

# NEWS:

## **Another new study (1) showed the interest of quantitative LC-MS/MS proteomics in order to understand UVB effect and active ingredient effects on UVB action.**

Photodamage is extrinsically induced by overexposure to ultraviolet (UV) radiation, and it increases the risk of various skin disorders. Therefore, discovery of novel biomarkers of photodamage is important. In this study, using LC-MS/MS analysis of epidermis from UVB-irradiated hairless mice, 57 proteins were identified whose levels changed after UVB exposure, and selected 7 proteins related to the tricarboxylic acid (TCA) cycle through pathway analysis. Dihydrolipoyl dehydrogenase (DLD) was the only TCA cycle-associated protein that showed a decreased expression after the UVB exposure. Then a targeted analyse of TCA cycle showed that DLD and its associated metabolites, malic acid and fumaric acid, may be candidate biomarkers of UVB-induced skin photoaging. Furthermore the effects of an *Aloe vera* extract on these parameters could be determined by the follow-up of these biomarkers.

This study is the first example of an integration of proteomic and metabolite analysis techniques to find new biomarker candidates for the regulation of the UVB-induced skinphotoaging. DLD, malic acid, and fumaric acid can be used for development of cosmeceuticals and nutraceuticals regulating the change of skin metabolism induced by the UVB overexposure. Moreover, this is also the first attempt to investigate the role of the TCA cycle in photodamaged epidermis. Our integration of the proteomic and targeted metabolite analyses will lead to a better understanding of the unidentified photobiological results from UVB-irradiated models and can elicit new diagnostic and treatment strategies based on altered metabolism.

(1)Dihydrolipoyl dehydrogenase as a potential UVB target in skin epidermis; using an integrated approach of label-free quantitative proteomics and targeted metabolite analysis. Moon E and all. 2015 <http://www.ncbi.nlm.nih.gov/pubmed/25576851>

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