COMPARATIVE MITOPROTEOMICS: A POWERFUL TECHNOLOGY TO STUDY MITOCHONDRIAL PLASTICITY.

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Proteomics represents an integral part of the modern biochemist's toolbox. Organelle science does not escape proteomics and mitochondrial physiology is increasingly investigated using proteomic technologies. Two lines of research related to mitochondrial proteomes (or mitoproteomes) are currently acknowledged: (i) structural proteomics that focuses on the elucidation of mitoproteome components; (ii) comparative proteomics that studies adaptations in mitoproteome patterns in response to environmental modifications. Two-dimensional differential in-gel electrophoresis – 2D-DIGE – is the last-born technology available in gel-based comparative proteomics. 2D-DIGE takes advantage of differential fluorescence protein labeling and sample multiplexing to improve accuracy and reliability of comparative analyses. Accordingly, 2D-DIGE enables subtle changes in mitoproteomes under comparison to be identified and opens a new path toward the understanding of the mitochondrial plasticity in response to changes in the cell physiology. This is illustrated by several examples of mitoproteome plasticity, namely: *Saccharomyces cerevisiae* mitoproteome plasticity in response to recombinant uncoupling protein 1 from rat brown fat and in response to recombinant alternative oxidase from *Hansenula anomala* , steatosis-induced proteomic changes in liver mitochondria of inbred hyperphagic obese mice and mitoproteome adaptation of rat brown adipocytes in response to cold acclimation. The results presented demonstrate complex cross-talks between mitochondria and the nucleus regulating the expression of key enzymes in energy homeostasis that are consequently adjusted in response to various mitochondrial metabolic statuses, reflecting a tremendous plasticity of the mitochondrial proteome.