rates of base substitutions through comparative studies of nucleotide sequences. Journal of molecular evolution. 1980 Jun;16(2):111-20.
8. Lee I, Chalita M, Ha SM, Na SI, Yoon SH, Chun J. ContEst16S: an algorithm that identifies contaminated prokaryotic genomes using 16S RNA gene sequences. International journal of systematic and evolutionary microbiology. 2017 Jun;67(6):2053-7.
9. Liu Y, Zhou J, Omelchenko MV, Beliaev AS, Venkateswaran A, Stair J, Wu L, Thompson DK, Xu D, Rogozin IB, Gaidamakova EK. Transcriptome dynamics of *Deinococcus radiodurans* recovering from ionizing radiation. Proceedings of the national academy of sciences. 2003 Apr 1;100(7):4191-6.
10. Makarova KS, Aravind L, Wolf YI, Tatusov RL, Minton KW, Koonin EV, Daly MJ. Genome of the extremely radiation-resistant bacterium *Deinococcus radiodurans* viewed from the perspective of comparative genomics. Microbiology and molecular biology reviews. 2001 Mar 1;65(1):44-79.
11. Tamura K, Stecher G, Kumar S. MEGA11: molecular evolutionary genetics analysis version 11. Molecular biology and evolution. 2021 Jul 1;38(7):3022-7.

12. Tamura K, Nei M. Estimation of the number of nucleotide substitutions in the control region of mitochondrial DNA in humans and chimpanzees. Molecular biology and evolution. 1993 May 1;10(3):512-26.
13. White O, Eisen JA, Heidelberg JF, Hickey EK, Peterson JD, Dodson RJ, Haft DH, Gwinn ML, Nelson WC, Richardson DL, Moffat KS. Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1. Science. 1999 Nov 19;286(5444):1571-7.
14. White O, Eisen JA, Heidelberg JF, Hickey EK, Peterson JD, Dodson RJ, Haft DH, Gwinn ML, Nelson WC, Richardson DL, Moffat KS. Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1. Science. 1999 Nov 19;286(5444):1571-7.

Figures

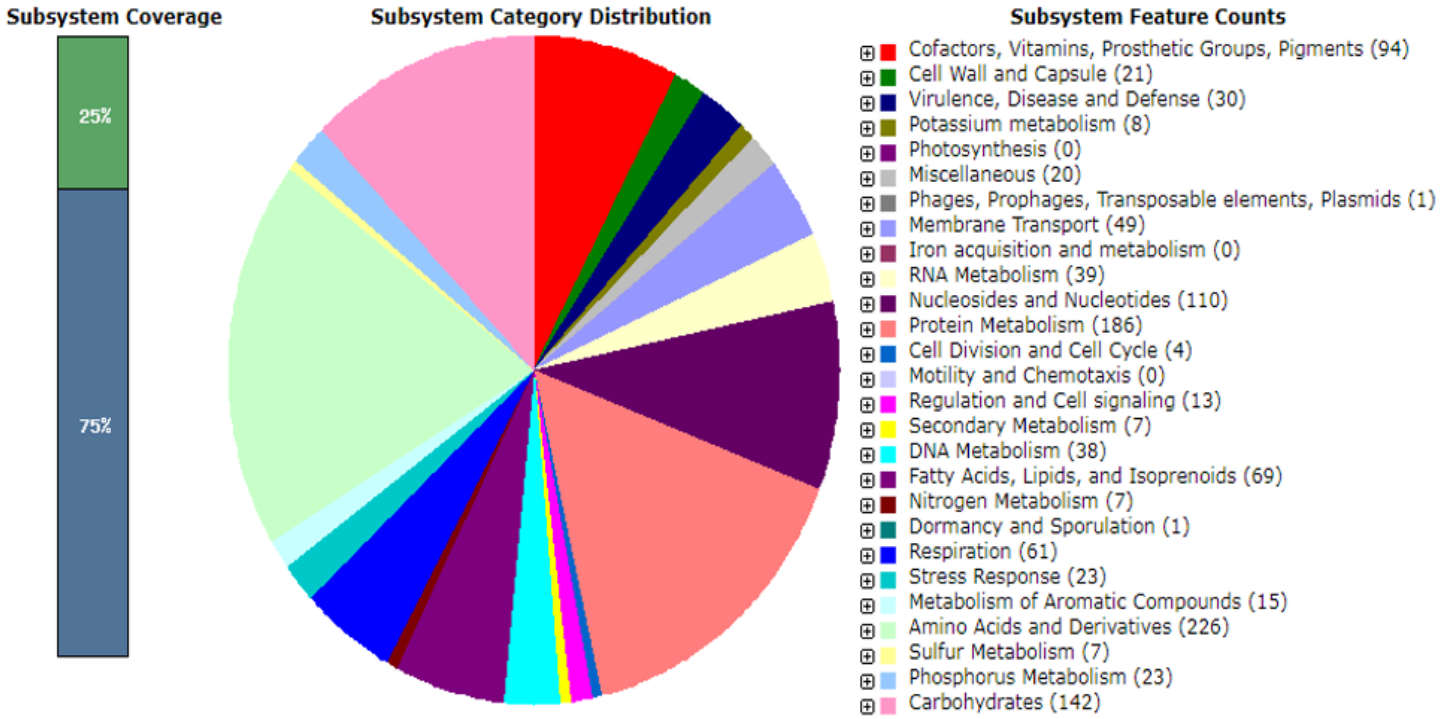


Figure 1

The subsystem category distribution statistics for *D. radiodurans* R1 DSM 20539^T. The whole-genome sequence of the strain was reannotated using the Rapid Annotation System Technology (RAST) server.

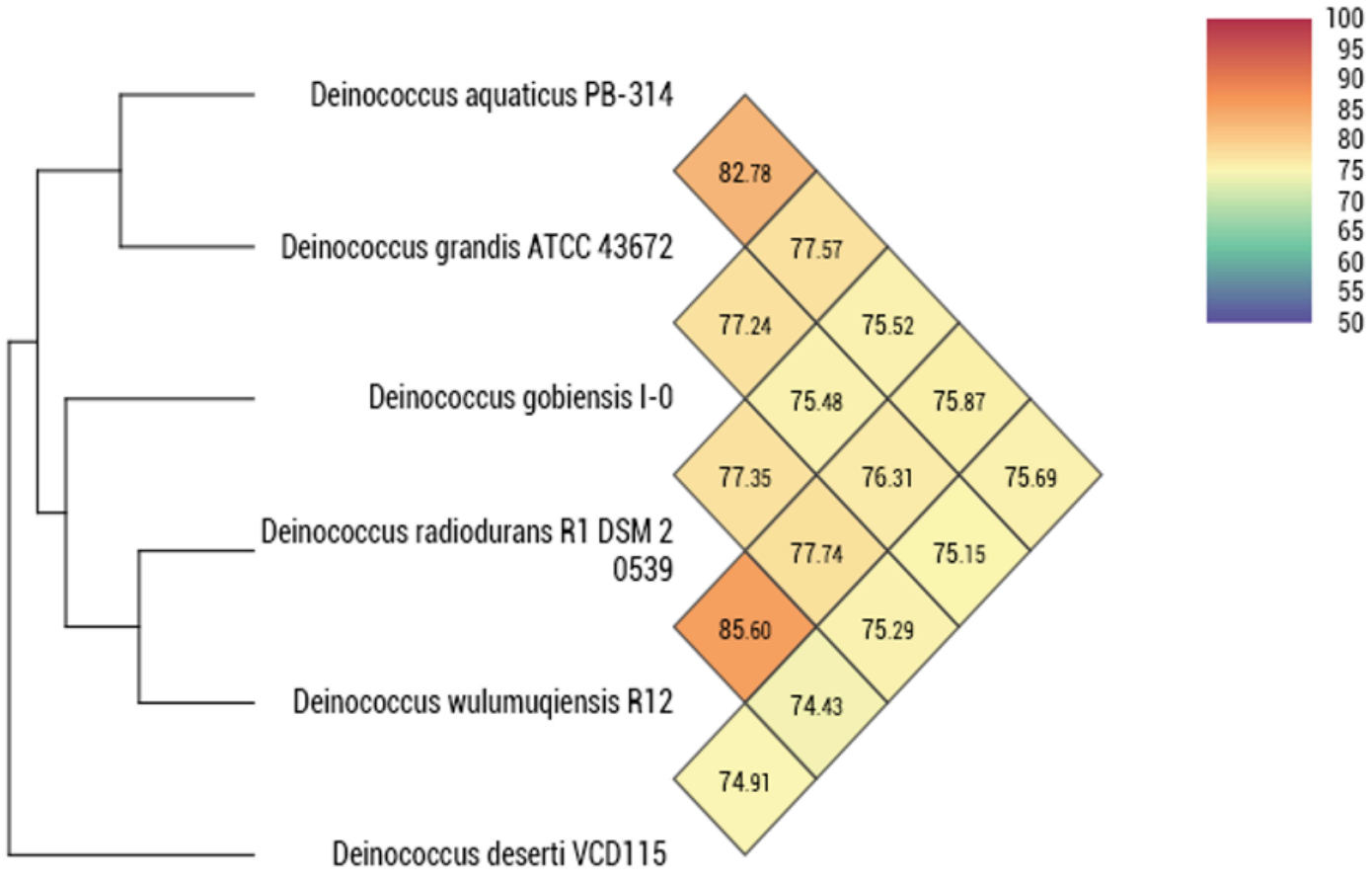


Figure 2

Heatmap showing the average nucleotide identity by orthology (OrthoANI) between strains: Ortho ANI results calculated with available genomes of *D. radiodurans* strain R1 and the other five (*D. aquaticus* strain PB-314, *D. deserti* VCD115, *D. gobiensis* I-0, *D. grandis* ATCC 43672, *D. radiodurans* DSM 20539 and *D. wulumuqiensis* R12) strains. OrthoANI measures the overall similarity between two genome sequences (Lee *et al*. 2015). Values larger than 96% indicate that strains belong to the same species. The results between two strains are given in the junction point of the diagonals departing from each strain, *i.e*., OrthoANI value between *Deinococcus equaticus* and *Deinococcus deserti* is 75.69%.

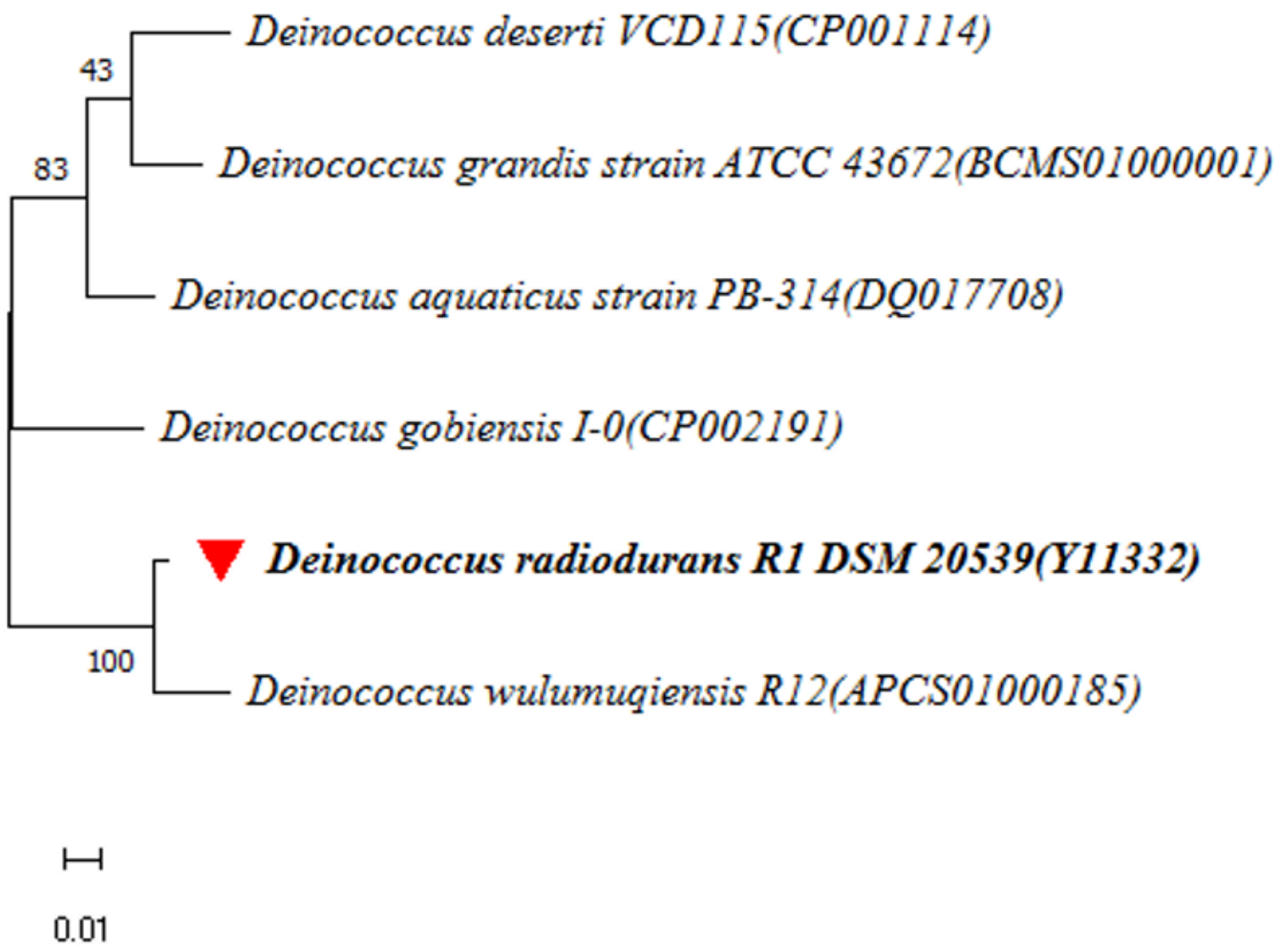


Figure 3

Evolutionary relationships of taxa and phylogenetic tree for 16S rRNA gene sequences of *Deinococcus* sp. The evolutionary history was inferred by using the Maximum Likelihood method and Tamura-Nei model (Tamura and Nei, 1993). The tree with the highest log likelihood is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the Tamura-Nei model, and then selecting the topology with superior log likelihood value. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. This analysis involved 6 nucleotide sequences. There were a total of 1502 positions in the final dataset. Evolutionary analyses were conducted in MEGA11 (Tamura *et al.*,2021).

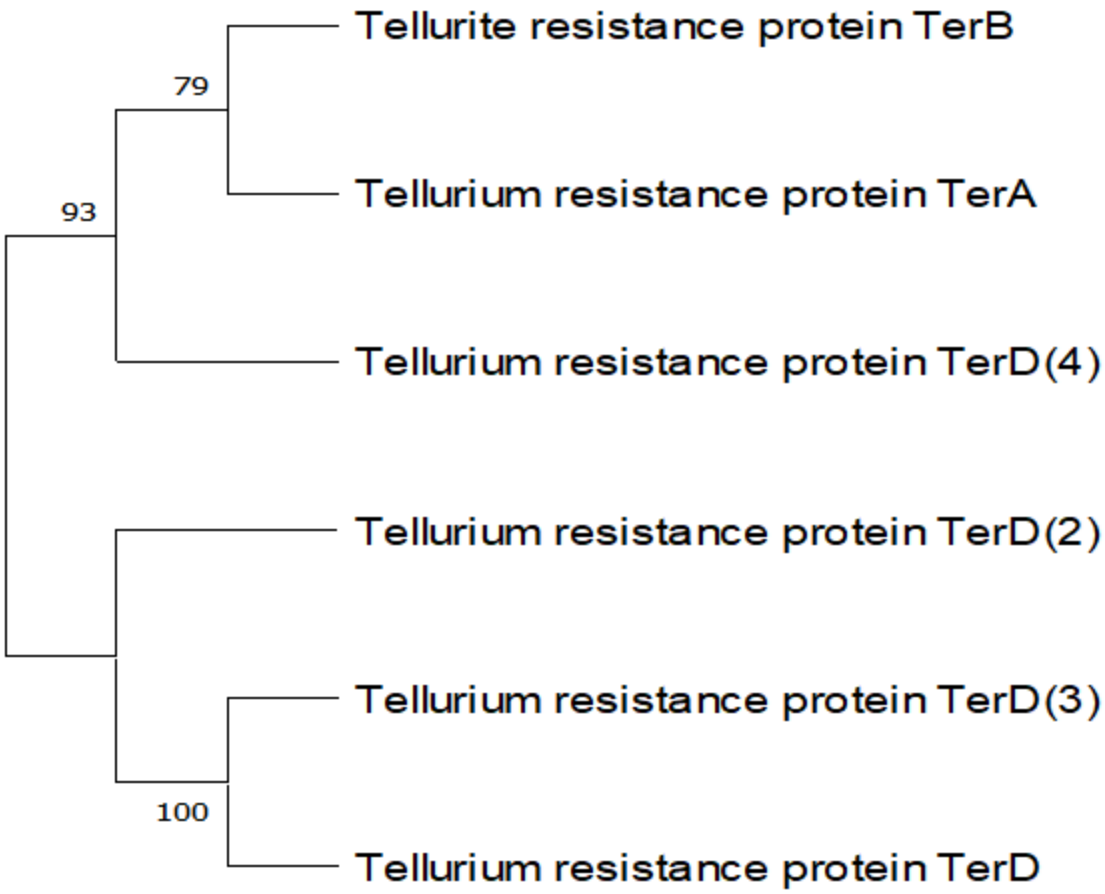


Figure 4

Evolutionary analysis by Maximum Likelihood method: The evolutionary history was inferred by using the Maximum Likelihood method and Kimura 2-parameter model (Kimura, 1980). The bootstrap consensus tree inferred from 1000 replicates (Felsenstein, 1985). is taken to represent the evolutionary history of the taxa analyzed. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test 1000 replicates) are shown next to the branches (Felsenstein, 1985). Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach, and then selecting the topology with superior log likelihood value. This analysis involved 6 nucleotide sequences. There were a total of 1336 positions in the final dataset. Evolutionary analyses were conducted in MEGA11 (Tamura *et al.,* 2021).

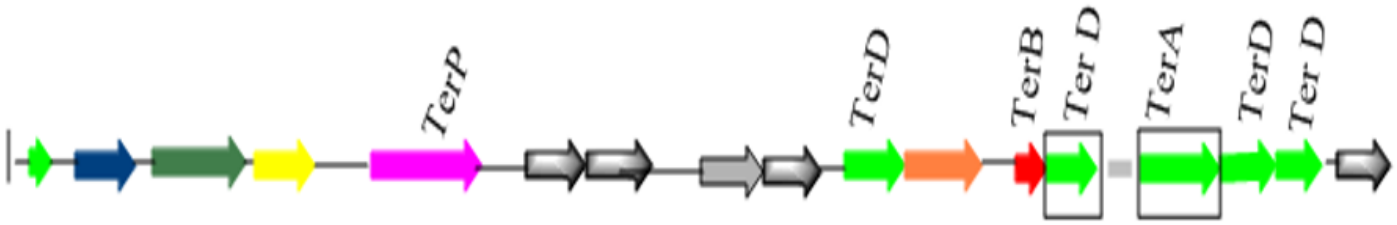


Figure 5

Organization of genes encoding the Tellurium resistant Proteins in *D.radiodurans* R1 DSM 20539^{T}: Sets of genes with similar sequence are grouped with the same color. Genes whose relative position is conserved are functionally coupled share gray background boxes.

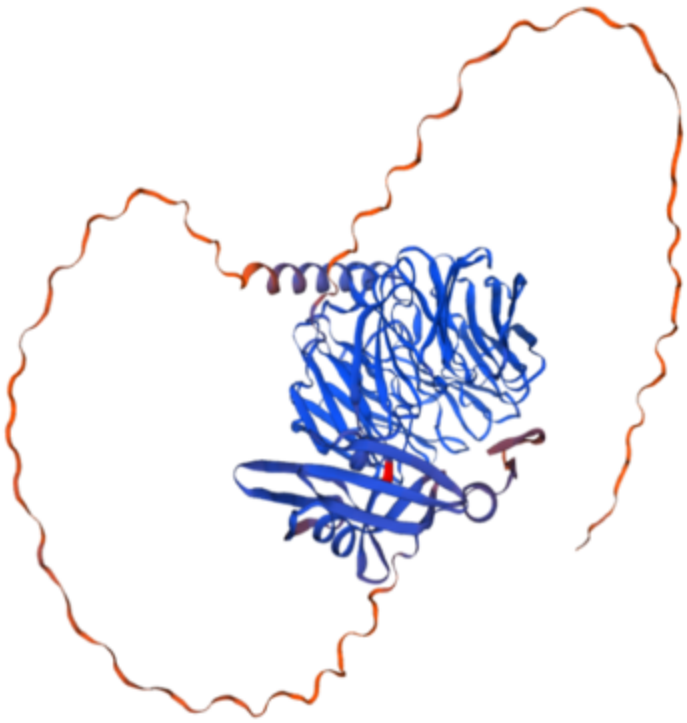


Figure 6

Three-dimensional structure of the template (*DR_1769*)