NEWS

We had the opportunity to study the UV effects on various models of skin cells and tissues by LC-MS/MS proteomics followed by CORAVALID analysis.

It showed metabolic changes on different scales and degrees, in effectors and regulators.

We were able to unravel the mechanisms underlying changes in interactions in the **extracellular matrix**, by examining interactors and protein domains. We could link part of the activities and variations to specific promoters, **catalytic or biological functions** (inflammation, immune cells interactions, vesicular transport, DNA repair**), metabolic** (anti-oxydant mechanisms, vitamin biosynthesis, energetic components, ubiquitination) and **signaling pathways** (apoptosis, NFkB, Ras/Jun, PP2A, PKC, calcineurin, cell cycle and proliferation regulations), and even specific compartments involved in the matter at work. It was even possible to correlate the changes with **pathological mechanisms** like atopic dermatitis, Cantú syndrome, or photosensitivity, and to accurately identify various **changes in cellular equipment** like ribosomal proteins, various structural proteins (collagens, actins, integrins, dynamins, desmosomes components, fibronectin, keratins, ankyrins), transporters (ATPases mitochondrial channels, RCPG or VOC subunits).

The exhaustivity of the method allowed interpreting the results to objectively explain the phenomena in progress depending on the parameters of the experimental context, discriminating the changes between apoptosis, cornification or senescence, with the advantage of taking post-translational modifications and signaling pathway interplay into account.

Results allow quick integrations of these into current researches, multiple metabolic pathways displays allowing additionally to replace the intervention level in the whole picture of the assessed as pertinent mechanisms.

High-resolution nano LC-MS/MS quantitative proteomics and CORAVALID™ data processing: The efficient tool

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