Integration of multiple capabilities in Structures for Lossless Ion Manipulations (SLIM) for achieving ultra-high-resolution ion mobility - MS with complex samples

Liulin Deng[2], Sandilya V. B. Garimella[1], Ian K. Webb[1], Ahmed M. Hamid[2], Spencer A. Prost[1], Randolph V. Norheim[1], Yehia M. Ibrahim[1], Richard D. Smith[1]
[1]Pacific Northwest National Laboratory, Richland, WA
[2]Mobilion Systems Inc. Exton, PA

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Overview

- Lossless CRIMP ion compression Improves sensitivity of multi-pass IM .
- Ultrasensitive SLIM Serpentine Ultralong Path with Extended Routing (SUPER) IM-MS enabled differentiation of D and L Aβ peptide isomers.
- 'Zoom in' multi-pass SLIM SUPER IM-MS can analyze complex samples.

Introduction

- Ion mobility-mass spectrometry (IM-MS) is a highly versatile analytical tool potentially for more complete analysis of complex samples.
- CRIMP accumulation and compression[1] and ultra-high IM resolution[2] have been achieved in SLIM which potentially provides significant benefits for the analysis of complex samples.
- This presentation describes new approaches involving integration of CRIMP compression, CID and ion selection in multi-pass SLIM IM-MS.

Methods

- The multi-pass SLIM SUPER module incorporated CRIMP compression.
- 13.5-m serpentine path.
- Two surfaces spaced by 2.75-mm.
- 2.5 torr N_2.
- Two independently-controlled sections.
- An ion switch was used to reroute ions for multiple passes.

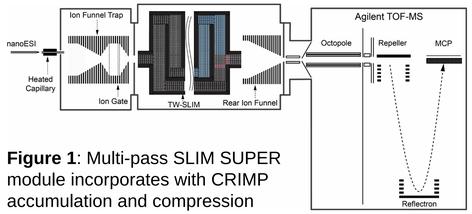

Figure 1: Multi-pass SLIM SUPER module incorporates with CRIMP accumulation and compression

Results

Lossless ion transmission

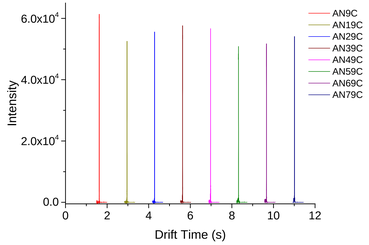

Figure 2: Lossless ion transmission was achieved after different passes in travel trap (i.e. surfing) mode.

Improved Sensitivity and Resolution

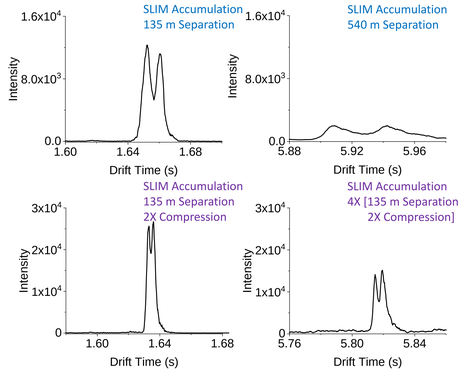

Figure 3: Improved sensitivity and IM resolution using CRIMP ion compression.

CID in SLIM

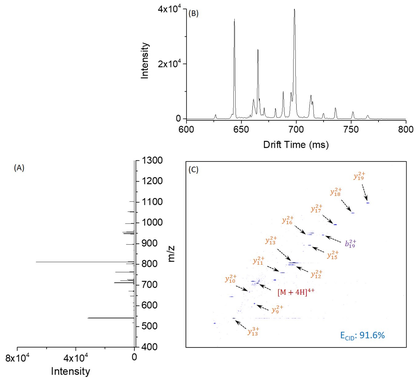

Figure 4: High efficiency CID in SLIM (See **MP 365**).

D and L Aβ Peptide Isomer Separation

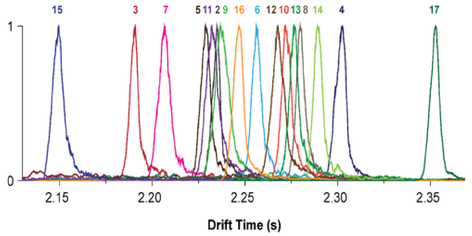

Figure 5: SLIM IM separation for 16 D and L Aβ peptide isomers.

	Sequence	Feature	DT (s)
2	LVFFAEDVGSDK	L-Asp, L-Asp	2.234
3	LVFFAEDVGS(dD)K	L-Asp, D-Asp	2.190
4	LVFFAEDVGS(bD)K	L-Asp, L-isoAsp	2.301
5	LVFFAEDVGS(dbD)K	L-Asp, D-isoAsp	2.229
6	LVFFAE(dD)VGSDK	D-Asp, L-Asp	2.256
7	LVFFAE(dD)VGS(dD)K	D-Asp, D-Asp	2.207
8	LVFFAE(dD)VGS(bD)K	D-Asp, L-isoAsp	2.280
9	LVFFAE(dD)VGS(dbD)K	D-Asp, D-isoAsp	2.238
10	LVFFAE(bD)VGSDK	L-isoAsp, L-Asp	2.272
11	LVFFAE(bD)VGS(dD)K	L-isoAsp, D-Asp	2.232
12	LVFFAE(bD)VGS(bD)K	L-isoAsp, L-isoAsp	2.268
13	LVFFAE(bD)VGS(dbD)K	L-isoAsp, D-isoAsp	2.277
14	LVFFAE(dbD)VGSDK	D-isoAsp, L-Asp	2.289
15	LVFFAE(dbD)VGS(dD)K	D-isoAsp, D-Asp	2.149
16	LVFFAE(dbD)VGS(bD)K	D-isoAsp, L-isoAsp	2.246
17	LVFFAE(dbD)VGS(dbD)K	D-isoAsp, D-isoAsp	2.352

Table 1: The amino acid sequence, feature and drift time of 135 meters SLIM IM separation for 16 D and L amino acid containing Aβ peptide isomers (**Figure 5**).

"Zoom in" Mode for Complex Samples

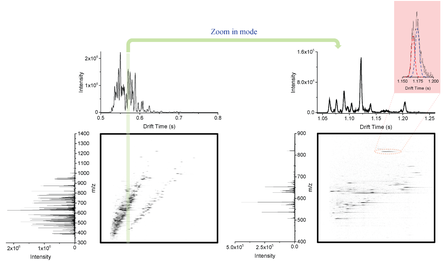

Figure 6: Ion selection was applied in multi-pass SLIM for complex sample analyses.

Conclusions

- Lossless ion compression was achieved using CRIMP in multi-pass SLIM.
- Improved sensitivity and resolution for multiple pass IM separations using CRIMP compression.
- High efficiency CID was achievable in SLIM.
- Ultrahigh resolution SLIM IM separation enables to differentiate complex D and L Aβ peptide isomers.
- "Zoom in" mode in multi-pass SLIM IM-MS can conduct complex sample analyses.

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1. Deng, L., Garimella, S. V. B., et al.: Compression Ratio Ion Mobility Programming (CRIMP) Accumulation and Compression of Billions of Ions for Ion Mobility-Mass Spectrometry Using Traveling Waves in Structures for Lossless Ion Manipulations (SLIM). Anal. Chem. **89** (12), 6432-6439, **2017**.
2. Deng, L., Webb, I.K., et al.: Serpentine ultralong path with extended routing (SUPER) high resolution traveling wave ion mobility-MS using structures for lossless ion manipulations. Anal. Chem. **89**(8), 4628-4634, **2017.**

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CONTACT: Richard D. Smith
Biological Sciences Division
Pacific Northwest National Laboratory
E-mail: rds@pnnl.gov

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