

Development and evaluation of Nano-ESI coupled to a triple quadrupole mass spectrometer for quantitative proteomics research

ASMS 2013 ThP 115

Shannon L. Cook¹, Hideki Yamamoto², Tairo Ogura²,
Yusuke Osaka², Ichiro Hirano²

¹Shimadzu Scientific Instruments. 7102 Riverwood
Drive Columbia, MD 21046, USA ²Shimadzu
Corporation.

1, Nishinokyo-Kuwabaracho Nakagyo-ku, Kyoto
604-8511, Japan

Development and evaluation of Nano-ESI coupled to a triple quadrupole mass spectrometer for quantitative proteomics research

1. Introduction

Recently, the promotion of proteomic analysis has resulted in the identification of many proteins. Analyzing the proteins function, such as its various signaling pathways, is a clue to understanding disease. Historically, quadrupole time-of-flight mass spectrometry has been preferred over more quantitative, but less sensitive, triple quadrupole based mass spectrometric methodologies. Our aim is to develop a triple quadrupole based system to quantitatively

analyze peptide fragments through a shotgun proteomics approach. We developed both a conventional and nano-flow quantitative system for proteomic analyses utilizing liquid chromatography (LC) coupled to a triple quadrupole mass spectrometer (triple Q MS). We also demonstrate the sensitivity enhancement of the triple Q MS as a function of the MS front-end LC at analytical and nano-flow rates (Fig. 1).



Fig. 1 Nano-flow LC and LCMS-8040 triple quadrupole mass spectrometer

2. Methods and Materials

2-1. Methods

Samples were measured by ESI-MS coupled to either an UHPLC system or a nano-flow HPLC system.

Analysis by UHPLC coupled to triple Q MS (conventional LC-MS)

UHPLC conditions (Nexera system)

Column	: Shim-pack XR-ODS III 2 mm I.D. × 50 mm L., 1.6 µm
Mobile phase A	: 0.5% acetic acid in aq.
B	: acetic acid / Water / Acetonitrile (0.5/19.5/80)
Flow rate	: 0.2 mL/min
Time program	: B conc.5%(0 min) - 60%(10 min) - 100%(10.01-20 min) - 5%(20.01-30 min)(Fig. 2)
Injection vol.	: 1 µL
Column temperature	: 40°C

MS conditions (LCMS-8040)

Ionization	: ESI
Events	: Positive MRM mode
Applied Voltage	: 4.5 kV
Desorption Liquid temp.	: 300°C
Heat Block temp	: 500°C
Nebulizer Gas flow rate	: 3 L/min
Drying Gas flow rate	: 10 L/min

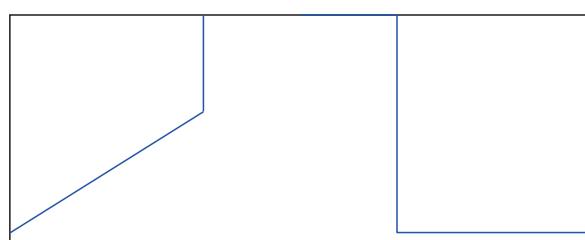


Fig. 2 The time program of conc.B gradient curve of the UHPLC system

Development and evaluation of Nano-ESI coupled to a triple quadrupole mass spectrometer for quantitative proteomics research

Analysis by nano-flow HPLC coupled to triple Q MS (nano-flow LC-MS)

nanoLC conditions (Prominence system)

Column	: column with nano spray tip 100 µm I.D. × 150 mm L., 3 µm (Reprosil® particles)
Mobile phase A	: 0.5% acetic acid in aq.
B	: acetic acid / Water / Acetonitrile (0.5/19.5/80)
Flow rate	: 500 nL/min
Time program	: B conc.5%(0 min) - 60%(30 min) - 100%(31-40 min) - 5%(45-65 min) (Fig. 3)
Injection vol.	: 1 µL
Column temperature	: Room Temp.

MS conditions (LCMS-8040)

Ionization	: nano-ESI (sprayed by nano spray tip)
Events	: Positive MRM mode
Applied Voltage	: 2.5 kV
Desorption Liquid temp.	: 250°C
Heat Block temp.	: 200°C
Nebulizer Gas flow	: None
Drying Gas flow	: None

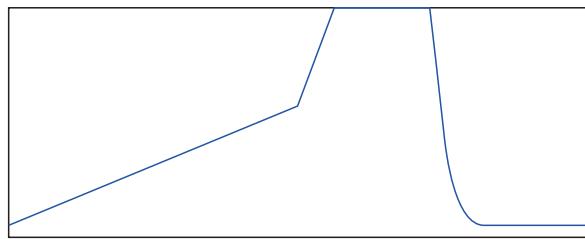


Fig. 3 The time program of conc.B gradient curve of the nanoLC system

The nano-flow HPLC system consists of binary pumps and autosampler. The flow channel is illustrated below (Fig. 4).

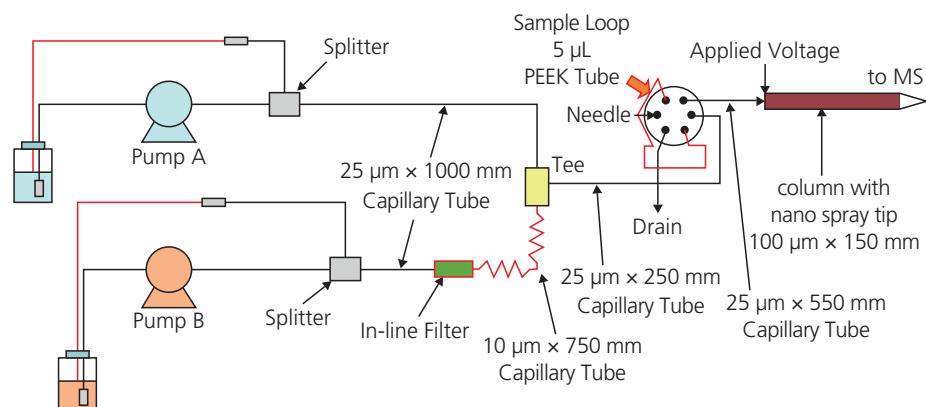


Fig. 4 The flow channel configuration of the nano-flow HPLC system

2-2. Materials

Digested BSA (Bovine Serum Albumin) was analyzed to optimize the conditions of the LC and the triple Q MS parameters.

Development and evaluation of Nano-ESI coupled to a triple quadrupole mass spectrometer for quantitative proteomics research

Digestion of BSA

1 mg/mL of BSA in 50 mM Ammonium Bicarbonate (ABC) and 8 M Urea solution
 ↓ Add 10 mM of dithiothreitol, 37°C 30 min
 ↓ Add 50 mM of 2-iodoacetamide, 37°C 30 min
 ↓ Add 10 µL of LysC (1 µg/µL), 37°C 4h
 ↓ Diluted by 3 mL of 50 mM ABC
 ↓ Add 20 µg of Trypsin, 37°C overnight
 Quenched by 10% trifluoroacetic acid (TFA) in aq.

Desalination of peptides

Add 1 mL of Buffer B to Stage Tip
 ↓ Centrifuge 500 g 3 min
 Add 1 mL of Buffer A to Stage Tip
 ↓ Centrifuge 500 g 3 min
 Add 1 mL of BSA Digestion to Stage Tip
 ↓ centrifuge 500 g 4 min
 Add 1 mL of Buffer A to Stage Tip
 ↓ centrifuge 500 g 4 min
 Add 250 µL of Buffer B to Stage Tip
 ↓ Centrifuge 300 g 2 min
 Preserve elution buffer at -20°C

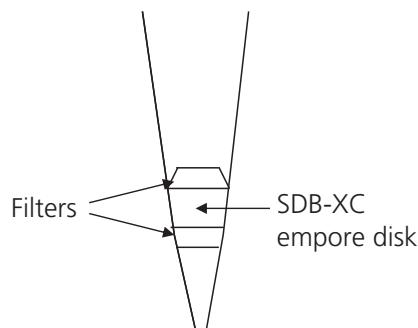


Fig. 5 Structure of Stage Tip.

Buffer A: TFA / H₂O / ACN (0.1/4.9/95),
 Buffer B: TFA / H₂O / ACN (0.1/19.9/80)

3. Results

Most peptides in digested BSA were detected as protonated divalent or trivalent molecules([M+2H]²⁺ or [M+3H]³⁺) in ESI positive ion mode. The precursor ions were monitored by Q1 SIM measurement. Mass spectrometric parameters for MRM analysis, such as product ion and collision energy, were optimized by an automatic MS optimization procedure. The chromatographic and automatic MS optimization produced 107 MRM transitions for 11 peptides for both the nano-flow LC-MS method and the conventional LC-MS methods. Quantitative analyses were performed for peptides containing at least 7 amino acids (Table 1).

Calibration curves were generated from each MRM transition with linearity improving when analyzed by nano-flow LC-MS as opposed to conventional LC-MS. Concentration ranges of the conventional LC-MS method and the nano-flow LC-MS method were 1-50 pmol and 10-500 fmol. Additionally, the LOD and LOQ of each transition analyzed by the nano-flow LC-MS method is several hundred fold lower than the conventional LC-MS method (Table 1, Fig. 6). In summary, we improved the sensitivity of a triple Q MS by reducing the LC flow rate to nL/min. A few femtmoles of injected peptides could be analyzed by nano-flow LC-MS.

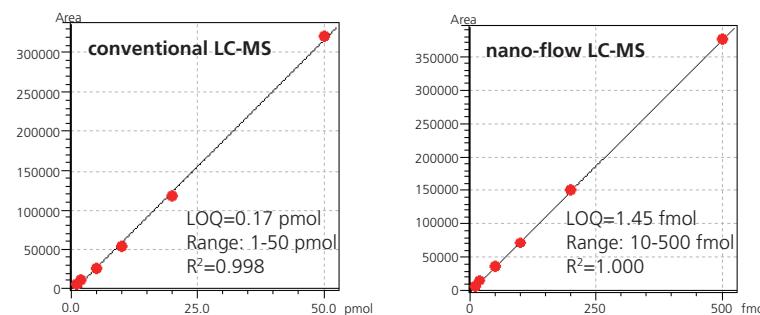


Fig. 6 Representative calibration curve [DDSPDLPK>b2(443.70>230.90)]

Development and evaluation of Nano-ESI coupled to a triple quadrupole mass spectrometer for quantitative proteomics research

4. Conclusions

• Nano-flow LC enhanced the sensitivity of a triple Q MS, as a function of the MS front-end LC, as opposed to conventional LC while improving the linearity of calibration curves.

- We developed and evaluated a novel quantitative system for proteomics with the results suggesting that this system could be applicable as a tool for shotgun proteomics.

Table 1 MRM transitions of BSA Digests and the LOD, LOQ, and relation coefficient (R^2) of each transition for both the nano-flow LC-MS method and the conventional LC-MS method.

MRMtransition	<i>m/z</i>	conventional LC-MS			nano-flow LC-MS		
		LOD(pm mol)	LOQ(pm mol)	coefficient(R^2)	LOD(fm mol)	LOQ(fm mol)	coefficient(R^2)
ECCDKPPLKEK>y2+++H2O	646.30-129.30	0.41	1.24	0.996	0.58	1.74	1.000
ECCDKPPLKEK>y1	646.30-147.00	0.36	1.08	0.999	1.67	5.02	1.000
ECCDKPPLKEK>y10++H2O	646.30-637.35	0.08	0.24	0.995	0.27	0.80	0.999
ECCDKPPLKEK>y3++	646.30-130.20	0.29	0.86	0.996	3.92	11.75	0.999
ECCDKPPLKEK>b4+++H2O	646.30-183.30	0.30	0.91	0.997	2.25	6.75	0.999
ECCDKPPLKEK>y2-H2O	646.30-258.10	0.19	0.56	0.997	1.94	5.83	0.995
CCTESLNVNR>b4+++H2O	569.75-178.00	0.03	0.10	0.998	0.41	1.24	1.000
CCTESLNVNR>y9++H2O	569.75-560.95	0.03	0.09	0.998	1.20	3.61	0.999
CCTESLNVNR>y7	569.75-818.45	0.02	0.06	0.997	0.32	0.97	0.999
CCTESLNVNR>y1	569.75-175.20	0.03	0.09	0.996	1.91	5.72	0.998
CCTESLNVNR>b2	569.75-320.85	0.06	0.17	0.994	0.37	1.12	1.000
CCTESLNVNR>y2	569.75-289.05	0.09	0.28	0.999	1.58	4.73	1.000
CCTESLNVNR>y5	569.75-588.15	0.06	0.17	0.996	0.29	0.88	0.998
CCTESLNVNR>y6	569.75-717.15	0.05	0.15	0.996	0.58	1.74	0.998
CCTESLNVNR>y3	569.75-388.35	0.09	0.26	0.995	1.81	5.42	0.998
CCTESLNVNR>b5+++	569.75-213.10	0.11	0.32	0.992	1.01	3.02	0.998
DDSPDLPK>b2	443.70-230.90	0.06	0.17	0.998	0.48	1.45	1.000
DDSPDLPK>y2	443.70-244.20	0.06	0.17	0.998	0.29	0.88	1.000
DDSPDLPK>y6	443.70-656.35	0.05	0.16	0.998	0.07	0.20	1.000
DDSPDLPK>b2-H2O	443.70-212.70	0.15	0.45	0.995	0.79	2.37	0.999
DDSPDLPK>y5	443.70-569.20	0.11	0.34	0.999	0.27	0.82	1.000
DDSPDLPK>y1	443.70-147.25	0.13	0.40	0.999	1.65	4.95	1.000
DDSPDLPK>y6++H2O	443.70-319.90	0.08	0.24	0.996	3.12	9.37	0.998
DDSPDLPK>y5++	443.70-285.30	0.21	0.64	0.996	1.14	3.42	1.000
DDSPDLPK>b3-H2O	443.70-300.20	0.12	0.36	0.993	2.22	6.66	0.999
DDSPDLPK>y6+++H2O	443.70-213.40	0.51	1.54	0.999	1.88	5.64	0.997
DDSPDLPK>b4+++	443.70-139.10	0.30	0.89	0.998	3.33	9.99	1.000
DLEEEHFK>y6	487.75-746.20	0.05	0.14	0.989	0.36	1.07	1.000
DLEEEHFK>b2	487.75-229.05	0.05	0.15	0.988	0.27	0.82	0.999
DLEEEHFK>b3+++	487.75-96.45	0.21	0.62	0.981	1.26	3.79	0.994
DLEEEHFK>y2+++	487.75-98.45	0.86	2.57	0.965	2.46	7.37	0.997
DLEEEHFK>y6+++	487.75-249.20	0.08	0.24	0.992	0.37	1.11	0.995
DLEEEHFK>y6++	487.75-373.45	0.11	0.32	0.983	0.38	1.15	0.999
GACLLPK>y2	379.70-244.10	0.05	0.14	0.991	0.40	1.19	1.000
GACLLPK>b2	379.70-129.20	0.03	0.08	0.990	0.35	1.04	1.000
GACLLPK>y5+++	379.70-315.70	0.04	0.12	0.990	0.37	1.11	1.000
GACLLPK>y5	379.70-630.35	0.04	0.13	0.990	0.38	1.13	1.000
GACLLPK>y1	379.70-147.20	0.04	0.12	0.992	0.45	1.34	1.000
GACLLPK>b2	379.70-289.10	0.04	0.12	0.990	0.39	1.16	1.000
GACLLPK>y3	379.70-357.15	0.05	0.14	0.991	0.32	0.95	1.000
GACLLPK>y4	379.70-470.40	0.05	0.14	0.993	0.39	1.16	1.000
GACLLPK>y6+++	379.70-351.51	0.04	0.12	0.991	0.31	0.94	0.999
GACLLPK>b4	379.70-402.25	0.03	0.08	0.994	0.57	1.71	0.999
GACLLPK>b4+++	379.70-201.25	0.03	0.10	0.992	0.68	2.03	0.999
LVTDLTK>y5	395.25-577.35	0.03	0.09	0.991	0.37	1.10	1.000
LVTDLTK>b2	395.25-212.90	0.04	0.11	0.991	0.38	1.14	1.000
LVTDLTK>y7++H2O	395.25-386.20	0.02	0.05	0.989	0.50	1.51	1.000
LVTDLTK>y2	395.25-248.05	0.05	0.14	0.989	0.40	1.20	0.999
LVTDLTK>y1	395.25-147.30	0.04	0.11	0.991	0.64	1.93	0.999
LVTDLTK>y6	395.25-676.35	0.03	0.08	0.991	0.17	0.52	0.999
LVTDLTK>y3	395.25-361.10	0.05	0.16	0.991	0.20	0.59	0.999
LVTDLTK>y2-H2O	395.25-230.10	0.25	0.75	0.990	0.35	1.04	0.998
AEVFEVTK>b2	461.75-201.15	0.04	0.11	0.991	0.27	0.81	1.000
AEVFEVTK>y6	461.75-722.40	0.03	0.10	0.992	0.41	1.24	1.000
AEVFEVTK>y2	461.75-248.30	0.03	0.10	0.993	0.34	1.01	0.999
AEVFEVTK>y5	461.75-575.30	0.05	0.16	0.994	0.29	0.88	0.999
AEVFEVTK>y6++	461.75-361.60	0.06	0.17	0.991	0.25	0.74	0.999
AEVFEVTK>y4	461.75-476.30	0.03	0.08	0.991	0.36	1.07	0.999
AEVFEVTK>y3	461.75-346.95	0.04	0.11	0.989	0.26	0.77	0.998
AEVFEVTK>y2-H2O	461.75-230.40	0.04	0.11	0.993	0.23	0.70	0.998
AEVFEVTK>b2-H2O	461.75-183.00	0.04	0.12	0.996	0.22	0.65	0.997
AEVFEVTK>y3++H2O	461.75-110.05	0.08	0.25	0.988	0.38	1.14	0.997
EACFAVEGPK>y1	554.25-147.25	0.05	0.16	0.996	1.06	3.19	0.996
EACFAVEGPK>y2	554.25-244.25	0.04	0.13	0.994	0.39	1.18	1.000
EACFAVEGPK>b3-H2O	554.25-342.95	0.04	0.12	0.991	0.36	1.09	1.000
EACFAVEGPK>y6	554.25-600.25	0.03	0.08	0.991	0.41	1.22	1.000
EACFAVEGPK>y3	554.25-301.00	0.04	0.12	0.993	0.50	1.49	0.999
EACFAVEGPK>y7	554.25-747.20	0.02	0.07	0.992	0.67	2.02	0.999
EACFAVEGPK>b2-H2O	554.25-182.95	0.05	0.16	0.992	0.49	1.47	0.999
EACFAVEGPK>y5	554.25-529.35	0.02	0.05	0.990	0.30	0.90	1.000
EACFAVEGPK>y4	554.25-430.05	0.03	0.10	0.989	0.35	1.06	0.999
EACFAVEGPK>y8++	554.25-454.25	0.04	0.12	0.991	0.39	1.17	1.000
EACFAVEGPK>y9++	554.25-490.05	0.02	0.06	0.988	0.34	1.02	0.999

First Edition: June, 2013

