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Study of the Metabolic Reprograming by Magnetic Resonance Spectroscopy

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Abstract:

The metabolome is the last step of the omic cascade, reflecting the modification in the upper omic levels but also the environmental changes that may affect the development of the disease, even the efficacy of a therapeutic approach. Whereas genes and proteins are subject to regulatory epigenetic processes and post-translational modifications, respectively, metabolites represent downstream biochemical end products that are closer to the phenotype. Accordingly, it is easier to correlate metabolomic profiles with phenotype compared to genomic, transcriptomic and proteomic profiles. The study of the metabolic changes associated with a disease include the analysis of the metabolic profile obtained from biological samples by high resolution spectroscopy techniques such as Magnetic Resonance Spectroscopy MRS or Mass Spectrometry (MS), but also the analysis of the metabolic fluxes. MRS in combination with hyperpolarized (HP) carbon-13 precursors is the only technique that allows the monitoring of metabolic fluxes in vivo and in real time using the DNP HP Technology. The aim of this presentation is to provide an overview of the potential of MRS technology in the study of cancer and cardiopulmonary diseases.

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