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Ionizing Radiation Resistance in *Deinococcus Radiodurans*

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Abstract

Deinococcus radiodurans is unmatched among all known species in its ability to resist ionizing radiation and other DNA-damaging factors. It is considered a model organism in the study of DNA damage and repair. Treatment of *D. radiodurans* with an acute dose of 5,000 Gy of ionizing radiation with almost no loss of viability, and an acute dose of 15,000 Gy with 37% viability. The extreme radiation resistance of this bacterium is due to efficient DNA repair capacity, high antioxidant activities, and unique cell structure. Based on the latest findings, the general characteristics and ionizing radiation resistance mechanisms of *D. radiodurans* are reviewed and discussed in this paper.

Key words: Ionizing radiation; *Deinococcus radiodurans*; DNA repair; Reactive oxygen species

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INTRODUCTION

D. radiodurans is unmatched among all known species in its ability to resist ionizing radiation (Cox & Battista, 2005). It was first described by Anderson in 1956 (Anderson, Nordon, Cain, Parrish, & Duggan, 1956).

Treatment of *D. radiodurans* with an acute dose of 5,000 Gy of ionizing radiation with almost no loss of viability, and an acute dose of 15,000 Gy with 37% viability (Daly, 2009; Ito, Watanabe, Takeshia, & Iizuka, 1983; Moseley & Mattingly, 1971). In contrast, 5 Gy of ionizing radiation can kill a human, 200-800 Gy of ionizing radiation will kill *E. coli*, and more than 4,000 Gy of ionizing radiation will kill the radiation-resistant tardigrade. *D. radiodurans* can survive 5,000 to 30,000 Gy of ionizing radiation, which breaks its genome into hundreds of fragments (Daly & Minton, 1995; Minton, 1994; Slade & Radman, 2011). Surprisingly, the genome is reassembled accurately before beginning of the next cycle of cell division.

The extreme radiation resistance of this bacterium is mainly due to a powerful repair system that achieves an efficient and precise assembly of DNA fragments. The research of radiation resistance in *D. radiodurans* with great significance, and caused the attention of many scientists, especially the microbiologists, the radiation biologists and cancer researchers. We give a current outlook on *D. radiodurans* strategies of combating ionizing radiation in this review.

1. GENERAL CHARACTERISTICS OF *DEINOCOCCUS RADIODURANS*

1.1. Classification and Name

Initially, *D. radiodurans* was placed in the genus *Micrococcus*, mainly due to its morpha similarity to members of the genus *Micrococcus*. After research on *M. radiodurans* over 30 years, based on evaluation of ribosomal RNA sequences and other evidences, this species was reclassified and placed in its own genus *Deinococcus*; which is closely related to the genus *Thermus* of heat-resistant bacteria (Battista, 1997; Hensel, Demharther, Kandler, Kroppenstedt, & Stackebrandt, 1986; Omelchenko et al., 2005; Rainey, Nobre, Schumann,

Stackebrandt, & da Costa, 1997; Weisburg, Giovannoni, & Woese, 1989; Woese, 1987; Woese, Stackebrandt, Macke, & Fox, 1985). *Deinococcus* from the Greek words 'deinos', meaning strange or unusual, and 'coccus', meaning a grain or berry. The *Deinococcus* include *D. proteolyticus*, *D. radiopugnans*, *D. grandis*, *D. radiophilus*, *D. geothermalis*, *D. murrayi*, *D. indicus*, *D. frigans*, *D. saxicola*, *D. marmoris* (Cox & Battista, 2005).

D. radiodurans is divided into two subtypes of *D. radiodurans* R1 and *D. radiodurans* Sark. The former with the ability to easily chromosomal transformation and plasmid transfer, it is preferred to the best model organism for the study of bioremediation.

1.2 Physiological Features

D. radiodurans is a Gram-positive, nonsporulating, nonmotile, nonpathogenic, red-pigmented bacterium (Cox & Battista, 2005; Slade & Radman, 2011). It exists as single cells, diads and tetrads with an average cell diameter of 1µm (range, 0.5 to 3.5 µm) in liquid culture (Cox & Battista, 2005; Slade & Radman, 2011). Each *D. radiodurans* cell has two perpendicular furrows that result in a tetrad morphology. The four compartments contain an equal amount of DNA and it adopted a distinctive toroidal shape (Levin-Zaidman et al., 2003; Minsky, Shimoni, & Englander, 2006). The cell envelope of *D. radiodurans* consists of the plasma and outer membranes, which include at least five layers with a total thickness of 150 nm (Work & Griffiths, 1968). The first layer is the cytoplasmic membrane; the next layer is a rigid peptidoglycan-containing holey layer, containing glucose, galactose, rhamnose and mannose, but no heptose; the third layer is the compartmentalized layer and appears to be divided into many fine compartments; the fourth layer is the interior layer and the fifth layer is the fragile soft layer, consists of regularly packed hexagonal protein subunits (S-layer), containing carotenoids, lipids, proteins, and polysaccharides (Kubler & Baumeister, 1978; Slade & Radman, 2011; Work & Griffiths, 1968). *D. radiodurans* is generally grown at 30°C in rich TGY medium (0.5% tryptone, 0.1% glucose, 0.15% yeast extract) with aeration, where cell doubling spends 1.5 to 3h (Venkateswaran et al., 2000).

1.3 Features of the Genome

The genome of *D. radiodurans* R1 (ATCC BAA-816) has been sequenced by the United States Department of Energy, and the results published in "Science" magazine (White, 1999). The *D. radiodurans* chromosome is 3,284,156 bp, with an average GC content of 66.6% and protein coding region accounted for 90.9%. The genome composed of four replicons: two chromosomes (chromosome I: 2,648,638 bp, chromosome II: 412,348 bp), a megaplasmid (177,466 bp) and a small plasmid (45,704 bp). There are 3,187 open reading frames (ORFs) with an average size of 937 bp in the genome. 2185 (69%)

of the *D. radiodurans* ORFs matched sequences available in public databases, and 1 493 assigned putative function, 511 matched hypothetical proteins, 181 function unknown. The chromosome I contains 2,633 genes, the chromosome II contains 369 genes, the megaplasmid contains 145 genes, and the small plasmid contains 40 genes. Chromosome II encodes the genes for amino acid utilization, cell envelope formation, and transporters. Genes for origins of replication are encoded on chromosome I and II, such as *dnaA* and *dnaN* for chromosome I and *parA* for chromosome II, but chromosome I contains *ParA* (*ParA1*) homologue (Charaka & Misra, 2012). Megaplasmid and small plasmid encodes some regulators and protein kinases, such as *RadR*, *RadS* for megaplasmid (Desai, Rajpurohit, Misra, & Deobagkar, 2011) and *DrC0012* for small plasmid. This unique structure of the genome may be an important factor for its superior resistance to radiation.

2. IONIZING RADIATION RESISTANCE MECHANISMS OF DEINOCOCCUS RADIODURANS

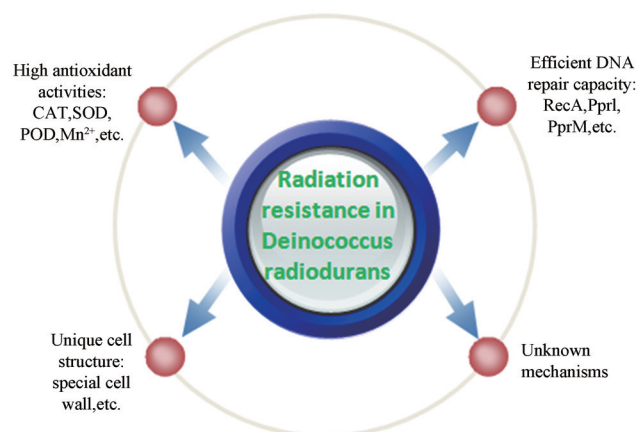


Figure 1
Radiation-Resistance Mechanisms of *Deinococcus Radiodurans*

Note. The high antioxidant activities, efficient DNA repair capacity and unique cell structure are contributed to the extreme radiation resistance of *D. radiodurans*.

Ionizing radiation is generated by the decay of radioactive elements. The cells are exposed to ionizing radiation will cause ionization and excitation of the biological molecules, so that the DNA or RNA strand breaks, the peptide strand breaks and loss of biological function. *D. radiodurans* with extreme radiation resistance and the exponentially grown cells can endure 15,000 Gy of ionizing radiation. *D. radiodurans* is the only survivor exposed to 20 kGy irradiation on earth. It is reported that

the maximum tolerated dose of ionizing radiation is 50 kGy in *D. radiodurans* (Ghosal et al., 2005). The extreme radiation resistance of this bacterium is due to many factors (Figure 1).

2.1 DNA Repair Mechanisms

DSBs are the most lethal damage caused by ionizing radiation. *D. radiodurans* can survive high doses of ionizing radiation, not because it can prevent the generation of DSBs, but it has a highly accurate and effective ability to repair DNA damage. Both of *D. radiodurans* and *E. coli* exposed to high levels of ionizing radiation can produce hundreds of genomic double-strand breaks, but the former usually repairs 100 ~ 200 DSBs in its chromosomes within 12–24 hours and the latter can only repairs 2 to 3 DSBs. DNA damage withstood by *D. radiodurans* is due to the diversity of DNA repair pathways: direct damage reversal, base and nucleotide excision repair, mismatch repair, and recombinational repair. The recombinational repair pathway is the main way to repair DNA damage.

2.1.1 The RecF Pathway

Homologous recombination (HR) between a resident plasmid and the chromosome following irradiation in *D. radiodurans* is widespread (Daly & Minton, 1997). It is carried out by the RecBCD or the RecFOR pathway in bacteria (Rocha, Cornet, & Michel, 2005). *D. radiodurans* does not encode RecB and RecC homologs, or SbcB, but it contains all components of the RecFOR pathway, RecF (DR_1089), RecO (DR_0819), RecR (DR_0198), and RecJ (DR_1126) (Bentchikou, Servant, Coste, & Sommer, 2010; Khairnar, Kamble, & Misra, 2008; Venkateswaran et al., 2000). It is suggested that the RecFOR pathway plays a key role in homologous recombination repair of *D. radiodurans*. Recently, Katsuya Satoh and his colleagues suggested that the RecF protein is involved in the RecA activation and RecR protein contribution to the stability of incoming DNA during RecA-mediated homologous recombination processes that initiated the ESDSA pathway in *D. radiodurans* (Satoh et al., 2012). RecO is essential for DNA Damage Repair and plays a vital role in extreme radiation resistance of *Deinococcus radiodurans* (Xu et al., 2008). The RecJ is the only 5'–3' exonuclease in *D. radiodurans*, and it is considered to process broken DNA ends for the RecF pathway (Bentchikou et al., 2010; Cao, Mueller, & Julin, 2010). In addition to these four proteins, the RecF pathway also requires other proteins, such as RecA (DR_2340), RecN (DR_1477), RuvA (DR_1274), RuvB (DR_0596), RuvC (DR_0440), SbcC (DR_1922), SbcD (DR_1921) (Cox & Battista, 2005). RecN is an SMC family member which stimulates the intermolecular ligation of linear DNA molecules in the presence of DNA ligase and prevents the separation of DNA fragments (Reyes, Patidar, Uranga, Bortoletto, & Lusetti, 2010).

2.1.2 The PprI Pathway

There is an important pathway of homologous recombination repair in the *D. radiodurans*. This repair pathway is controlled by the pprI, and contains several important radiation damage repair related genes (or their products), such as pprI, pprA, recA, pprM. PprI is a protection switch gene, and its expression product PprI is a peculiar protein to *D. radiodurans* (Hua et al., 2003). PprI plays a central regulatory role in multiple pathways, including oxidative stress, energy metabolism, transcriptional regulation, signal transduction, protein folding and assembly (Gao et al., 2003; Hua et al., 2003). PprI can significantly and specifically induce the genes expression of recA and pprA to enhance the ability to repair DNA damage caused by ionizing radiation.

RecA is a helicase, which can control the double-stranded DNA molecule unwinds and open the double-stranded structure, thereby providing single-stranded DNA template for recombination repair. RecA plays a crucial role in DNA recombination repair and chain exchange process (Repar et al., 2010).

The *D. radiodurans* RecA protein (RecADr) is 57% identical (72% similar) to the *E. coli* RecA protein (RecAEc) (Cox & Battista, 2005; Makarova et al., 2001). RecADr forms filaments on DNA that are similar to those formed by the RecAEc, it hydrolyzes ATP, dATP and promotes DNA strand-exchange reactions (J. I. Kim, 2006; J. I. Kim et al., 2002). However, the RecADr shows its own unique features. The *E. coli* RecA protein and other hitherto known filament-forming homologues first combine with the DNA single strand in DNA strand-exchange reaction, while the *D. radiodurans* RecA protein is the exact inverse of this established pathway, binding the duplex DNA first and the homologous single-stranded DNA substrate second (Cox & Battista, 2005; J.I. Kim & Cox, 2002). It suggests that RecADr may play a unique role in DSBs repair. RecA with a high level of transient expression following exposure to ionizing radiation (Lipton et al., 2002), such as RecA gene expression is induced 8 times following 15 kGy of ionizing radiation (Liu et al., 2003). The recA deletion mutant cell is highly sensitive to ultraviolet and ionizing radiation (Gutman, Carroll, Masters, & Minton, 1994).

PprA (DR_A0346) is an essential repair gene and contributes to the extreme resistance of this bacterium to a variety of genotoxic assaults (Kota, Charaka, Ringgaard, Waldor, & Misra, 2014; Narumi et al., 2004). PprA is necessary for accurate cell division of γ -irradiated *D. radiodurans* (Devigne, Mersaoui, Bouthier-de-la-Tour, Sommer, & Servant, 2013), and may participate in a RecA-dependent process during recovery from radiation damage (Tanaka et al., 2004). PprA protein preferentially binds to double-stranded DSBs, and inhibit the activity of exonuclease III to promote DNA end-joining by DNA ligase (Narumi et al., 2004). These results suggested

that PprA plays a key role in non-homologous end-joining (NHEJ) of this species. PprA expression level was upregulated obviously after ionizing radiation and desiccation (Liu et al., 2003; Tanaka et al., 2004), and pprA mutant *D. radiodurans* strain was significantly sensitive to ionizing radiation, MMC (Narumi et al., 2004). Besides, PprA also contributes to maintain the integrity of the damaged *D. radiodurans* genome by interacting with topoisomerases (Kota et al., 2014).

PprI, recA, and pprA are the critical component of the PprI pathway in *D. radiodurans*. Studies have shown that these three genes for resistance to ultraviolet of *D. radiodurans* are indispensable (Bauermeister, Bentchikou, Moeller, & Rettberg, 2009). Inactivation of pprA promoter and up-regulation of pprA expression by the PprI protein is triggered at the transcription initiation level (Ohba, Satoh, Yanagisawa, & Narumi, 2005). But PprI doesn't directly bind to promoter regions of pprA and cinA-recA. It shows that PprI itself does not directly regulate the expression of pprA and recA. So there may be hitherto unknown components of PprI-mediated signal transduction pathway in *D. radiodurans*. Ohba and colleagues identified PprM protein was a novel component of the PprI pathway (Ohba, Satoh, Sghaier, Yanagisawa, & Narumi, 2009). The pprM mutant *D. radiodurans* strain was significantly sensitive to ionizing radiation, and the pprA/pprM double deletion mutant strain showed higher sensitivity than pprA or pprM single mutant strain, which suggested that PprM regulates PprA and other unknown protein(s) important for radiation resistance. However, Hua and colleagues identified the PprI protein could directly combine with the promoter region of recA and pprA (Lu, Chen, Xu, Shah, & Hua, 2012). PprI and DrRRA may work together in response to extreme ionizing radiation in *D. radiodurans* (Wang et al., 2012). In summary, the PprI pathway is an enormously complex DNA repair regulatory network, which is worthy of further study.

2.1.3 Novel Deinococcal DNA Repair Genes

In addition to the RecF and PprI pathway, there are many other genes involved in DNA repair of *D. radiodurans*. RecX could inhibit the expression of DNA repair proteins RecA, SSB, PprA and facilitate the expression of some metabolism-related proteins in *D. radiodurans* (Sheng, Jao, Li, Xu, & Zhang, 2009), which suggesting RecX is a DNA damage stress switch. DR_0171 mutant strain is highly sensitive to ionizing radiation and DR_0171 serves as a regulator of the transcriptional response to radiation damage in *D. radiodurans* (Lu et al., 2011). Besides, DdrB is a novel single-stranded DNA binding protein (SSB) that contains a novel fold (Sugiman-Marangos & Junop, 2010). Recently, a novel protein encoded by the DR_1245 gene was identified as an interacting partner of DdrB (Norais et al., 2013). Further studies show the structure of the DR_1245 protein is similar to YbjN and numerous type III secretion chaperones. It suggests that the

DR_1245 protein with chaperone activity towards DdrB and possibly other substrates. Interestingly, there are many insertion sequences (IS) in the *D. radiodurans* genome, but only ISDra2 is strongly induced by γ irradiation and provides the major source of induced mutations, and TnpB regulate the transposition of ISDra2 (Pasternak et al., 2013). Moreover, Onodera T and colleagues identified *D. radiodurans* ygdD (DR_0382) and yeaZ (DR_0756) genes play a role in the repair of DNA cross-links (Onodera, Satoh, Ohta, & Narumi, 2013). In conclusion, *Deinococcus radiodurans* DNA damage repair mechanism will be a research hotspot in the future.

2.2 High Antioxidant Activities

2.2.1 Catalases and Superoxide Dismutases

Although many studies have shown that the radiation resistance of *D. radiodurans* is due to its efficient DNA repair ability, however, ionizing radiation will produce large amounts of free radicals, which indirectly cause DNA, RNA and protein damage. In general, the *D. radiodurans* cells possess high antioxidant activity to scavenge free radicals. The catalase activity during exponential phases is 127 times and stationary phases are 32 times higher it in *E. coli* (P. Wang & Schellhorn, 1995). In addition, Tian and colleagues' research showed the catalase activity is 15 folds in *D. radiodurans* higher in *E. coli* (Tian et al., 2004). Catalases and peroxidases can remove H₂O₂, which is the byproduct of superoxide dismutases (SOD) eliminate superoxide free radicals from the cells (Abreu et al., 2008). There are three catalases (katE catalases DR_1998 and DR_A0259 and eukaryotic-type DR_A0146), four superoxide dismutases (Mn-dependent DR_1279 and Cu/Zn-dependent DR_1546, DR_A0202, and DR_0644), a cytochrome c peroxidase (DR_A0301), and an iron-dependent peroxidase (DR_A0145) in *D. radiodurans* (Lipton et al., 2002; Slade & Radman, 2011). DR_1279 is constitutively expressed, and its product can be efficient removal of superoxide radicals (Abreu et al., 2008). Recently, Hua et al. identified extracellular dGMP induced catalase (DR_1988) activity, and enhanced *D. radiodurans* tolerance to H₂O₂ and gamma-radiation significantly (Li et al., 2013). These results suggest that catalases and SODs protect macromolecules from ROS-mediated damage in vivo of *D. radiodurans*.

2.2.2 Carotenoids

D. radiodurans also contains other oxidative defense components, such as glutaredoxin, thioredoxin, thioredoxin reductase, alkyl hydroperoxide reductase, and carotenoids (Slade & Radman, 2011; White, 1999). Carotenoids are efficient scavengers of reactive oxygen species (ROS) and belong to the group of lipophilic antioxidants (Tian & Hua, 2010). Carotenoids are able to detoxify various forms of ROS, which protect DNA from oxidative damage, proteins from carbonylation, and

membranes from lipid peroxidation (Slade & Radman, 2011; Tian et al., 2009). *D. radiodurans* carotenoids can eliminate all types of reactive oxygen species in vitro, such as hydroxyl radicals, superoxide radicals, hydrogen peroxide and singlet oxygen (Zhang et al., 2007). Furthermore, *D. radiodurans* carotenoids also remove RNS (reactive nitrogen species) such as 2,2-diphenyl-1-picrylhydrazyl (DPPH•) (Tian et al., 2009). *D. radiodurans* possess 13 genes involved in carotenoids biosynthesis, and with a perfect biosynthetic pathway (Tian & Hua, 2010). Deinoxanthin as a major product in the carotenoid synthetic process of *D. radiodurans*, which has a stronger eliminate capabilities than two carotenes (lycopene, β -carotenoids) and two xanthophylls (zeaxanthin, lutein) to remove hydrogen peroxide and singlet oxygen (Tian, Xu, Sun, Lin, & Hua, 2007). However, carotenoids seems to have little effect on the radiation resistance, block carotenoid biosynthesis pathway (knockout *crtB*) only a weak increase in *Deinococcus* to ionizing radiation, drying and UV radiation sensitivity (Luan et al., 2014; Tian et al., 2007; Zhang et al., 2007). It suggests that carotenoids may not be the main ROS scavengers in vivo of *D. radiodurans*.

2.2.3 Manganese Complexes

The *D. radiodurans* ultrafiltrate is enriched in Mn, phosphate, peptides, nucleosides and bases, which protect proteins from ionizing radiation-induced ROS damage (Daly et al., 2010; Daly et al., 2004). *D. radiodurans* cells have unusually high manganese content, which up to 0.2 ~ 4.0 mmol/L (15-150 times higher than radiosensitive bacteria) (Daly et al., 2007; Daly et al., 2004). The majority of cellular Mn in *D. radiodurans* is present as small complexes with orthophosphate and amino acids or peptides, and Mn-peptide complexes are the most protective (Daly et al., 2010; Daly et al., 2007). Mn²⁺ metabolite defenses are key to preserving the activity of repair enzymes in *Deinococcus radiodurans* exposed to ionizing radiation (Culotta & Daly, 2013), which by scavenging O₂^{•-} and H₂O₂, specifically protect proteins against oxidative damage (Daly et al., 2010; Daly et al., 2007). The nucleotide residues (e.g., uridine) also form complexes with Mn²⁺ and orthophosphate, which with a higher ability to eliminate ROS than Mn²⁺-orthophosphate alone (Daly et al., 2010). Further research shows, as much as 40% of the total Mn²⁺ is in manganese superoxide dismutase, which is the most effective for regulating superoxide in *Deinococcus radiodurans* (Tabares & Un, 2013). In vitro, the superoxide free radical scavenging relies on manganese threshold concentration (Barnese, Gralla, Cabelli, & Valentine, 2008; Daly et al., 2010; Daly et al., 2007). Divalent manganese ions (Mn²⁺) scavenge superoxide radicals by binding phosphate (Barnese et al., 2008), and hydrogen peroxide in combination with bicarbonate salts, amino acid or polypeptide in the extracellular (Berlett, Chock, Yim, & Stadtman, 1990).

Manganese may not only be a chemical scavenger

but may also replace Fe in Fe-loaded enzymes, thereby preventing the iron in the Fenton reaction to cause oxidative damage to the protein (Anjem, Varghese, & Imlay, 2009). *D. radiodurans* has a high intracellular manganese-to-iron (Mn/Fe) ratio of 0.24 (Daly et al., 2004), which contribution to extreme ionizing radiation resistance (Daly et al., 2004; Sun et al., 2012), desiccation resistance (Fredrickson et al., 2008) and low levels of protein oxidative damage (Daly et al., 2007). There is more than one regulator of Mn/Fe homeostasis that involves its high intracellular Mn/Fe ratio in *D. radiodurans* (Sun et al., 2012).

2.3 Unique Cell Structure

D. radiodurans cell is divided into four compartments by two perpendicular furrows, and each compartment contains an equal amount of DNA and it adopted a distinctive toroidal shape. This rare DNA compartments and the ringlike shape of the chromatin contribute to its extremely radiation-resistant (Levin-Zaidman et al., 2003; Minsky et al., 2006). *D. radiodurans* is gram-positive bacteria, but its cell wall is similar to gram-negative bacteria. This cell wall includes a plurality of layers as thick as 150 nm (Work & Griffiths, 1968), which play an important role in its extremely radiation-resistant. The fragile soft layer is tightly to cell walls in *D. radiodurans* that consists of regularly packed hexagonal protein subunits (S-layer or HPI-layer), containing carotenoids, lipids, proteins, and polysaccharides (Baumeister et al., 1986; Kubler & Baumeister, 1978; Work & Griffiths, 1968). The S-layer with a number of functions, include cell adhesion, enzyme attachment, prevention of adsorption of macromolecules and cellular rigidity, which contribute to the extremely radiation-resistant of *D. radiodurans* (Rothfuss, Lara, Schmid, & Lidstrom, 2006). Many genes are involved in building the S-layer and maintain the integrity of the cell envelope in *D. radiodurans* (Farci et al., 2014; Rothfuss et al., 2006). Besides, membrane proteins are important structural components and function in many physiological processes. Tian and colleagues did a proteomic analysis of membrane proteins from *Deinococcus geothermalis*, identified the special protein composition and functions in the cell membrane of *Deinococcus* (Tian et al., 2010). DR_2518 is a DNA damage-responsive membrane protein kinase plays an important role in radiation resistance and DNA strand break repair in *D. radiodurans* (Rajpurohit & Misra, 2010). These results suggest that the particular membrane proteins are involved in the extreme radiation resistance of *D. radiodurans*.

3. CONCLUSION

In summary, recent researches have shown that the tolerance of *D. radiodurans* to radiation is owe to efficient DNA repair capacity, high antioxidant activities, and unique cell structure. The high DNA repair rates make *D.*

radiodurans with a powerful repair system that achieves an efficient and precise assembly of DNA fragments. The high antioxidant activities can scavenge free radicals and protect macromolecules from ROS-mediated damage in vivo of *D. radiodurans*. The unique cell structure of *D. radiodurans* also contributes to its extreme radiation resistance. All of above show that *D. radiodurans* have a complex network system contains many genes, proteins and other substances to cope with its DNA damage and repair, which can help *D. radiodurans* survive in extreme levels of ionizing radiation.

Researches on the molecular mechanisms of DNA repair not only has important theoretical significance, but also has extensive practical application prospects. Aging and cancer are tightly associated with DNA, RNA and protein oxidative damage due to ROS generation (Choudhari, Chaudhary, Gadbaill, Sharma, & Tekade, 2014; Kryston, Georgiev, Pissis, & Georgakilas, 2011; Lee & Wei, 2007), it suggests that the radioresistance mechanism of *D. radiodurans* help us to understand the formation mechanism of cancer and aging. Engineering of *D. radiodurans* with good application prospects in environmental remediation (Appukuttan, Rao, & Apte, 2006; Appukuttan, Seetharam, Padma, Rao, & Apte, 2011; Brim et al., 2000; Chaturvedi & Archana, 2014). Moreover, some functional genes of *D. radiodurans* are used to plant breeding for disease resistance and desiccation tolerance (J. Battista, Park, & McLemore, 2001; Sun et al., 2012) Therefore, we have every reason to believe that with further research of *D. radiodurans* will show more attractive prospects.

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