

Rapid Discovery of Differentially Expressed Proteins in T2D Plasma Samples Using Improved UHPLC Chromatography and pSMART Data Acquisition

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Overview

Purpose: Develop a robust, comprehensive workflow to perform large-scale global protein differential expression analysis facilitating putative groups of protein biomarkers.

Methods: Combine high-flow UHPLC chromatography with pSMART data acquisition and Pinnacle software for robust and efficient workflow support.

Results: Over 500 proteins (>5000 peptides) were quantified in 134 samples originating from 4 groups generated distinct sets of biologically and statistically relevant proteins translated into more targeted studies.

Introduction

Translational proteomics links global protein discovery to targeted quantification with the ultimate goal of identifying and verifying relevant groups of proteins that collectively form potential biomarkers. To increase the effectiveness of the assay, two changes are made to traditional translational proteomics, increased number of proteins/peptides quantified across larger numbers of samples per biological group. These two changes facilitate robust determination of biological and statistical relevancy. These requirements introduce tremendous challenges for the experimental methods to maintain thorough identification and quantification without sacrificing throughput. We introduce a workflow to handle the increased analytical demands by incorporating ultra-high performance liquid chromatography (UHPLC)¹ with pSMART² to generate comprehensive LC-MS and MS/MS records for plasma peptides. In addition, we utilize the Pinnacle software for qualitative and quantitative data processing.

Methods

Sample Preparation

A set of 134 plasma samples were collected at the Joslin Diabetes Center representing five different biological groups. A total of 49 samples were classified as controls, 12 as type 2 diabetes (T2D), and 29, 25, and 23 samples for three other groups. The samples were digested with trypsin in the BRIMS Center using standard protocols and spiked with the PRTC kit prior to analysis.

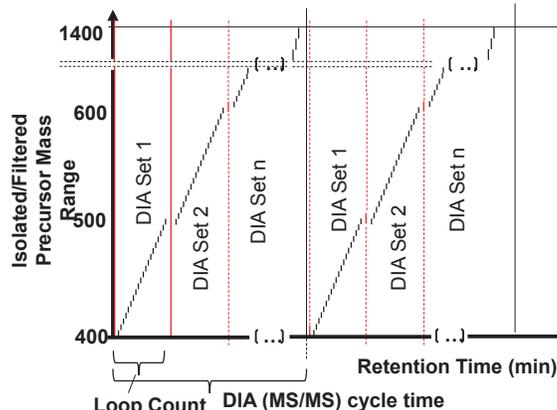
Liquid Chromatography (or more generically Separations)

A Thermo Scientific™ Vanquish™ UHPLC autosampler and pump delivered an analytical flow rate of 200 $\mu\text{L min}^{-1}$ for a linear gradient of 0.49% min^{-1} in 85 minutes using A) 0.2% formic acid and B) MeCN (0.2% formic acid). A UHPLC column comprised of three individual 250 x 2.1 mm Thermo Scientific™ Acclaim™ 120 C18 columns aligned in series and heated to 55 °C. A cycle time of 110 minutes was used from injection to injection.

Mass Spectrometry

All experiments were performed on the Thermo Scientific™ Orbitrap Fusion™ Tribrid™ mass spectrometer. The first analysis was performed using data dependent acquisition (DDA) scheme using a top 10 experimental method with MS resolving power of 120k and 15k for MS/MS data acquisition. A maximum ion fill time of 100 msec was used for all scan events. The resulting data was used to build a consolidated spectral library. The second data acquisition method used pSMART, which is comprised of two independent acquisition cycles for MS and narrow DIA spectral acquisition events. See Figure 1 for more details. The resolution settings and maximum ion fill times used for pSMART were the same as those listed for the DDA experiments. A loop count of 10 was used to meter the DIA acquisition events in between the MS scans.

FIGURE 1. The pSMART acquisition scheme used for global protein profiling shows the interspersed MS and narrow DIA acquisition scheme. Ten narrow DIA spectra (Loop Count) are acquired after every MS spectra. The total acquisition cycle acquires at least 9 full scan MS spectra and 80 narrow DIA events were acquired covering a precursor m/z range of 400-1400 Da. The goal of pSMART is to acquire 9 HR/AM MS data points and at least 1 narrow DIA spectrum under each peptide elution profile.

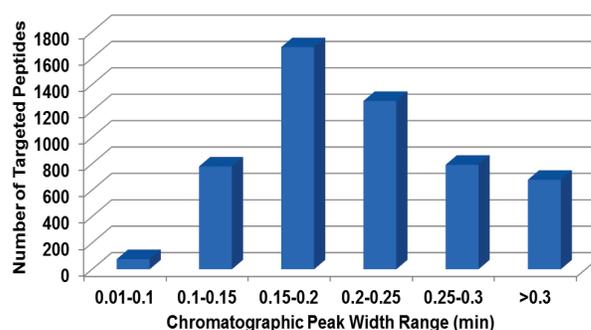


Data Analysis

An unbiased search was performed for all DDA data using Thermo Scientific™ Proteome Discoverer™ 1.4 software. The search results were consolidated to form a spectral library. All translational proteomics studies were performed using the Pinnacle software loaded on a Velocity data processing computer. (both products from Optys Technologies, Philadelphia, PA) The DDA spectral library was used to determine all targeted proteins and peptides as well as all LC and MS information. This reference information was imported into Pinnacle for post-acquisition data extraction, verification, and quantification. In addition, the Pinnacle software performed statistical relevancy analysis using receiver operator curve (ROC) analysis and p- and q-value determination. Biological relevancy was determined using Ingenuity Pathway Analysis software (Qiagen, Redwood City, CA).

Results

FIGURE 2. Incorporation of UHPLC pumps, columns, and high flow rates significantly increases the chromatographic performance for peak capacity, sensitivity, selectivity, and reproducibility. Figure 2 shows the reproducibility of repetitively measured retention times for all peptides across the month-long study.



Conclusion

The presented research workflow demonstrates a high-throughput analytic method for global protein profiling. The incorporation of high-flow UHPLC provides significant advantages for handling complex biological samples in a highly reproducible manner. Future studies will evaluate smaller bore UHPLC columns and lower flow rates while maintaining the similar chromatographic performance. Additional benefits of the workflow include:

- UHPLC generated excellent separation facilitating MS analysis of non-depleted digest samples
- The UHPLC set up facilitated extremely reproducible separations over the month-long study
- Data collection using pSMART data acquisition facilitated reproducible analyte sampling by HR/AM MS and MS/MS
- The Pinnacle software automated ca. 92 MB of data processing in 1.5 hrs resulting in comprehensive qualitative, quantitative, and statistical analyses for over 500 proteins and 5000 peptides

References

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2. Prakash, A., Peterman, S., Ahmad, S., Sarracino, D., Frewen, B., Vogelsang, M., Byram, G., Krastins, B., Vadali, G., Lopez, M. Hybrid data acquisition and processing strategies with increased throughput and selectivity: pSMART analysis for global qualitative and quantitative analysis *J. Proteome Res.*, **2014**, *13(12)*, 5415-30

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