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Dissecting the extreme radiation resistance of *Deinococcus radiodurans* at proteome level

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World's most radiorestant microbe, *Deinococcus radiodurans*, possesses an efficient DNA repair capability that confers resistance to all forms of DNA damage caused by ionizing radiations, UV, desiccation or mutagenic chemicals. Post-irradiation, the organism enters a growth arrest phase during which it reassembles it's shattered genome with absolute fidelity and recycles the radiation-damaged biomolecules. Towards this goal, *D. radiodurans* genome harbors DNA repair pathways for RecFOR mediated homologous recombination (HR) and nucleotide/base excision repair (NER/BER) along with few ORFs homologous to eukaryotic DNA repair machinery, such as strand annealing (SA) and non-homologous end joining (NHEJ), but also displays some important omissions in universal prokaryotic DNA repair pathways such as RecBCD mediated HR, photo-reactivation and SOS response. In the present study, the proteomic changes were investigated during the 4h growth arrest phase of post-irradiation recovery (PIR), by two dimensional protein electrophoresis coupled with mass spectrometry. Nearly 100 radiation-responsive proteins belonging to the functional categories of DNA repair, oxidative stress alleviation and protein translation/folding were identified. The upregulated DNA repair proteins belonged to SA, NER, NHEJ and HR pathways. The kinetics and dynamics of proteomic changes during PIR revealed (a) differences between transcriptomic and proteomic changes, and (b) relative versus fold induction levels of proteins, and established (i) chronology of events in DNA repair, and (ii) proteolytic processing of induced proteome post-repair. The proteomic data, in conjunction with transcriptomic analysis, knockout mutagenesis and biochemical evidences, revealed requirement of induced as well as constitutively expressed proteins, for the extreme radioresistance of *D. radiodurans*.

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