## Deciphering non thermal plasma effects on human cell lines by proteomics

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Non thermal plasmas are promising tools for different medical applications. To identify and basically understand the effect of non thermal plasmas on cells and tissues as well as to support plasma tuning efforts a deep insight into plasma – cell interaction is desirable.

The cellular proteome covers the complete protein composition of a biological cell at a given time. Therefore, the snapshot of a cellular proteome – the cell's toolbox – enables in-depth findings on the cellular status.

To understand the cellular behavior after non thermal plasma treatment by an argon based plasma jet (kinpen, Neoplas Tools) we established a time (hours past treatment) and space (localization within a cellular compartment) resolved protocol to identify and quantify the intracellular proteins of a human keratinocytes cell line (HaCaT). Using an ABSciex TripleTOF 5600 high resolution mass spectrometer, we were able to identify 3000+ human proteins within different cellular compartments in a gel free approach. Proteins detected cover a wide range of molecular functions (e.g. antioxidant activities) and a broad spectrum of biological processes (e.g. regulation of apoptosis; DNA replication).



Measured protein abundances differ specifically between argon jet plasma treated cells and controls. Among the most regulated proteins are proteins involved in reactive oxygen/reactive nitrogen (RONS) metabolism and cell division, indicating an oxidative influence on cellular macromolecules. We also give evidence of the activation of protective and pro-proliferative signal molecules indicating specific (and transient) cell activation after kinpen treatment and encouraging a possible use of such plasmas in wound care.

Together with transcriptomic data the presented overview of HaCaT proteome after nonthermal plasma treatment helps streamlining the identification of both biological and physical key players and the conclusion of further research topics.

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