# **ASMS 2005**

## **OVERVIEW**

A micro scale hydrophilic interaction chromatography (HILIC) SPE cartridge is applied to enrich and fractionate N-linked glycans released from glycoproteins. The fractionation of glycans from HILIC SPE is achieved by using low and high pH stepped elutions. Fractionation enables isolation and enrichment of sialylated glycans, therefore, simplifying the identification and structural characterization of these glycans using MALDI MS analysis.

### Scheme 1. Micro scale HILIC SPE Protocol



A 96 well micro scale HILIC SPE plate operated via a vacuum manifold was used to extract and fractionate neutral and acidic glycans.

#### **MALDI MS**

- Waters MALDI micro MX<sup>TM</sup>, MALDI QTof Ultima<sup>TM</sup>
- MALDI Matrix: MassPREP<sup>TM</sup> DHB (20 mg/ml in 100% ETOH)
- HILIC SPE extracted sample was mixed with MALDI matrix in 1:1 ratio directly on the target and dried at ambient temperature. After crystallization, 0.8 µl of EtOH was spotted on the target to recrystallize the sample. The glycans spotted on the MALDI target are released from 10 to 100 pmol of proteins
- MALDI-TOF positive and negative ion mode was used to acquire spectrum
- MS/MS fragmentation was performed on the AGP glycans after neuraminidase treatment

### INTRODUCTION

Characterization of oligosaccharides from glycoproteins is challenging due to their structural heterogeneity and low abundance. Glycans released from glycoproteins contain both neutral and acidic glycans. Extensive fragmentation of sialylated glycans (loss of sialic acids) occurs with MALDI and multiple peaks are generally observed as a result of the fragmentation. Since the desialylated fragment ions can have the same mass as the corresponding native neutral glycans, this complicates glycan assignment.

HILIC SPE was used for the removal of salts and detergents from hydrophilic analytes such as oligosaccharides. In addition, we developed a method for SPE fractionation of glycans based on their acidity. The fractionation is performed using two elution steps (Scheme 1). The first elution uses an acidic solution and neutral glycans are released from the SPE exclusively; the second elution is a pH neutral solution which elutes the remaining glycans that contain acidic glycans only.

The fractionated glycans are analyzed separately, which reduces the complexity of the sample, allows an easier assignment of sialylated glycans.

# **METHODS**

#### Deglycosylation

Glycoproteins, RNase B, and a1-acid glycoprotein (Sigma) were solubilized in 0.1% surfactant, RapiGest<sup>TM</sup> SF. DTT was added to the solution to a final concentration of 10mM before heating the sample at 100°C for 5 minutes. The protein sample was buffered using equal volume of 100 mM NH<sub>4</sub>HCO<sub>3</sub>. PNGase F was used to remove N-linked glycans.

The released glycans were desalted using Waters 96 well MassPREP™ HILIC µElution plate.

Sialic acids from AGP glycans were removed by using neuraminidase (sigma)

# TO DOWNLOAD A COPY OF THIS POSTER VISIT WWW.WATERS.COM/POSTERS



Figure 1. MALDI-TOF MS negative ion analysis of 25 ng of sialylated glycan A2F. A) Control sample, A2F was analyzed directed without desalting. B) HILIC µElution SPE was used to desalt A2F (see method for protocol). No A2F ions were observed from the first elution fraction which contains 0.1% formic acid. C) A2F was eluted from the HILIC SPE using 10 mM ammonium citrate (pH 7).

# RESULTS



Figure 2. MALDI-TOF MS of mixed glycans. A) MALDI TOF MS positive ion mode of control sample of mixed neutral glycan (Maltoheptaose) and acidic glycan A2F, extensive fragmentation of A2F ions were observed. B) MALDI-TOF positive ion mode showed that Maltoheptaose was fractionated in the low pH elution. C) MALDI-TOF negative ion showed that the A2F was eluted using the high pH elution.

#### 3. Mixed glycans released from glycoprotein, RNase B and $\alpha$ 1-Acid Glycoprotein (AGP) RNase B contains neutral glycans while AGP contains only sialylated glycans



Ying Qing Yu, Jennifer Kaska, Martin Gilar and John C. Gebler Waters Corporation, Milford, MA, 01757



### CONCLUSIONS

- This micro scale HILIC SPE device removes salts and detergents from glycans released from glycoproteins enzymatically prior to mass spectrometry analysis
- The low and high pH stepped elution can effectively fractionate neutral and acidic glycans (sialylated), since
  - 1. Neutral glycans retain on HILIC SPE due to hydrophilic interaction
  - 2. Acidic glycans retain on HILIC SPE due to both hydrophilic interaction and weak anion exchange mechanism
- The fractionation of glycans simplifies glycan samples and the sialylated glycan assignment



Figure 4. MALDI-QTof MS/MS fragmentation was performed on the desialylated AGP glycans. The fragment ion peak list and their intensity was submitted to Glycosuite database (ProteomeSystems) for structural identification. The structure with the highest score was proposed for the likely structure and showed in the bottom spectrum. Ions labeled with a solid green circle were partially desialylated ions. The top MS/MS spectrum is shown as an example. Ions generated from glycosidic bond cleavages are labeled