Improvements in Peptide MRM Sensitivity Using Multiplex Monoclonal Antibody Capture (SISCAPA) and an Ion Funnel QQQ-MS at Standard Flowrate

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Introduction

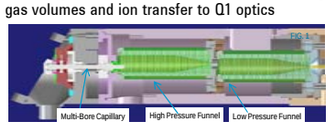
Quantitation of proteotypic peptides by SRM-MS allows specific, internally-standardized measurement of protein biomarkers in digests of plasma and can achieve sub-nanogram/ml detection levels when specific anti-peptide antibodies are used to enrich target peptides from the digest (SISCAPA). We have evaluated a multiplex SISCAPA panel based on 11 rabbit monoclonal antibodies to specific peptides from 10 proteins spanning a wide plasma concentration range. Use of an ion-funnel-equipped triple quadrupole instrument yielded high sensitivity at a flow rate of 400 µl/min, providing a workable alternative to nanoflow LC-SRM for SISCAPA assays.

Here we have sought to characterize the SISCAPA-enriched analyte peptides using more conventional (and robust) flow (2.1 mm column at 400 µl/min) chromatography in combination with a novel ion delivery system. The sensitivity and ion sampling efficiency of ESI ionization has been challenged over decades by several researchers primarily due to the significance for various analytical applications including peptide quantitation.

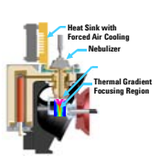
Ion Funnel Technology

The Agilent 6490 QQQ incorporates iFunnel technology which is a combination of three fundamental innovations:

- Agilent Jet Stream technology – ESI with thermal gradient ion focusing confinement
- Hexabore sampling capillary with 6 independent parallel bores to enable sampling a much larger fraction of the ions
- Dual-stage ion funnel for efficient removal of large gas volumes and ion transfer to Q1 optics



- Agilent JetStream is ESI with thermal gradient ion focusing confinement
- The standard heat sink was modified to provide additional shielding of the nebulizer to accommodate low flow rates



SISCAPA Methodology

Proteotypic tryptic peptides (initially 5 peptides per protein) were selected representing known protein biomarkers: PAI3 (protein C inhibitor), LPS binding protein, transferrin receptor, osteopontin, ferritin light chain, mesothelin, alpha-fetoprotein, HER2/neu, CA-125 and thyroglobulin. Proteotypic peptides for thyroglobulin included those reported by Hoofnagle.

Each peptide was synthesized with an added N-terminal cysteine and coupled to KLH. Pools of five such immunogens were injected into two rabbits, whose titers to each peptide were followed by a "peptide ELISA". Affinity-purified polyclonal antibodies against the two peptides for each protein showing highest titers were characterized in SISCAPA assays, after which rabbit monoclonal antibodies (RabMAbs) were prepared (Epitomics, Inc.) against the best performing peptide for each target, except for Tg, for which mAb's were made against two peptides. RAbMAbs were selected for high affinity binding to peptides in solution by surface plasmon resonance analysis.

Each RAbMAb was independently covalently immobilized on magnetic beads and a pool of all 11 RabMAb reagents was used in an automated procedure to capture the 11 corresponding stable isotope labeled internal standards and cognate endogenous peptides from plasma digest matrix, after which bound peptides were eluted for LC-SRM analysis.

Automation Development

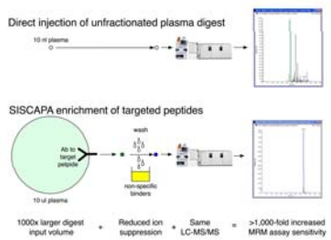
The multiplexed capture reaction setup, bead wash and analyte elution steps for a SISCAPA assay have been automated on a Bravo Automated Liquid Handling Platform (Agilent) to allow processing of 96 samples in less than 30 minutes.

The eluted peptides were delivered in a volume (20 µl) and solvent (5% acetic acid) suitable for subsequent injection into a reversed-phase LC system.

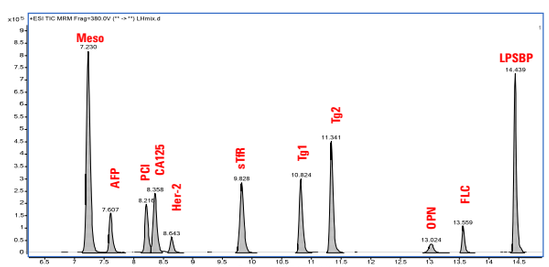
Results and Discussion

The near-purity of these analyte peptides, in contrast to the enormous matrix background of unfractionated plasma digests and their generally low absolute abundance (often sub-fmol) has to date focused attention on nanoflow chromatography and nanospray ESI as the preferred analytical platform despite its limited robustness for high-throughput applications in clinical laboratories.

With the increased sensitivity from thermal gradient ion focusing electrospray ionization and increased ion sampling with the hexabore capillary and dual ion funnel gain, standard flow LC becomes a workable, sensitive alternative to nanoflow LC-SRM for SISCAPA assays.



SISCAPA: Enrich target peptides and decrease sample complexity



Chromatographic separation developed for the analysis of the multiplexed SISCAPA samples.

Parameters for each of the 11 target peptides and cognate labeled standards were optimized, permitting use of retention-time scheduled SRM data collection. All peptides yielded narrow, well-shaped peaks at distinct elution times and displayed a wide range of peak areas (which are normalized in the figure above).

The 2.1 mm column provides superior loading and peak capacity compared to nanoflow which results in excellent separation and retention time reproducibility. In general, the retention time for all analytes showed less than 0.2% RSD across the concentration range for the standard curves (both forward and reverse curves).

LC/MS Conditions

MS: dynamic MRM with 400 ms cycle time, positive mode AJS source, Unit resolution on precursor and wide resolution on product ion

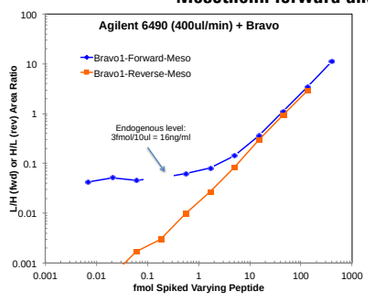
LC: Zorbax Eclipse Plus C18 **2.1 x 150 mm** column, 1.8 um particles. Flow rate **0.4 mL/min.**
Solvent A = 0.1% formic acid in water
Solvent B = 0.1% formic acid in 90% acetonitrile in water
Gradient: 3% at 0 min, 10% at 1 min, 20% at 10 min, 35% at 14 min, 90% at 15 min, 90% at 19 min, then 3% at 20 min

Stop time: 21 min
Post time: 4 min

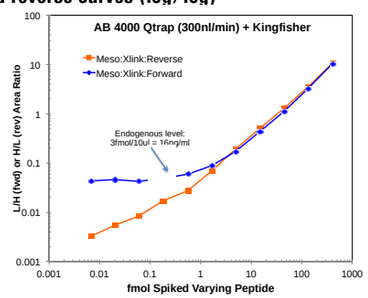
Results and Discussion

Using twelve-point dilution curves of both labeled internal standard peptides (i.e., reverse curves) and of unlabeled synthetic peptide (i.e., standard addition curves), we have characterized the response of these 11 assays in pooled human plasma digest matrix. The data clearly demonstrate that a majority of the analytes can be measured in the digest of 10 µl plasma using the optimized standard chromatography-ion-funnel MS method.

Mesothelin forward and reverse curves (log/log)

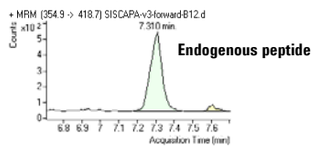


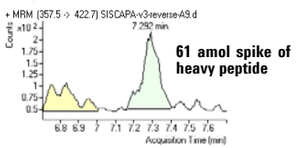
Standard flow ion funnel QQQ-MS



Nanoflow QQQ-MS

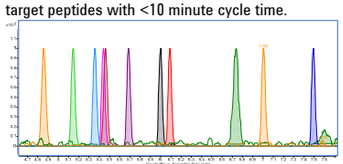
The figures above shows example standard curves obtained by adding varying amounts of either the heavy internal standard peptide ("Reverse" curve: 3-fold dilutions down from 400 fmol per peptide) or a synthetic version of the endogenous (unlabeled, light) peptide ("Forward" or standard addition curve). The difference between the curves is the presence of endogenous light peptide derived from the mesothelin protein in the plasma sample digested to provide the analytical matrix. The figures below show the endogenous level from the forward curve (left) and lowest level from the reverse curve (right).





Reducing LC/MS Analysis Time

The cleanliness of SISCAPA samples reduces the possibility of interferences in the MRM transitions, thus it is feasible to greatly reduce the analysis time. The figure below shows a separation for the target peptides with <10 minute cycle time.



Conclusions

- Multiplexed SISCAPA sample preparation can be automated for high-throughput assays
- Standard flow LC/MS using ion funnel technology on a QQQ mass spectrometer was equivalent to that achieved previous using nanoflow LC/MS
- Future development of will focus on LC/MS analysis times of <10 minutes for a multiplexed SISCAPA assay