Profiling Lysine Acetylation of Rat Liver Mitochondria Enriched Fraction and its Potential Interplay with Protein Phosphorylation.

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Acetylation of the lysine side-chain is a reversible and highly regulated post-translational modification. Due to neutralization of the positive charge at the Lys amino group, lysine acetylation may change protein structure and biological function. Recent studies showed that this modification plays not only a crucial role in the nucleus but is also abundant in mitochondria. Therefore, several mitochondrial processes may be affected, and lead to mitochondrial dysfunction pathologies like type-2 diabetes. On the other hand, phosphorylation-desphosphorylation events are key regulators in numerous cell signaling pathways related to energy metabolism and apoptosis. In this study, we profiled Lys-acetylated and phosphorylated mitochondrial proteins. Modified peptides from rat liver tissue were enriched using anti-acetyl-Lys immunoprecipitation and TiO2 methodology. The mass spectrometry analysis was performed using LTQ-OrbiTrap mass spectrometry. The identification list revealed about 100 acetylated proteins, mostly mitochondrial, and about 200 phosphoproteins, from which at least 50 proteins contain both modification types. Fatty acid metabolism and tricarboxylic acid cycle are examples of the over-represented pathways involving these modified proteins. Finally, the study predicts potential cross-talk between some of the observed modifications.

Word Keys: mitochondria, post-translational modifications, lysine acetylome, phosphoproteome and mass spectrometry.

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