

Hybridation of Mass Spectrometry and Infrared Ion Spectroscopy for Glycoanalytics

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Deciphering the sequence of carbohydrates is a major challenge in glycosciences today. Whereas spectroscopic approaches (NMR, Raman, ...) and Mass Spectrometry (MS) offer valuable information on carbohydrate structure, they also suffer from severe technical limitations: on one hand, spectroscopy provides refined structural detail but requires a relatively large amount of purified sample, on the other hand MS applies to complex samples in small amounts, but does not disambiguate all carbohydrate isomerisms.

In this context, we have developed a unique hybrid Glycoanalytical approach, which adds a spectroscopic dimension to MS analysis. Based on this technology, it is possible to measure simultaneously the MS spectrum and the spectroscopic fingerprint of a carbohydrate. This enables the disambiguation of all kinds of carbohydrate isomerisms (monosaccharide content, regiochemistry and stereochemistry of the glycosidic bond, and positional isomers of functional modifications) without the need for chemical modification, labelling, or thorough purification.

While this new carbohydrate metric mitigates the lack of structural specificity of MS without the limitation of traditional spectroscopy, the identification of a carbohydrate however still relies on the availability of referenced standards. In order to enable true “de novo” analysis, we have established a top-down sequencing strategy based on the demonstration of a memory of the carbohydrate sequence within MS fragmentation products. [1] The performance of de novo carbohydrate sequencing will be illustrated on various classes of carbohydrates.

1. B. Schindler et al. Nature Communications, 8 (2017).