**附件1：**

**Site-specific quantification of protein core-fucosylation by isotope incorporation and SRM-MS**

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Targeted researches on glycosylated proteins are considered increasingly as a ways to find novel diagnostic or therapeutic targets, of which core fucosylation (CF) glycoproteomics has attracted particularly great interesting. Previous reports show that CF-glycoproteins are involved in many important physiological and pathological processes, especially during cancer progression. In our early study, a delicate approach was designed, which integrated molecular weight (MW) cut-off, neutral loss-dependent MS3 and database-independent candidate spectrum filtering and optimization, to effectively identify CF-glycoproteins in a large scale. The approach is promising in that it generated the highly accurate and largest dataset of core-fucosylated protein so far. However, it only provides a qualitative view of the CF-glycoproteins in a system, the development of a method for quantitative measurement of CF-glycoproteins is necessary.

Here, we tend to establish a quantification method for site-specific CF level of CF-glycoproteins by combining stable isotope incorporation, selected reaction monitoring (SRM) on triple quadrupole mass spectrometry and our enrichment methods in early research. Our results indicate that the simplified glycopeptides (peptide sequence attached with fucose-GlcNAc disaccharides) show different fragmentation pattern along with the change of collision energy in triple quadrupole, this tendency cannot be obtained from the fragmentation pattern in ion trap. The parent ion mass and neutral loss mass due to preferential loss of fucose provide the strongest SRM transition for quantitative analysis of CF-modification. The developed method was further applied to the analysis of 7 CF-glycopeptides from clinical serum from HCC patient, and the differential expression of some peptides could be inferred.

**Key words:**

core-fucosylation/ selected reaction monitoring/ isotope labeling/quantitation

**Reference:**

Jia W, Lu Z, Fu Y, Wang HP,*et al.*, A Strategy for Precise and Large Scale Identification of Core Fucosylated Glycoproteins. ***Mol Cell Proteomics.***2009,8(5):913-23.