

P064 The transcriptional response to low doses of UV-B in *Halobacterium* sp. NRC-1

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We have studied the transcriptional response of the sunlight-tolerant model archaeon, *Halobacterium* sp. NRC-1, to low doses of mid-wave UV (UV-B) to assess its response to UV radiation that is likely to be biologically relevant. Cells were irradiated with UV-B at doses equivalent to 30 J.m⁻² and 5 J.m⁻² of UV-C and transcriptional profiling was carried out 1 and 3 hours after irradiation, using oligonucleotide microarrays. In contrast to earlier experiments in which we used higher UV doses and short-wave UV (UV-C), only 12 genes were up-regulated 1.5-fold or more after both of these UV-B doses. The most strongly up-regulated gene was *radA1* the archaeal homologue of *RAD51/recA*.

Five of the consistently UV-B up-regulated genes, *radA1*, *vng17*, *top6B*, *vng280* and *npa* share a common 11-base pair motif, TTT(C/T)ACTTTCA, in the promoter region, upstream of the TATA box. We suggest that this motif is the binding site for a transcriptional regulator involved in the response to UV damage in this model archaeon. The same sequence is found in *radA* promoters of other halophilic archaea, as well as in the *radA* promoter of *Methanospirillum hungatei*. We have also analysed the transcriptional response of a repair-deficient $\Delta uvrA \Delta uvrC$ double-deletion mutant.