High-sensitivity, high-resolution MS-based quantitative proteomics by manipulation of protein isotope composition *in vivo*

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Many quantitative proteomics strategies rely on *in vivo* metabolic incorporation into proteins of amino acids with modified stable isotopes profiles. These methods give rise to multiple ions for each peptide, with possible distortion of the isotopologs distribution, making the overall analytical process complex. By reducing the isotopic composition of proteins *in vivo*, we bring a new dimension to in-depth, high resolution MS-based quantitative proteomics that alleviates these problems. We used U-[12C]-glucose as the metabolic precursor of all amino acids in yeast. This substantially increased the peptide monoisotopic ion intensity in bottom-up analyses, greatly improving identification scores and protein sequence coverage. Multiplexing samples of 12C composition varying from natural abundance to 100% 12C makes it possible to address quantitative proteomics, keeping all the critical information within a single isotopologs cluster. We applied this method to measure for the first time protein turnover at the proteome scale in the pathogenic yeast *Candida albicans*.

Biography

Jean-Michel Camadro is currently working as a Group Leader at Institut Jacques Monod, France.

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