

Detection of glycation sites in proteins by high-resolution mass spectrometry combined with isotopic labeling.

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The products of nonenzymatic glycation of proteins are formed in a chemical reaction between reducing sugars and the free amino group located either at the N terminus of the polypeptide chain or in the lysine side chain. Glycated proteins and their fragments could be used as markers of the aging process as well as diabetes mellitus and Alzheimer's disease, making them an object of interest in clinical chemistry. In this article, we propose a new method for the identification of peptide-derived Amadori products in the mixtures obtained by enzymatic hydrolysis of glycated proteins. Two proteins, ubiquitin and human serum albumin (HSA), were modified with an equimolar mixture of glucose and [$^{13}\text{C}_6$]glucose and were subjected to enzymatic hydrolysis. The obtained enzymatic digests were analyzed by high-resolution mass spectrometry (HRMS), and the peptide-derived Amadori products were identified on the basis of specific isotopic patterns resulting from ^{13}C substitution. The number of glycated peptides in the digest of HSA detected by our procedure was in agreement with the data recently reported in the literature.

Słowa kluczowe

glycation, mass spectrometry, Isotopic labeling

Adres publiczny

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