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Identification of metabolic alterations in tumor cell lines following treatment with cold physical plasma

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Abstract

Cold atmospheric plasma (CAP) is a new field in cancer therapy. It is produced by partially ionizing rare gases, which in turn generates Reactive Oxygen and Nitrogen Species (RONs). These oxidative species again exert their influence on the vitality and metabolism of the cells. Some cancer cells have been shown to be sensitive to the cold plasma, whereby others have been shown to be resistant. As metabolism and redox-status of the cells are highly intertwined, we propose metabolic adaptations as a possible cause of this difference.

We assessed the substrate mitochondrial activity of seven cancer cell lines following the treatment with cold plasma. Mitochondria functional assays were performed by determining the utilization of 31 substrates (MitoPlate™). Results indicate enhanced utilization of fatty acid, amino acid and glycolysis pathway following cold plasma treatment. Therefore we screened for the mrNA expression of 31 key genes involved in the amino acid and fatty acid pathways by qPCR. Differential gene expression analysis revealed that HK-1, PKM-2, GLS, MCT-1, MPC-2, ASCT2 and SLC3A2 were significantly upregulated following cold plasma treatment. Further molecular characterization of these genes are underway in order to implicate them as metabolic switches governing response to cold plasma

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