Trends in the design of new isobaric labeling reagents for quantitative proteomics.

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Modern mass spectrometry is one of the most frequently used methods of quantitative proteomics, enabling determination of the amount of peptides in a sample. Although mass spectrometry is not inherently a quantitative method due to differences in the ionization efficiency of various analytes, the application of isotope-coded labeling allows relative quantification of proteins and proteins. Over the past decade, a new method for derivatization of tryptic peptides using isobaric labels has been proposed. The labels consist of reporter and balanced groups. They have the same molecular weights and chemical properties, but differ in the distribution of stable heavy isotopes. These tags are designed in such a way that during high energy collision induced dissociation (CID) by tandem mass spectrometry, the isobaric tag is fragmented in the specific linker region, yielding reporter ions with different masses. The mass shifts among the reporter groups are compensated by the balancing groups so that the overall mass is the same for all forms of the reagent. Samples of peptides are labeled with the isobaric mass tags in parallel and combined for analysis. Quantification of individual peptides is achieved by comparing the intensity of reporter ions in the tandem mass (MS/MS) spectra. Isobaric markers have found a wide range of potential applications in proteomics. However, the currently available isobaric labeling reagents have some drawbacks, such as high cost of production, insufficient selectivity of the derivatization, and relatively limited enhancement of sensitivity of the analysis. Therefore, efforts have been devoted to the development of new isobaric markers with increased usability. The search for new isobaric markers is focused on developing a more selective method of introducing a tag into a peptide molecule, increasing the multiplexicity of markers, lowering the cost of synthesis, and increasing the sensitivity of measurement by using ionization tags containing quaternary ammonium salts. Here, the trends in the design of new isobaric labeling reagents for quantitative proteomics isobaric derivatization strategies in proteomics are reviewed, with a particular emphasis on isobaric ionization tags. The presented review focused on different types of isobaric reagents used in quantitative proteomics, their chemistry, and advantages offer by their application.

Słowa kluczowe

isobaric labeling reagents, quantitative proteomics, ESI-MS, ionization enhancers, quaternary ammonium salts

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