STABLE ISOTOPE LABELING BY AMINO ACIDS IN CELL CULTURE (SILAC) AS A TOOL IN CANCER RESEARCH

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Stable isotope labeling by amino acids in cell culture (SILAC) is a simple and accurate approach to quantify differential protein expression and dynamic regulation of posttranslational modifications. In a typical SILAC experiment, cells representing different biological conditions are grown in media supplemented with either “light” or “heavy” isotope-containing amino acids. Metabolic incorporation of labeled amino acids into all proteins from cells of one population and subsequent combination of differentially labeled samples in equal ratios enables relative quantification of proteins from each sample based on the intensities of the corresponding differentially labeled peptides. In the same mass spectrometric experiment, MS/MS can be carried out to obtain sequence information for protein identification. The high accuracy of quantitation provided by SILAC is a consequence of the metabolic incorporation of the isotopes which allows mixing of the labeled and unlabeled cells, therefore subsequent fractionation, purification or protein digestion steps do not introduce any errors in the quantitation.

In combination with mass spectrometry (MS), SILAC can be an effective means for characterization of different cellular events. The advantages of using SILAC in the cancer research field are significant because this approach allows the expansion to a proteomics scale of established biochemical and cell biological experiments that are frequently used to address cancer-related problems. Here I present some examples on how cancer research can benefit from the combination of SILAC and MS as a screening tool for the identification of potential biomarkers for early detection or disease prognosis, for the elucidation of biochemical pathways directly related with cell division and cancer, and for the study of the cellular mechanisms involved in tumor invasion and metastasis.