



Development of a Novel Mass Spectrometry-Based Method for Simultaneous Qualitative and Quantitative Protein Citrullination Analysis of Complex Biological Samples

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The Invention

UW-Madison researchers have developed a novel mass spectrometry (MS)-based method for simultaneous qualitative and quantitative protein citrullination analysis from biological and clinical samples. The key to this method is a novel thiol-containing biotin tag, which enables qualitative analysis of citrullinated proteins. The tag works together with 2,3-butanedione to specifically derivatize the ureido group at the side chain of peptidylcitrulline, enabling the concurrent biotinylation of citrullinated peptides and a mass shift from 0.984 Da to 254 Da upon citrullination. Following this, the biotin tag-modified citrullinated peptides can be enriched and released for MS-based identification. In addition, the enlarged mass shift allows for precise annotation of citrullination sites, eliminating the interference of deamidation. The method has been successfully applied to real biological sample analyses.

Furthermore, the biotin tag-assisted qualitative method can be integrated with various MS-based quantitative proteomics strategies, such as stable isotopic labeling strategies (e.g., SILAC & dimethyl labeling) or isobaric labeling strategies (e.g., TMT labeling & DiLeu labeling) for relative quantitation of citrullinated proteins. Consequently, this method is the first to enable simultaneous qualitative and quantitative analysis of post-translational modified (PTM) proteins, such as citrullinated and homocitrullinated polypeptides.

Additional Information

For More Information About the Inventors

- [Lingjun Li](#)

Tech Fields

- [Analytical Instrumentation, Methods & Materials : Mass spectrometry](#)

For current licensing status, please contact Jennifer Gottwald at jennifer@warf.org or 608-960-9854