



PHOTOBIOLOGY AND PHOTOPROTECTION

CIRCULAR RNA EXPRESSION PROFILE IN HUMAN FIBROBLAST PREMATURE SENESCENCE AFTER REPEATED UVB IRRADIATIONS REVEALED BY MICROARRAY

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Introduction: MiRNA and circRNA are both non-coding RNA. In the UVB-SIPS (stress induced premature senescence) HF field, we have found that miR-23a is a significant miRNA in photoaging.

Objective: The profiling and potential function of circRNA in UVB-SIPS are unclear. Hence, research on circRNA in UVB-SIPS was conducted.

Methods and materials: The model of UVB-SIPS was formed by using UVB irradiation. Microarray of circRNA profiles was conducted. The selected circRNAs were confirmed using qRT-PCR and relationship of circRNA_100797 with miR-23a was assessed using luciferase reporter assay and their functions were determined using qRT-PCR and Western blot. Gene Ontology and KEGG for pathway analysis were used to predict the potential function of dysregulated circRNAs.

Results: There were a total of 472 differentially expressed circRNAs occurred in UVB-SIPS (228 upregulated and 244 downregulated circRNAs). qRT-PCR confirmed five out of the eight differentially expressed circRNAs. The GO and KEGG analysis showed these differently expressed circRNAs function in biology process, cell component and molecular function, such as the cells against ultraviolet radiation, DNA double-strand break, p53 signaling, PPAR signaling pathways. Furthermore, we found circRNA_100797 was low expression in UVB-SIPS. However, when we overexpressed circRNA_100797, the acceleration of cell proliferation and alleviation of cell cycle arrest were observed. What's more, circRNA_100797 could directly target miR-23a-5p and miR-23a overexpression blocked the effect of overexpression circRNA_100797 on UVB-SIPS.

Conclusion: This study gives us a landscape about circRNA in human UVB-SIPS fibroblasts and circRNA_100797 acted as a sponge of miR-23a and function as anti-aging role in the UVB-irradiated fibroblasts.

