

KN6 Soft ionization and dissociation required for glycoproteomic studies

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New idea on the site-occupancy for O-glycosylation is provided.

MS of glycopeptides plays the key role in elucidating the structural issues of glycoproteins, and allows site-specific profiling of N-glycans of even the large glycoproteins [1-3]. By contrast, the analysis of O-glycosylated proteins is a formidable task. Unlike N-glycosylation, there are no reliable consensus sequences to predict O-glycosylation due to multiple GalNAc transferase isozymes, overlapping of their substrate specificities and clustered attachment. In addition, high proline content in the vicinity of glycosylated sites prevents collision-induced dissociation from elucidating the full sequence of peptides. As a result, less than 100 O-glycosylation sites have been recorded in the human protein database. Electron transfer dissociation is obviously a major breakthrough in the O-glycosylation study. With this new technology, we can determine the site occupancy as well as attachment sites. A line of our studies on the major O-glycosylated proteins such as IgA1, fetuin and hemopexin have suggested that the site occupancy is invariable among individuals.

In my talk, two other topics, quantitation of glycans by MS [4] and the MALDI MS using mid-IR laser, will be presented as well.

[1] Y. Wada, M. Tajiri, S. Yoshida, *Anal Chem* 2004, 76: 6560-6565.

[2] M. Tajiri, S. Yoshida, Y. Wada, *Glycobiology* 2005, 15: 1332-1340.

[3] M. Tajiri, C. Ohyama, Y. Wada, *Glycobiology* 2008, 18: 2-8.

[4] Y. Wada, et al., *Glycobiology* 2007, 17: 411-422.