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Improvement of core-fucosylated glycoproteome coverage via alternating HCD and ETD fragmentation

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Core-fucosylation (CF) plays important roles in regulating biological processes in eukaryotes. Alterations of CF-glycosites or CF-glycans in bodily fluids correlate with cancer development. Therefore, global research of protein core-fucosylation with an emphasis on proteomics can explain pathogenic and metastasis mechanisms and aid in the discovery of new potential biomarkers for early clinical diagnosis. In this study, a precise and high throughput method was established to identify CF-glycosites from human plasma. We found that alternating HCD and ETD fragmentation (AHEF) can provide a complementary method to discover CF-glycosites. A total of 407 CF-glycosites among 267 CF-glycoproteins were identified in a mixed sample made from six normal human plasma samples. Among the 407 CF-glycosites, 10 are without the N-X-S/T/C consensus motif, representing 2.5% of the total number identified. All identified CF-glycopeptide results from HCD and ETD fragmentation were filtered with neutral loss peaks and characteristic ions of GlcNAc from HCD spectra, which assured the credibility of the results. This study provides an effective method for CF-glycosites identification and a valuable biomarker reference for clinical research.

Biography

Cheng Ma has completed his PhD from Beijing Proteome Research Center (BPRC). His work as a research scientist in Georgia State University focused on development of novel techniques to analyze the sequence of glycopeptides through the fragment ions of MS/MS. He has a broad background in proteomics, glycoprotemics, glycomics, as well as bioinformatics. Meanwhile, He has more than eight years' experience in mass spectrometry operation.

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