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Microarray analysis of the transcriptional response to different doses of ionizing radiation in *Salmonella enterica* serovar Typhimurium

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Microarrays can be used to measure the expression of thousands of genes to identify the changes in expression between different biological states. To define the repertoire of *Salmonella typhimurium* genes responding to different doses of ionizing radiation (IR), 1, 10, and 100 Gy, transcriptome dynamics were examined using DNA microarrays. At least 74 genes were induced and 38 genes were repressed 2-fold or more by a dose of 100 Gy, while 26 genes were induced and 29 genes were repressed by a dose of 10 Gy. In particular, only 2 and 4 genes were up- and down-regulated significantly after 1 Gy IR exposure, respectively. We found that four SOS genes (*umuD*, *dinP*, *dinG*, and *uvrB*) are strongly and moderately induced by 100 and 10 Gy IR, respectively, but not by 1 Gy IR. However, interestingly, most of the genes showing the dose-dependent increase like the four SOS genes were found to be *Salmonella* prophage genes such as Fels-1 and Gifsy-1 and -2. In addition, heat shock genes (*dnaK* and *groELS*) also showed the dose-dependent expression. These results suggest that a dose of 1 Gy is not sufficient to provoke an IR response in bacteria. Considering the high expressional level of prophage genes compared to SOS genes, it is likely that an additional transcriptional regulatory mechanism may play a role in the induction of prophage genes.

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