MOBILIZING THE LIBRARY: USING IMS-MS DATA TO SUPPLEMENT GU LIBRARY SEARCHING FOR GLYCAN IDENTIFICATION

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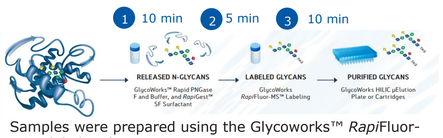
INTRODUCTION

Glycan analysis is a key area of research in many scientific disciplines, including the health sciences and the biopharmaceutical industry. The path to structural characterization requires careful navigation in data analysis and is complicated by the multiple isomeric possibilities for a single composition. Glycan characterization frequently employs multiple analytical techniques and often relies on mass spectrometry (MS) and tandem MS, the latter requiring significant skill in spectral interpretation and is a laborious process and may require additional confirmatory experiments (e.g. exoglycosidase digestions). Here, we present the use of ion mobility (IMS)-MS data to improve glycan identification when performing LC retention time-(normalized in glucose units) based scientific library searches.[1]

Key Words

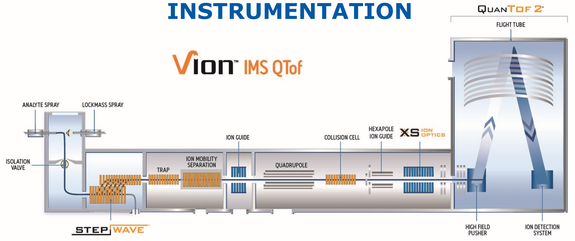
- IMS: Ion mobility spectroscopy
- RFMS: *Rapi*Fluor-MS™
- GU: Glucose unit
- CCS: Collision cross section
- rCC: reduced CCS
- HDMS: High Definition MS

SAMPLE PREPARATION



Samples were prepared using the Glycoworks™ *Rapi*Fluor-MS™ labeling kit.

INSTRUMENTATION



INSTRUMENT CONDITIONS

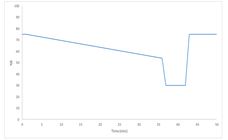
LC Conditions

LC System:	ACQUITY UPLC H-Class Bio
LC Column:	ACQUITY BEH Glycan Amide, 2.1 x 150 mm, 130 Å pore size, 1.7 µm particle size
Column Temp.:	60° C
Sample Temp.:	4° C
Fluorescence Detection:	Ex 265 nm/Em 425 nm

Gradient Conditions

Mobile Phase A:	50 mM ammonium formate, pH = 4.5
Mobile Phase B:	Acetonitrile

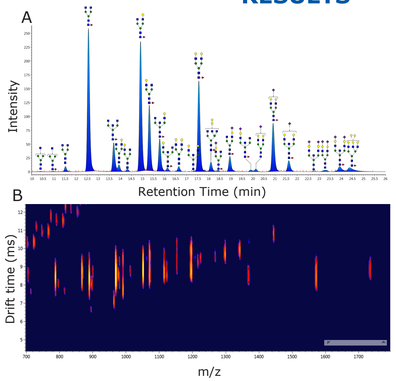
Time (min)	Flow Rate (mL/min)	%A	%B
0	0.4	25	75
36	0.4	46	54
37	0.4	70	30
42	0.4	70	30
43	0.4	25	75
50	0.4	25	75



MS Conditions

MS System:	Vion IMS QTof
Analyzer Mode:	ESI+, sensitivity mode
Capillary Voltage:	3.0 kV
Cone Voltage:	40 V
m/z Range	400-2000
Scan Rate:	1 Hz
Acquisition:	HDMS
Instrument Control:	UNIFI 1.8
Informatics:	UNIFI Glycan Application Solution
Scientific Library:	RFMS Glycan GU Library (co-developed with NIBRT, Ireland)

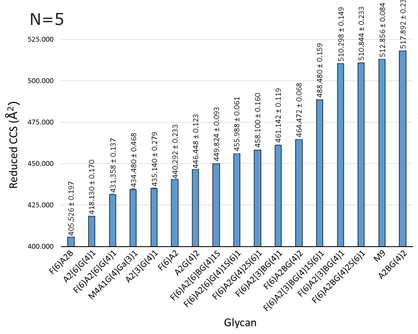
RESULTS



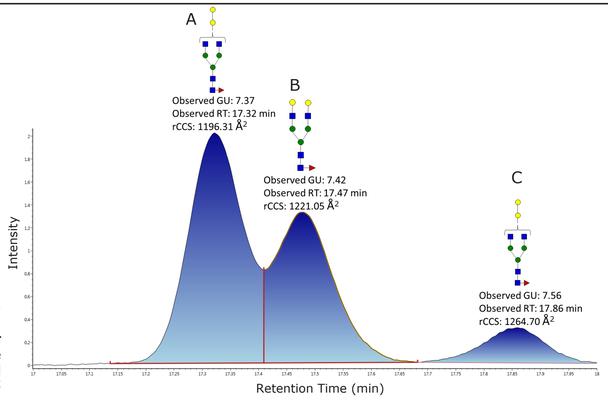
We identified 25 mass confirmed RFMS-labeled glycans from pooled human IgG using our Glucose Unit library, shown in Panel A. Panel B shows a plot of *m/z vs* drift time. The majority of the ions were doubly-charged and had drift times between 6.5-12.5 ms. From these drift times, Unifi automatically calculated collision cross sections (CCS) and reduced CCSs (rCCS) values, based on a calibration using a polyalanine ladder.

rCCS values were used due to their charge-independent nature and were calculated by CCS = (rCCS * $\mu^{1/2}$)/z where µ = (Mi * Mn) / (Mi + Mn), Mi = m/z * z, and Mn = Drift gas mass

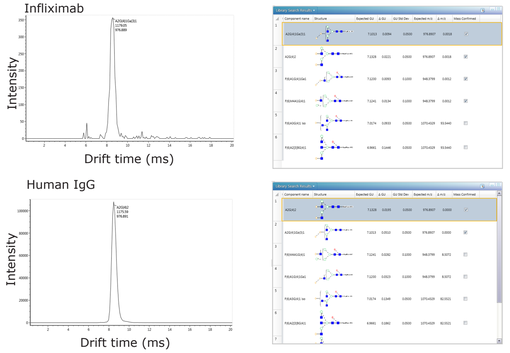
Reproducibility of Glycan Reduced Collision Cross Sections



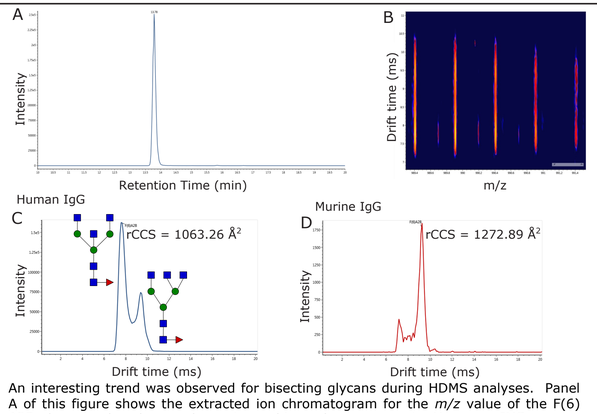
We studied the reproducibility of rCCSs of RFMS-labeled glycans through 5 injections of pooled human IgG. This graph demonstrates that rCCS values are very reproducible with RSDs less than 0.5%.



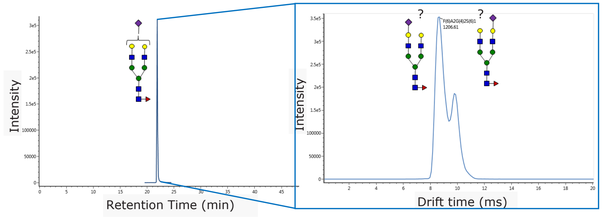
We investigated the use of rCCSs to assist our GU library searching. With a search tolerance of 0.2 GU units, we are sometimes challenged by isomeric species that have GU values that are within this tolerance, as shown in the FLR chromatogram above. However, Isomers A and B have rCCS values sufficiently different and we can correctly assign each peak without the need for additional experiments. To ensure that we did have the correct assignments, MS^E experiments were performed and Isomer A produced an abundant ion at *m/z* 528.19, indicating the presence of α-linked galactoses while Isomer B generated an intense ion at *m/z* 366.14, confirming both galactoses were attached to GlcNAcs.



This figure demonstrates the usefulness of rCCS values. In an infliximab sample, our library search indicated that the glycan eluting at 17.4 min was A2G(4)1Ga(3)1 based on GU values. Unfortunately for this low abundance glycan, tandem MS experiments were not able to conclusively confirm this assignment. However, the rCCS value (1179 Å²) was nearly identical to that of A2G(4)2 (1175 Å²) from human IgG where MS^E did confirm the assignment. Using rCCS values, we believe that that the correct assignment for this glycan in infliximab is A2G(4)2.



An interesting trend was observed for bisecting glycans during HDMS analyses. Panel A of this figure shows the extracted ion chromatogram for the *m/z* value of the F(6) A2B glycan and only one chromatographic peak was present. However, IMS separation, shown in Panels B and C, reveals two distinct peaks, suggesting a possible isomeric species was present in human IgG. Interestingly, the IMS profile shifted the predominant peak to the lower mobility species in a different monoclonal antibody. These two species were observed to have significantly different rCCS values.



IMS also appears to be able to resolve the sialic acid positional isomers of F(6) A2G(4)2S1. However, at this time, there is still some ambiguity as to which isomer is associated with each IMS peak.

CONCLUSIONS

- rCCS values can improve the confidence of GU library search results, particularly for isomeric glycans that have GU values within the search tolerance.
- rCCS values can add an extra dimension of knowledge and may be useful in cases when tandem MS data is inconclusive.
- Possible IMS resolution of glycan isomers within a given chromatographic peak was observed.

Reference

Yu, Y. Q. N-linked Glycan Characterization and Profiling: Combining the Power of Accurate Mass, Reference Glucose Units, and UNIFI Software for Confident Glycan Assignments. 2014.

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