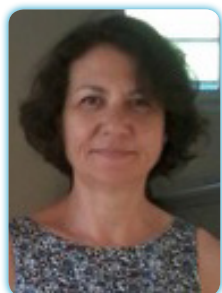


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Mitochondrial phosphoproteome

A large proportion of the proteome is subjected to post-translational modifications (PTMs), often associated with vital processes like cell cycle regulation, homeostasis, stress response, apoptosis, etc. Among the PTMs, phosphorylation is of key importance (at least 500 protein kinases and more than 100 phosphatases are predicted in the human genome) because, as a fast and reversible process, it potentially regulates almost all aspects of cell life. It is also known that abnormal phosphorylation events are associated with various cancers and neurodegenerative diseases. The steadily increasing number of known mitochondrial phosphoproteins, kinases and phosphatases in last few years suggests that reversible protein phosphorylation could be an important regulatory event in mitochondria that needs to be better understood. We have used two techniques to analyze protein phosphorylation state on isolated mitochondria. The first one relies on 2D BN SDS-PAGE electrophoresis associated to Pro-Q Diamond staining. The second one is quantitative and it uses multiplex stable isotope dimethyl labeling followed by fractionation by SCX and phosphopeptides enrichment by IMAC before LC-MS/MS analysis. This second approach allowed us to produce the first extensive study providing quantitative data on phosphosite responses to different carbon substrates in the yeast *Saccharomyces cerevisiae* (Renvoisé *et al.*, 2014, *J. Proteomics*). It is an essential step forward in the analysis of regulation of mitochondrial proteins by phosphorylation.

Biography

Lemaire Claire is a Biochemist specialized in Membrane Proteins. She began her career in the Photosynthesis field on the assembly and regulation of Photosynthetic Complexes. She then joined the CNRS (French National Center for Scientific Research) where she acquired an expertise in the Respiratory Complexes. She has developed a research project with her group focusing on the regulation of OXPHOS complexes by phosphorylation.

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