PHOTOBIOLOGY AND PHOTOPROTECTION

TRANSCRIPTIONAL PROFILE STIMULATED BY UVA AND UVB RADIATION IN HUMAN KERATINOCYTES

Huaping Li [1] - Runxiang Li [2] - Aili Gao [2] - Huiyan Deng [2] - Zhiyin Mo [2] - Huilan Zhu [2]

Guangzhou Institute Of Dermatology, Clinical Laboratory, Guangzhou, China [1] - Guangzhou Institute Of Dermatology, Departmrnt Of Dermatology, Guangzhou, China [2]

Background: Ultraviolet (UV) irradiation is the major environmental factor that causes pathological damage in the skin such as sunburn, photoaging and even skin cancers. According to wavelength, UV in sunlight reaching the earth surface is classified in UVA (320–400 nm) and UVB (280–320 nm). There is a significant diversity in transcriptional profiling of skin response to different wavelengths of UV. Although much progress has been made in understanding the signaling pathways induced by UV irradiation in the skin, the signaling molecules and gene expression that initiated by different wavelength UV remain unclear.

Objective: The aim of this study was to identify shared and distinctive expressed genes responses to UVA and UVB in immortalized human keratinocytes (HaCaT cells).

Materials and Methods: In the present study, HaCaT cells were irradiated with UVA (25 J cm−2) or UVB (300 mJ cm−2) then analyzed by RNA-Seq at 24 h after irradiation. Non-irradiated cells were used as a background control.

Results: Upon UVA radiation, 57 unigenes were up-regulated significantly and 88 unigenes were down-regulated significantly when compared to non-irradiated control. While upon UVB radiation, 51 unigenes were up-regulated significantly and 290 unigenes were down-regulated significantly. KEGG enrichment analysis identified 12 enriched pathways, such as MAPK signaling pathway, TNF signaling pathway, response to UVA irradiation but no UVB, whereas 17 enriched pathways, such as Jak-STAT signaling pathway, NF-kappa B signaling pathway and mTOR signaling pathway, response to UVB irradiation but no UVA. 7 shared pathways, such as cytokine-cytokine receptor interaction, transcriptional misregulation in cancer and rheumatoid arthritis, response to UVA as well as UVB.

Conclusions: Our data elucidated both common and distinctive transcriptional profiling responses to UVA and UVB irradiation in human keratinocytes that might be utilized to reduce UV-induced skin adverse photobiological effects on the skin.