

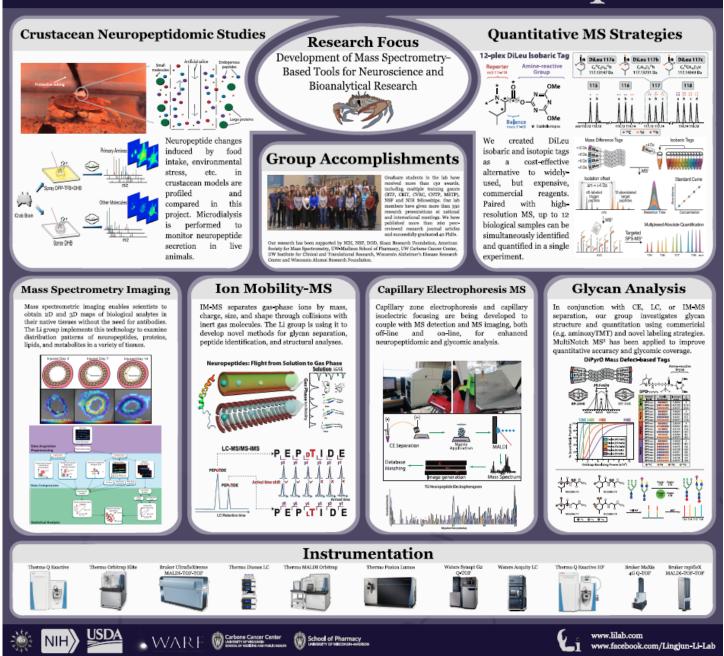


AP MALDI-Quadrupole-Orbitrap MS Platform for High Spatial and High Mass Spectral Resolution In Situ Analysis of Biomolecules Lingjun Li, Bingming Chen, Gongyu Li, Caitlin Keller, Yatao Shi, Qinjingwen Cao, Chuanzi Ouyang, Jill Johnson Vilas Distinguished Achievement Professor **Charles Melbourne Johnson Distinguished Chair**

School of Pharmacy & Department of Chemistry, University of Wisconsin, Madison, WI, USA

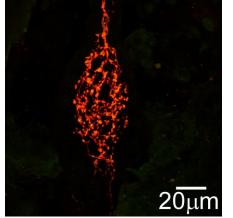
> MassTech Inc. Breakfast Seminar, ASMS 2019 Atlanta, GA, USA, June 3, 2019

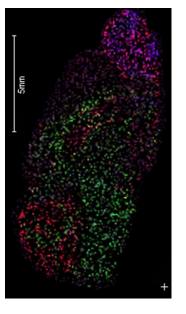
Li Research Group



Molecular Imaging Strategies







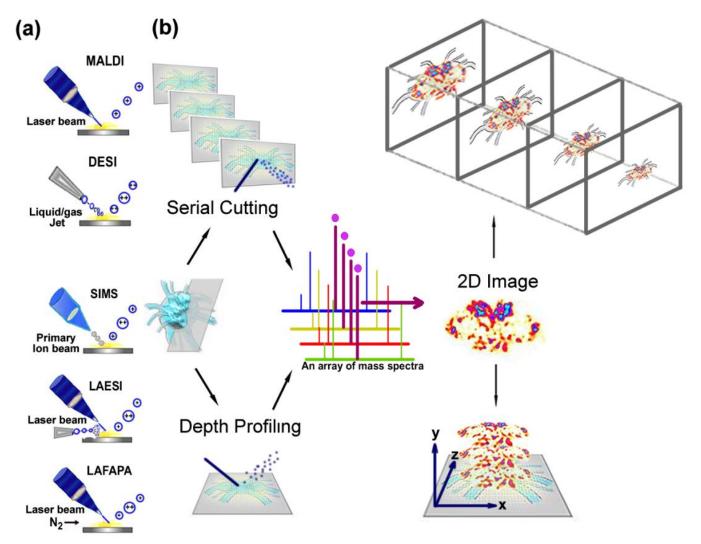
MS imaging advantages

- No Jabeling required
 - Biomolecules are functionally unmodified
- Image biomolecular modifications
 - PTM's
 - Metabolites
- Detailed information on molecular identity
- Large scope of different elements and molecules, discovery of unknowns
- Extend histopathology to a molecular level
 Multiplexing and highly parallel

Imaging Mass Spectrometry Liam A. McDonnell, Ron M. A. Heeren Mass Spectrometry Reviews (2007) **26** 606-643

Mass spectral imaging: Ionization methods and tissue preparation strategies

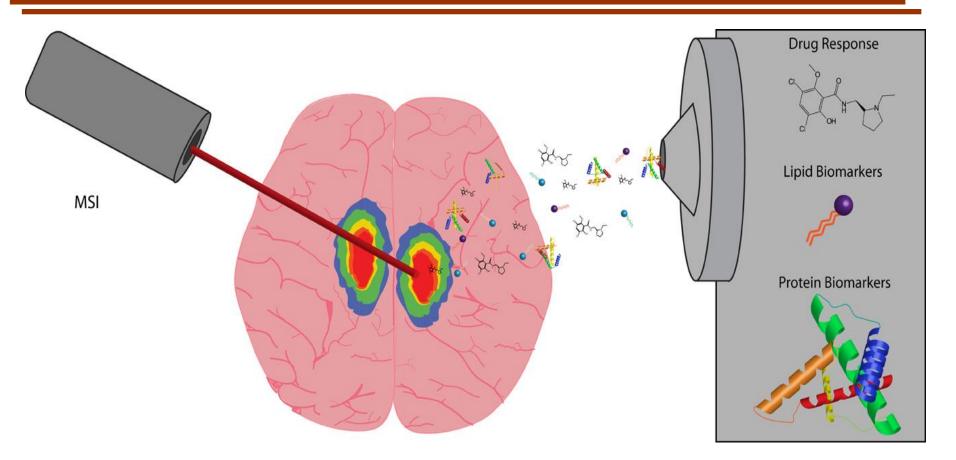




Ye, Greer, and Li, *Bioanalysis*, 3, 313-332 (2011)

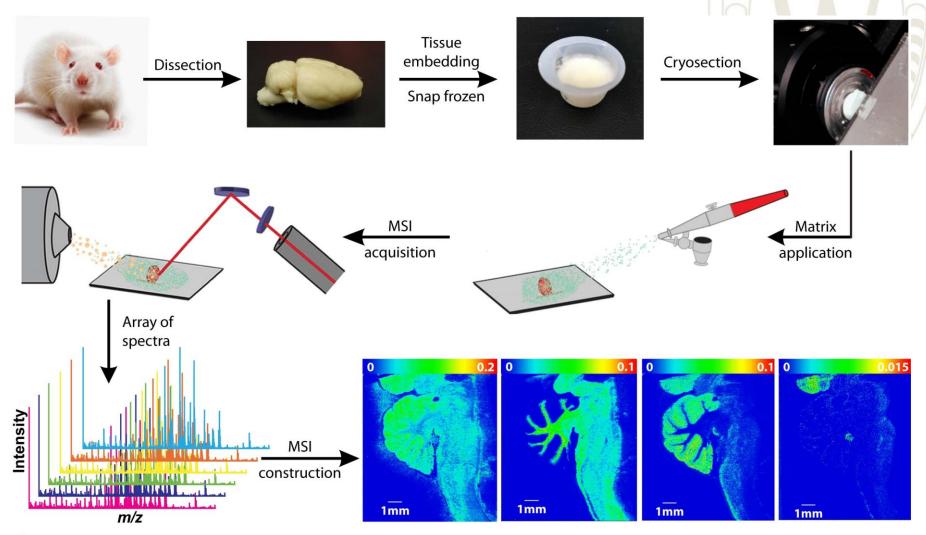
With MALDI MSI, we can...





H. Ye, E. Gemperline, and L. Li (2013). A vision for better health: Mass spectrometry imaging for clinical diagnostics. *Clinica Chimica Acta*. *420*, 11-22.

Typical MS Imaging Workflow





Chen[#], Gemperline[#] & Li (2014), *Bioanalysis*, 6(4), 525-540; (#Co-First authors) Angel & Caprioli (2013), *Biochemistry*, 52, 3818-3828; Gessel, Norris & Caprioli (2014), *J. Proteom.*, 107, 71-82. Part of artwork by Dr. Erin Gemperline.

Image Acquisition Animation

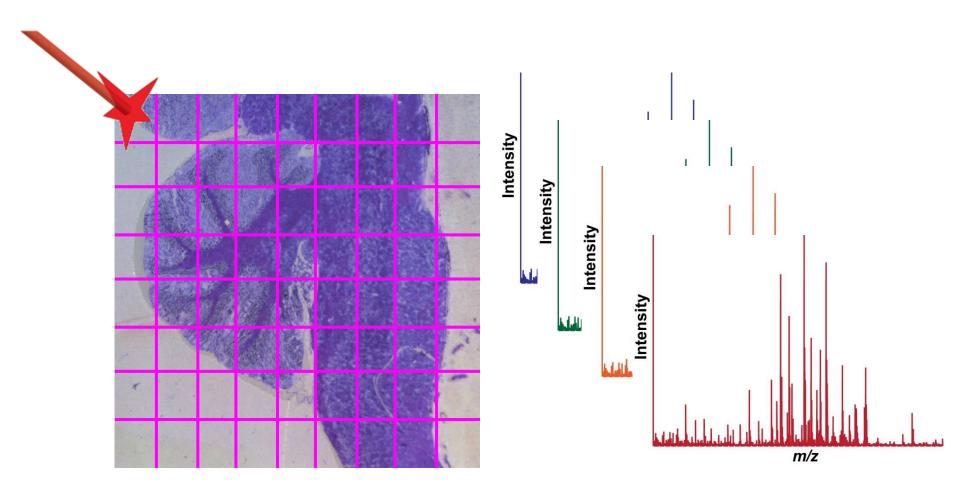
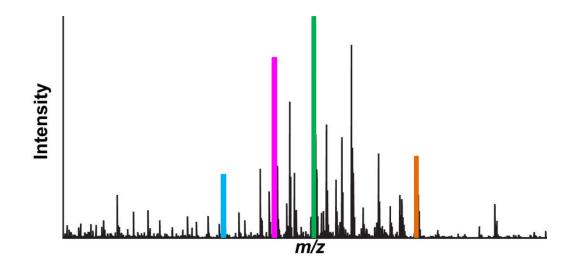
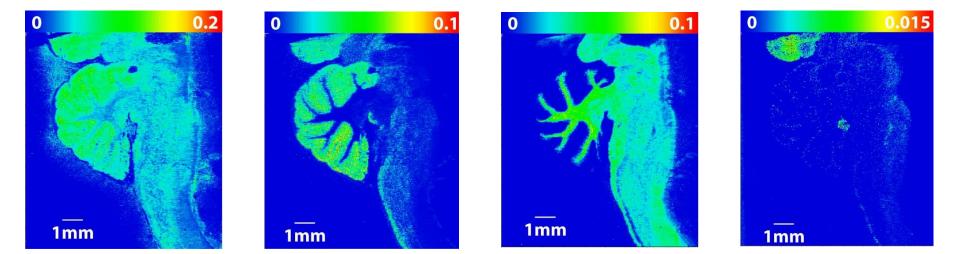


Image Data Analysis Animation



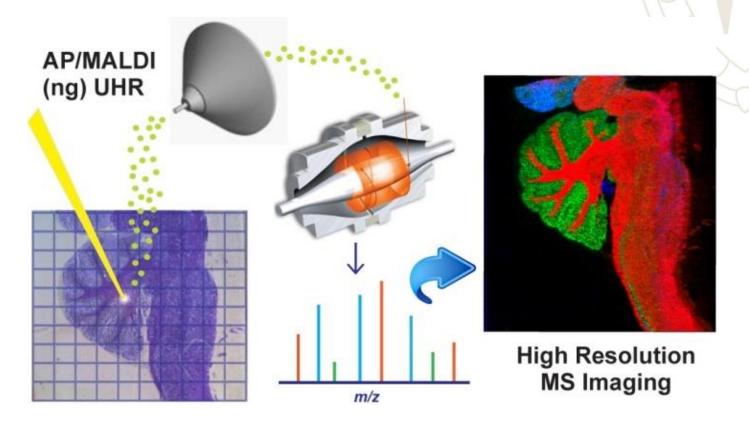


Ongoing Interest in MS Imaging

Project 1				
Improve spatial resolution Develop robust protocol	Project 2	Droject 2		
	Expand detection range of high resolution mass analyzer	Efficient biomolecule identification and structural elucidation and	Applications	
			MS imaging of neuropeptides, glycans, lipids and metabolites	



Project 1. A High Resolution Atmospheric Pressure MALDI-Quadrupole-Orbitrap Platform Enables *In Situ* Analysis of Biomolecules by Multi-Mode Ionization and Acquisition





AP/MALDI (ng) UHR source provided by MassTech.

AP/MALDI-Q-Orbitrap Capability

AP/MALDI: an alternative to vacuum MALDI

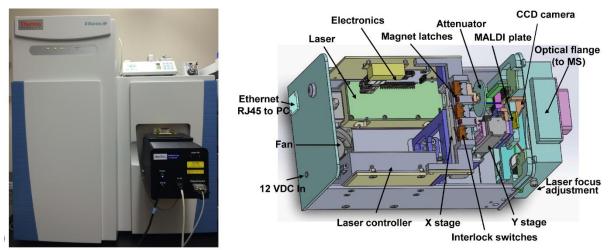
- Interchangeable with ESI source
- Ease of sample introduction and handling at AP condition
- Capable of analyzing volatile molecules
- Optimized source geometry design and ion transfer efficiency

Multiple types of ionization

MALDI, novel ionizations for multiply charged ions (LSI and MAI/MAIV)

High resolution MS imaging

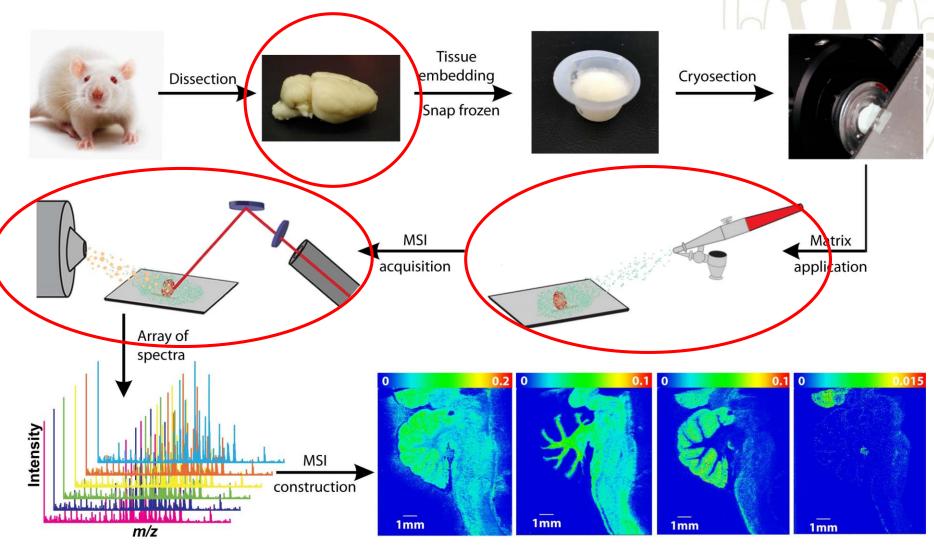
- In mass: 240k mass resolution at m/z 200
- In space: < 10 μm spatial resolution





Laiko et al. (2000), Analyt. Chem., 72, 652-657; Guenther et al., (2011), IJMS, 305, 228-237.

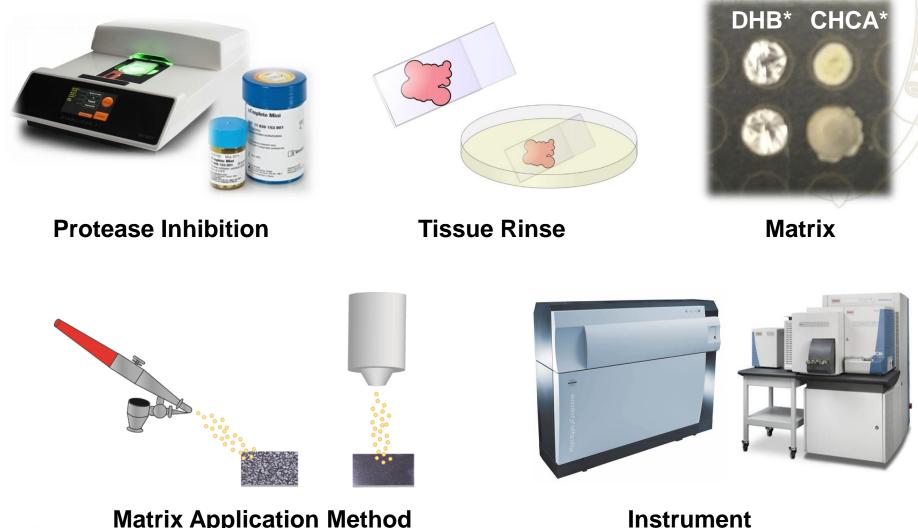
Optimization for MS Imaging





Chen[#], Gemperline[#] & Li (2014), *Bioanalysis*, 6(4), 525-540; ([#]Co-First authors) Angel & Caprioli (2013), *Biochemistry*, 52, 3818-3828; Gessel, Norris & Caprioli (2014), *J. Proteom.*, 107, 71-82. Part of artwork by Dr. Erin Gemperline.

Optimization for MS Imaging



Matrix Application Method

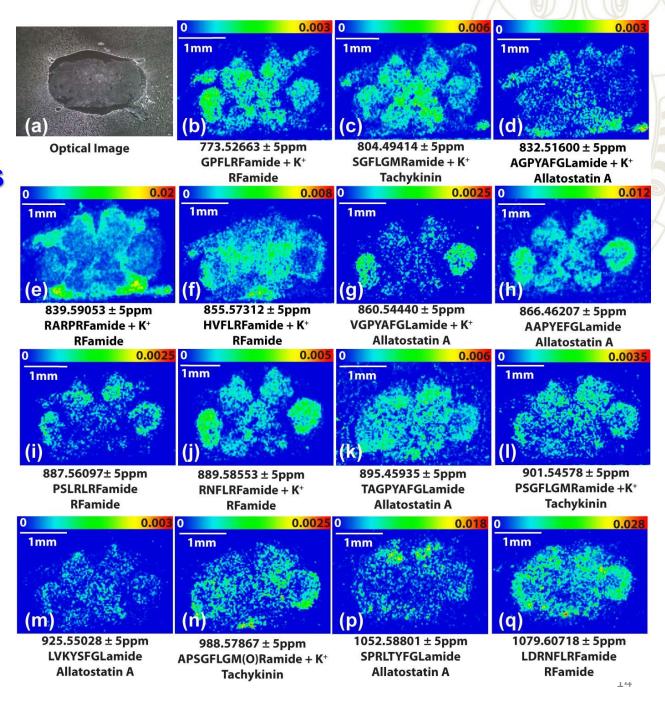


*DHB: 2,5-Dihydroxybenzoic acid *CHCA: α-Cyano-4-hydroxycinnamic acid

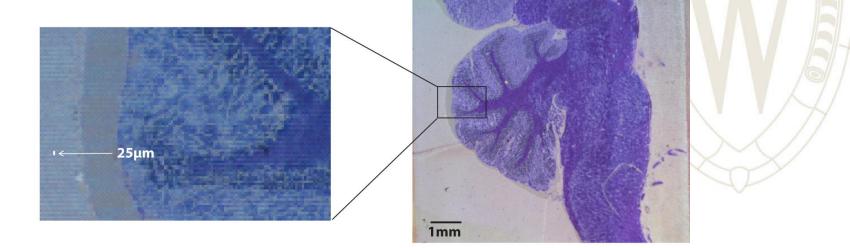
High Resolution **MSI of Neuropeptides** in Crustacean **Brain Tissue** Section by AP MALDI Q-Orbitrap Platform

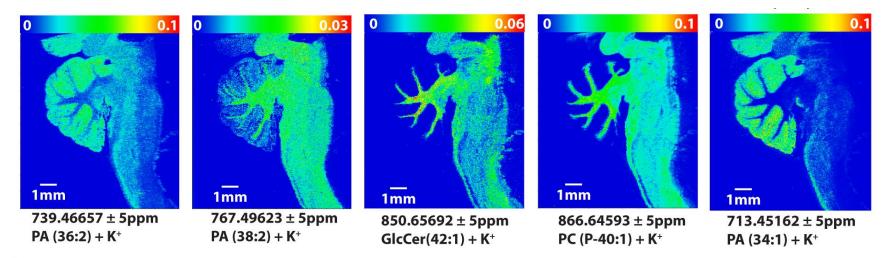
Chen et al., *Analytica Chimica Acta*, 1007, 16-25 (2018).





High Resolution MS Imaging

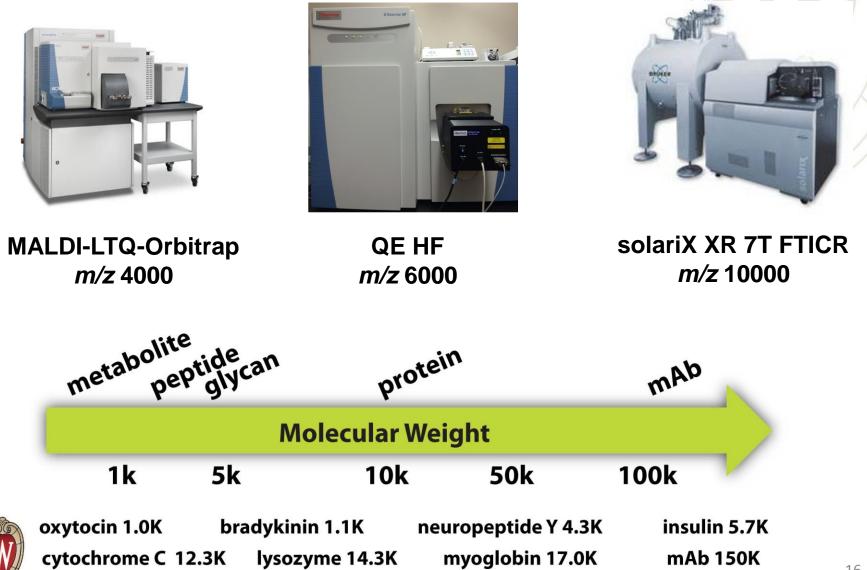




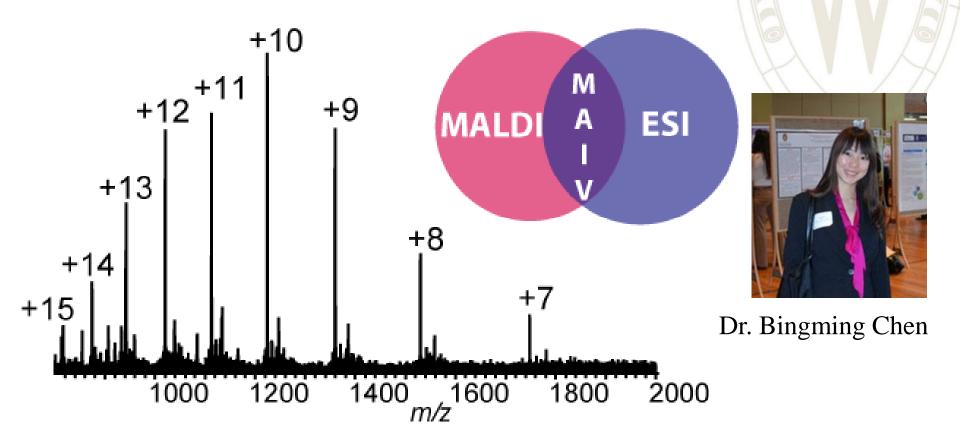


Chen et al., Analytica Chimica Acta, 1007, 16-25 (2018).

High Resolution Trade-off: Limited Mass Range



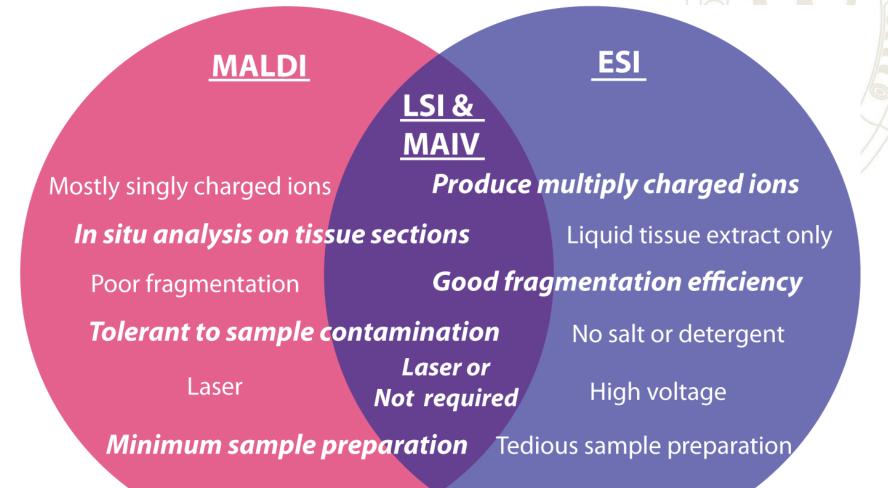
Project 2. "Magic" Ionization on High Performance Mass Spectrometers





B.Chen, C.B. Lietz, C.Ouyang, X. Zhong, M. Xu and L. Li (2016). Analyt. Chim. Acta., vol 916. p.52-59; B.Chen, C.B. Lietz, L. Li (2014). J. Am. Soc. Mass Spectrom., vol. 25 (12). p. 2177-80; B. Chen[#], C. Ouyang[#], Z. Tian, M. Xu and L. Li, To be submitted to Analyt. Chim. Acta. (#Co-First authors);

"Magic" Ionization – Multiply Charged MALDI





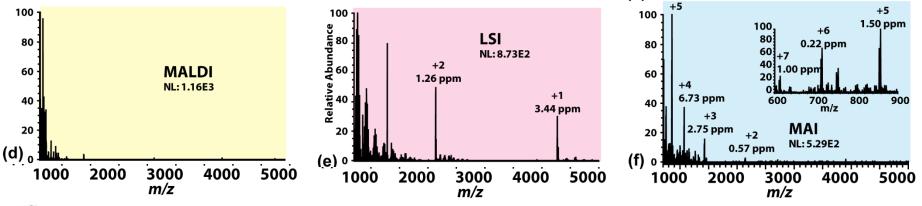
Chen, Lietz & Li, JASMS, 2014, 25, 2177-2180; Chen et al., Analyt. Chim. Acta, 2016, 916, 52-59; Trimpin, JASMS, 2016, 27 (1), 4-21. Trimpin et al., Mol Cell Proteomics 2010, 9, 362-367; Inutan et al., Mol Cell Proteomics 2011, 10, M110 000760; Inutan & Trimpin, Mol Cell Proteomics 2013, 12, 792-796

Multiply Charged Ions on AP/MALDI MS

100 +1 100 100 +2 +1 0.15 ppm 1.11 ppm 1.28 ppm Relative Abundance LSI 80 80 NL: 5.87E2 MAI +2 MALDI 60 NL:7.95E3 60 1.18 ppm NL:2.34E4 40 40 20 20 +1 0.36 ppm (b) o (c) (a) 0 700 800 1000 1100 500 600 800 900 600 700 800 900 1000 1100 500 600 700 900 1000 1100 500 m/z m/z m/z

Neuropeptide Y 4269.0808 Da

Bradykinin 1059.5608 Da

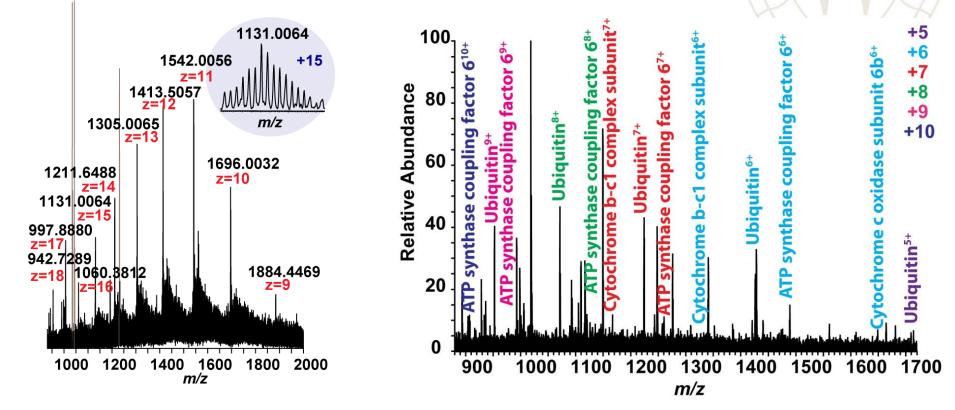




Extended Mass Range Enables Protein Detection

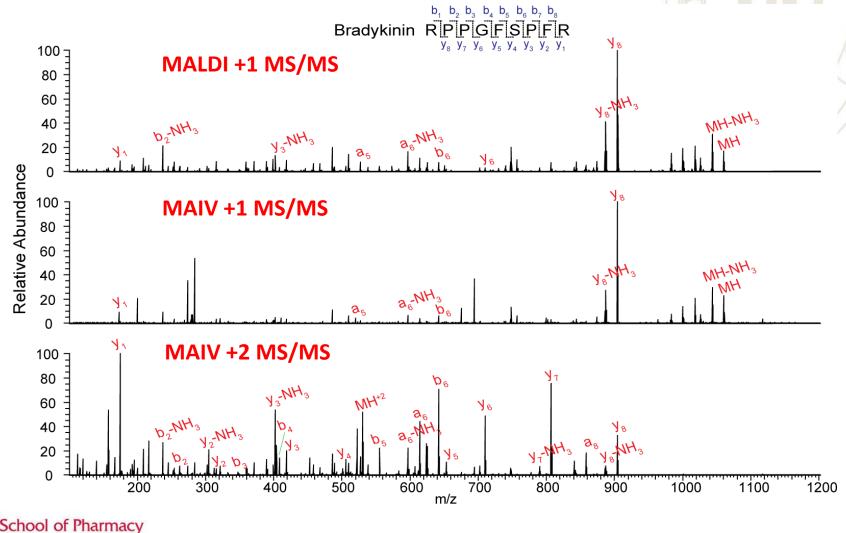
Myoglobin 17.0 kDa

Rat brain protein extraction



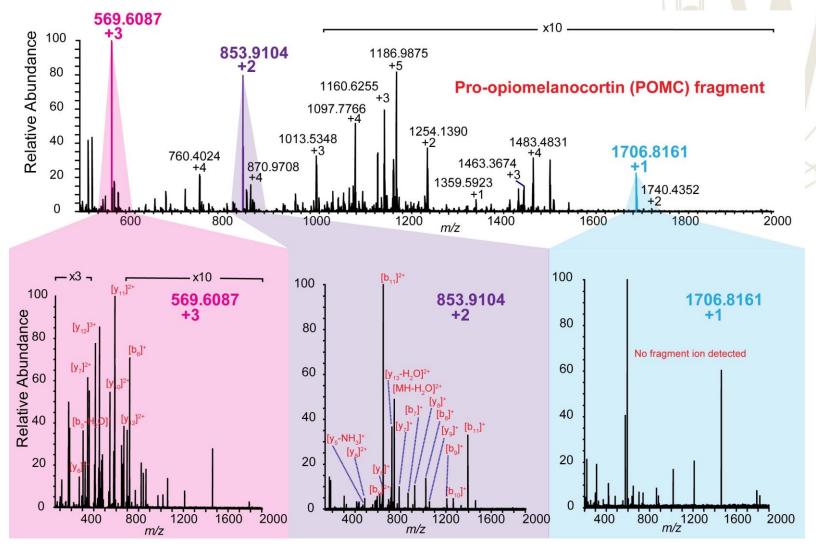


Improved Fragmentation: Bradykinin



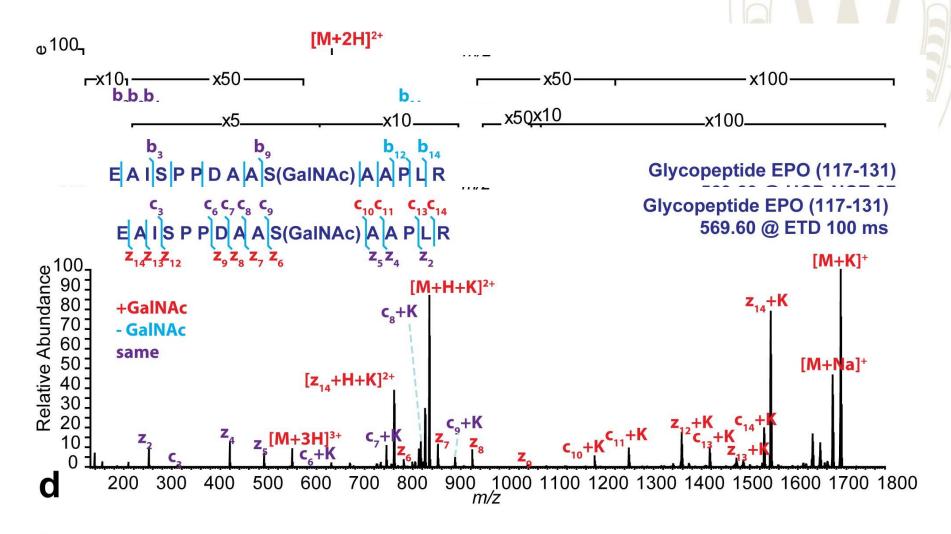
UNIVERSITY OF WISCONSIN-MADISON

Improved Fragmentation Efficiency





Labile Post-Translational Modification Analysis





Project 1 & 2. HR² AP/MALDI MS Conclusions

Achieved HR² MS imaging

- In mass (240K at *m/z* 200)
- In space (< 10 μm)

Produced multiply charged ions

- Mass range expanded for protein detection
- Fragmentation efficiency improved
- Possible to study labile PTMs

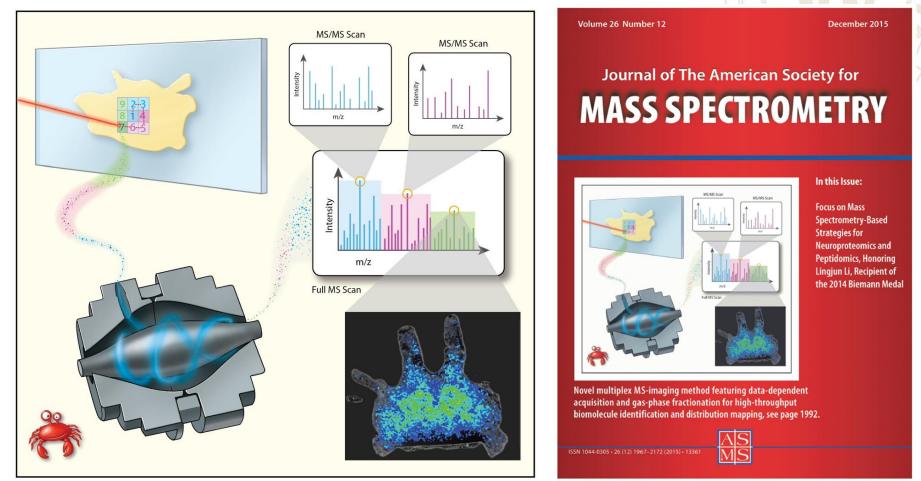


Ongoing Interest in MS Imaging

Project 1				
Improve spatial resolution Develop robust protocol	Project 2	Ducient 2		
	Expand detection range of high resolution mass analyzer	Project 3 Efficient	Applications] /
		biomolecule identification and structural elucidation	MS imaging of neuropeptides, glycans, lipids and metabolites	



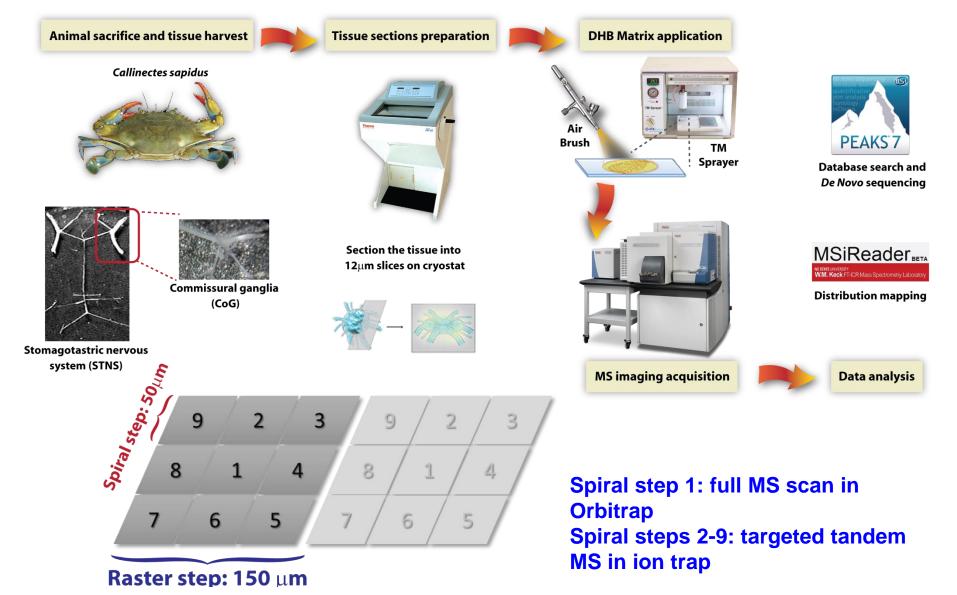
Project 3. High Throughput *In Situ* DDA Analysis of Neuropeptides by Coupling Novel Multiplex MS Imaging with Gas Phase Fractionation





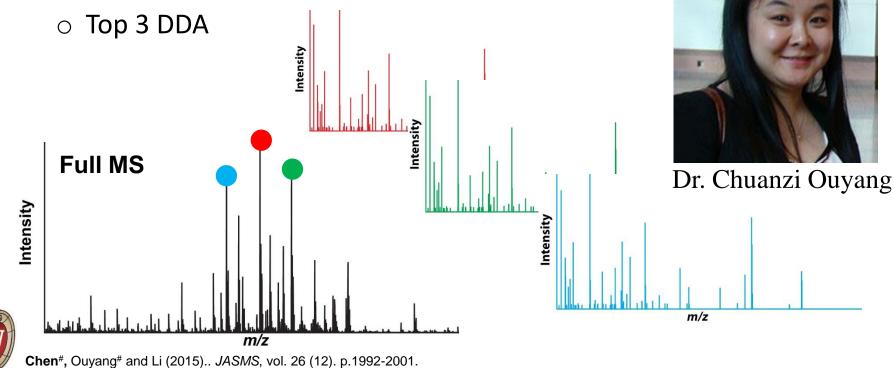
Chen[#], Ouyang[#] and Li (2015). High Throughput *In situ* DDA Analysis of Neuropeptides by Coupling Novel Multiplex Mass Spectrometric Imaging (MSI) with Gas-Phase Fractionation. *JASMS*, vol. 26 (12). p.1992-2001. Cover article (#Co-First authors), artwork by Sally Griffith-Oh

MSI Study of the Crustacean Stomatogastric Nervous System (STNS) by MALDI Orbitrap

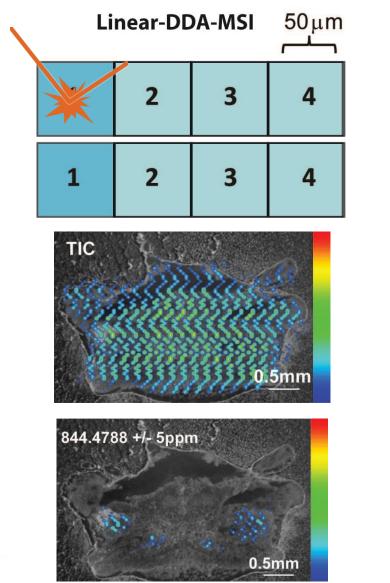


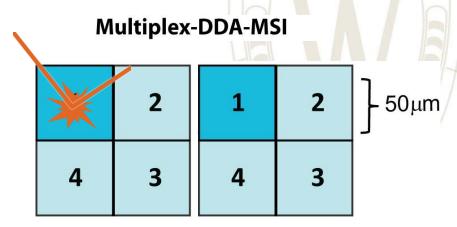
In Situ Biomolecule Identification

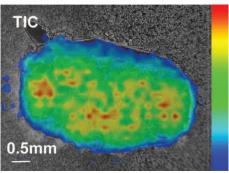
- A major challenge in MS imaging
 - Accurate mass matching: putative identification
 - Targeted MS/MS: confident identification and confirmation
- Data dependent acquisition (DDA)
 - Fragment top N ions after a full scan

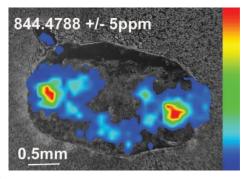


In Situ DDA: Linear vs. Multiplex MSI





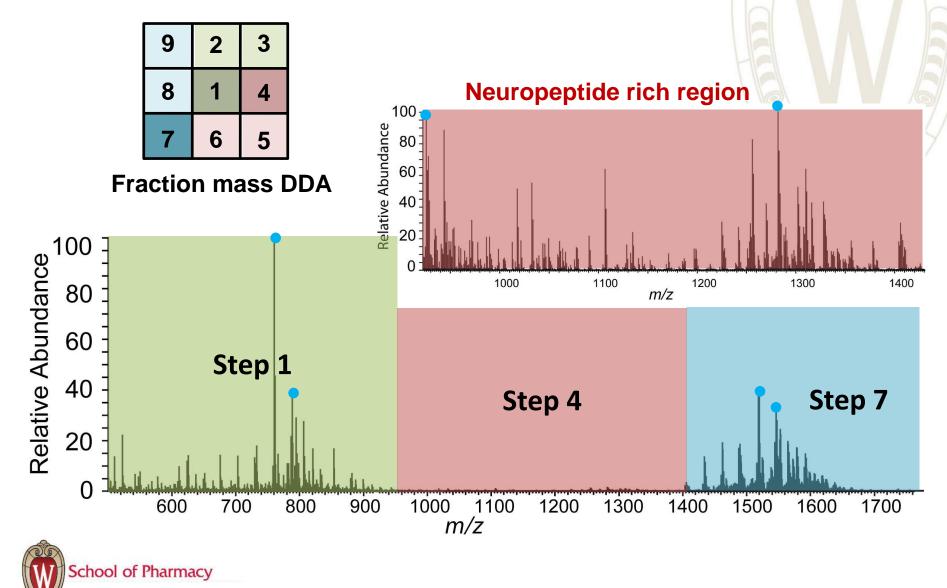






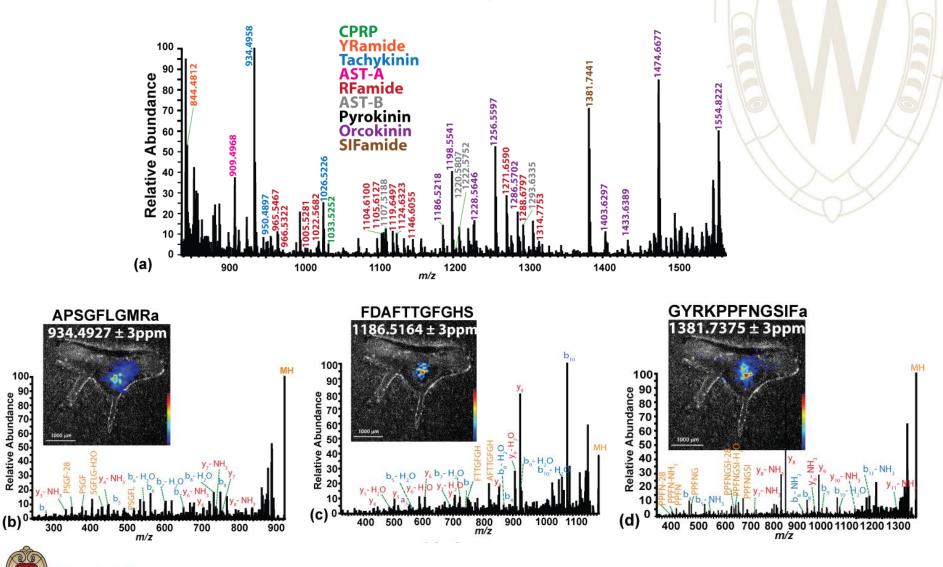
Chen#, Ouyang# and Li (2015).. JASMS, vol. 26 (12). p.1992-2001. (#Co-First authors)

Improving MS² Precursor Selection Efficiency



Chen#, Ouyang# and Li (2015).. JASMS, vol. 26 (12). p.1992-2001. (#Co-First authors)

In Situ DDA: Multiplex MSI Results

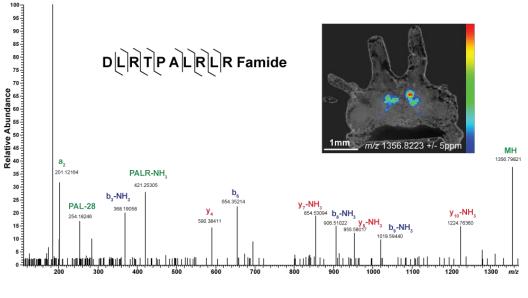


School of Pharmacy

Chen#, Ouyang# and Li (2015).. JASMS, vol. 26 (12). p.1992-2001. (#Co-First authors)

Multiplex DDA MSI Conclusions

- Simultaneous localization and identification
- Pseudo gas phase separation improved the precursor selection coverage
- Detection of novel neuropeptides by *de novo* sequencing
- **18** novel neuropeptides from crustacean neural tissue were identified by *in situ* MS/MS.



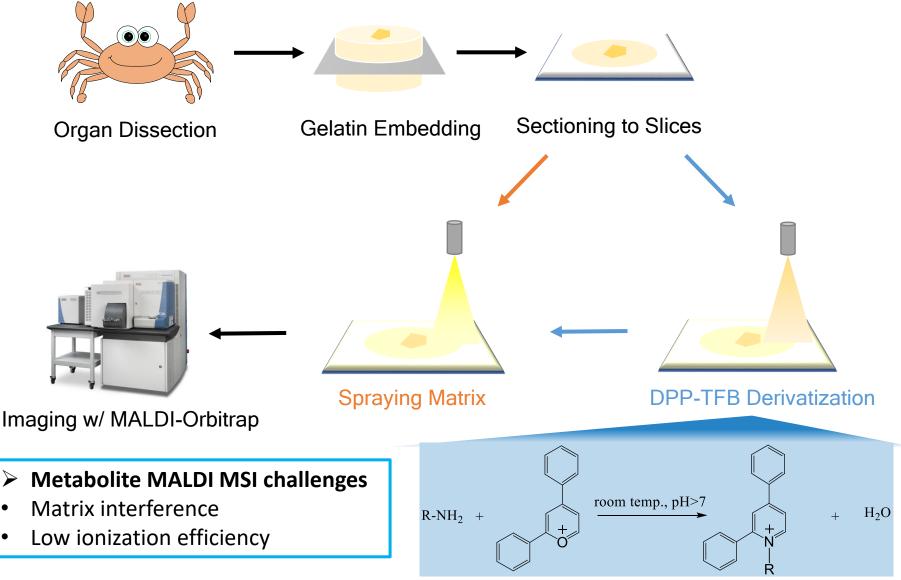


Novel RFamide identified in brain tissue of blue crab

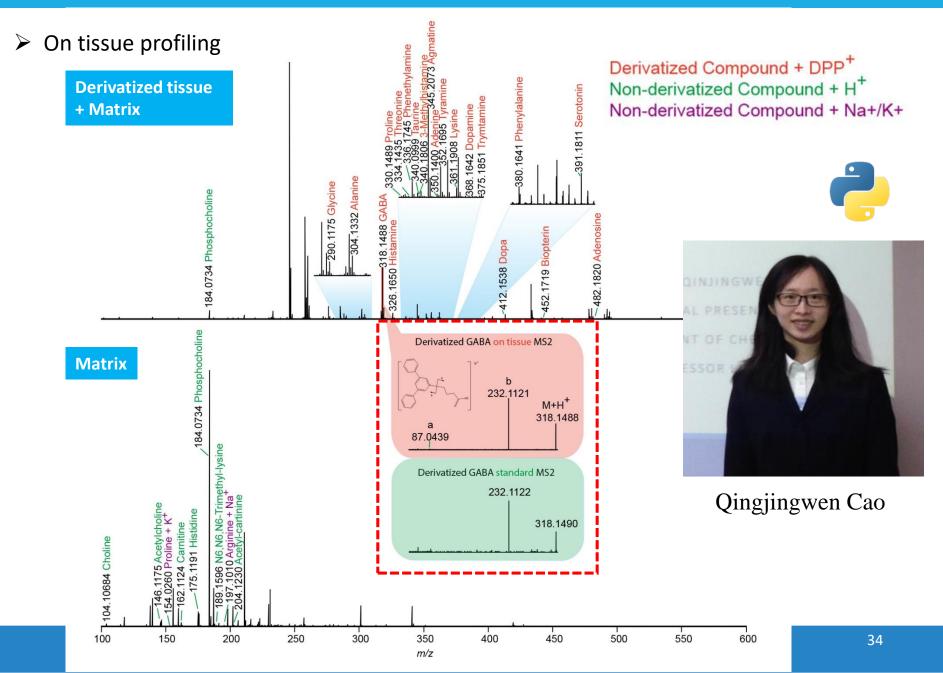
Chen[#], Ouyang[#] and Li (2015).. *JASMS*, vol. 26 (12). p.1992-2001. ([#]Co-First authors)

MALDI MSI Workflow

Workflow to achieve complementary metabolite coverage



Results

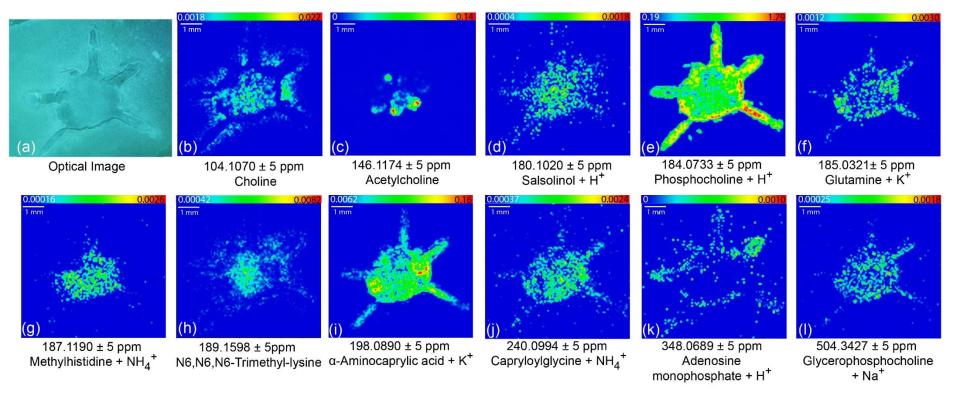


Results

Selected ion images from crab brain

Matrix

- Neurotransmitter: Acetylcholine
- Amino acids
- Lipids



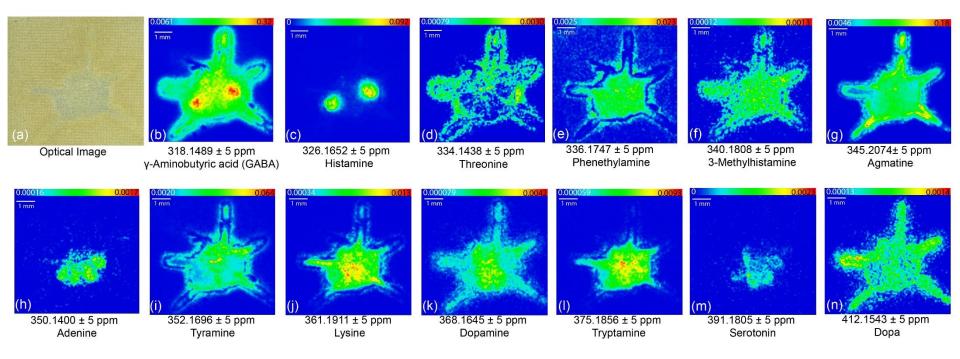
Results

Selected ion images from crab brain

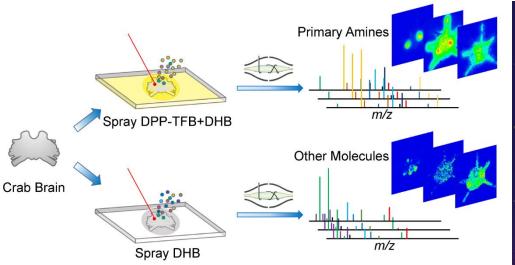
Derivatized tissue

+ Matrix

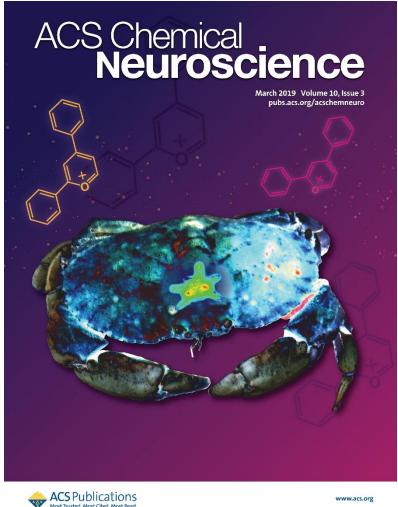
Many more neurotransmitters!



MALDI MSI Visualization and Identification of Neurotransmitters in Crustacean Brain



- On tissue chemical derivatization and reactionfree approaches enabled complementary signaling molecule visualization on crab brain sections via MALDI-LTQ-Orbitrap XL platform.
- Pyrylium salt served as a primary amine derivatization reagent and produced prominent signal enhancement of multiple neurotransmitters, including dopamine, serotonin, y-aminobutyric acid and histamine that were not detected in underivatized tissues.
- Molecules with other functional groups, such as acetylcholine and phosphocholine, were directly imaged after matrix application.



THE UNIVERSITY

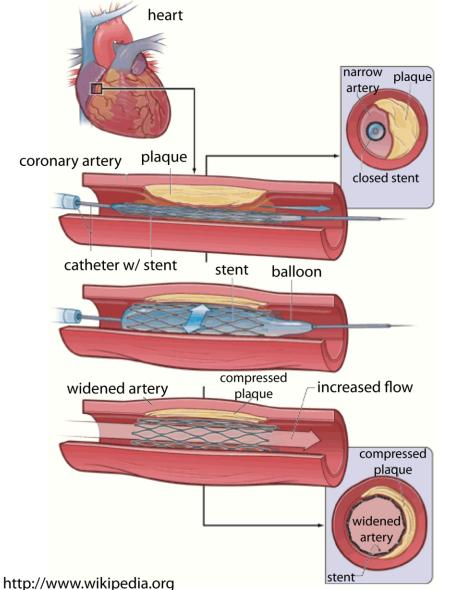
www.acs.org

Cao et al., ACS Chem Neurosci 2019 Mar 20;10(3):1222-1229. doi: 10.1021/acschemneuro.8b00730.

University of Wisconsin - Madison



Restenosis: An unintended consequence

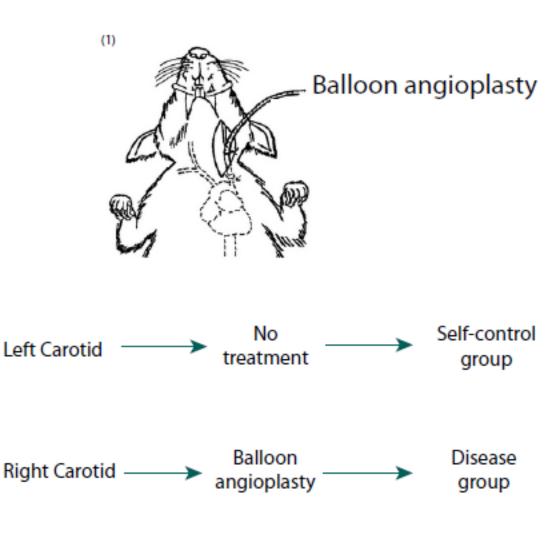


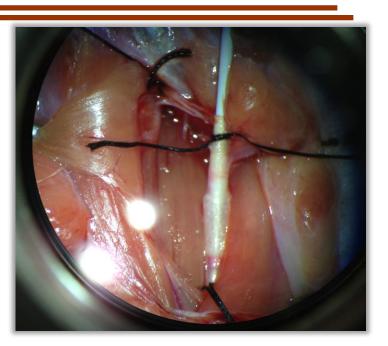
- Coronary atherosclerosis occurs when fatty plaques deposit on the interior wall of an artery and inhibits blood flow.
- Angioplasty is a common treatment wherein a balloon is inflated in the artery to clear the blockage.
- A stent is often placed after angioplasty to prevent future re-narrowing.

In collaboration with Dr. Craig Kent Lab

Rat Carotid Injury Model for Restenosis



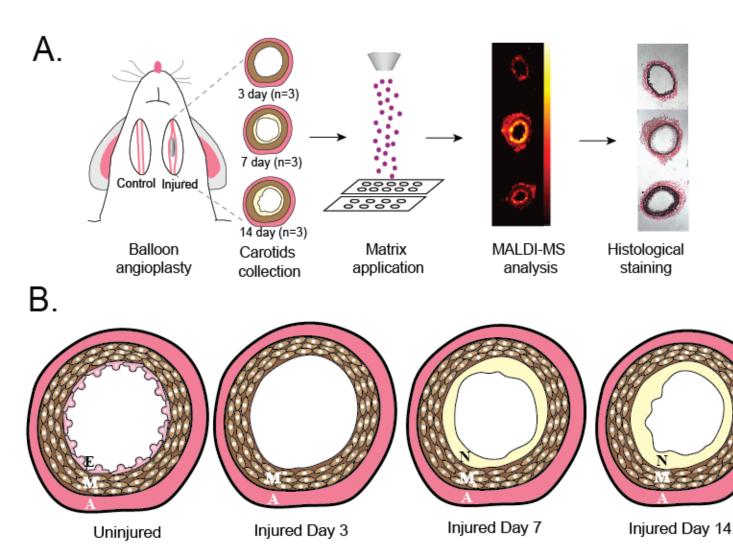




A rat model of restenosis is prepared by treating healthy rat carotid with balloon angioplasty. After surgery, the restenosis will gradually occur and rat carotid samples will be collected on 3, 7, 14 days after surgery, respectively.

MALDI MSI Workflow to Reveal Dynamic Changes of Signaling Lipids in Restenosis



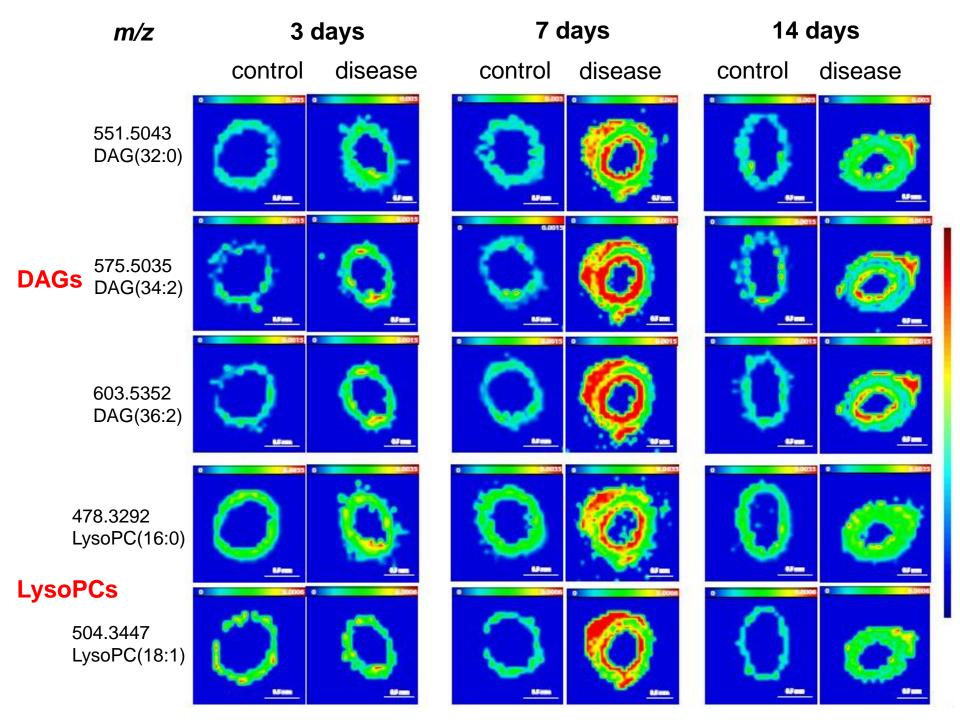




Yatao Shi

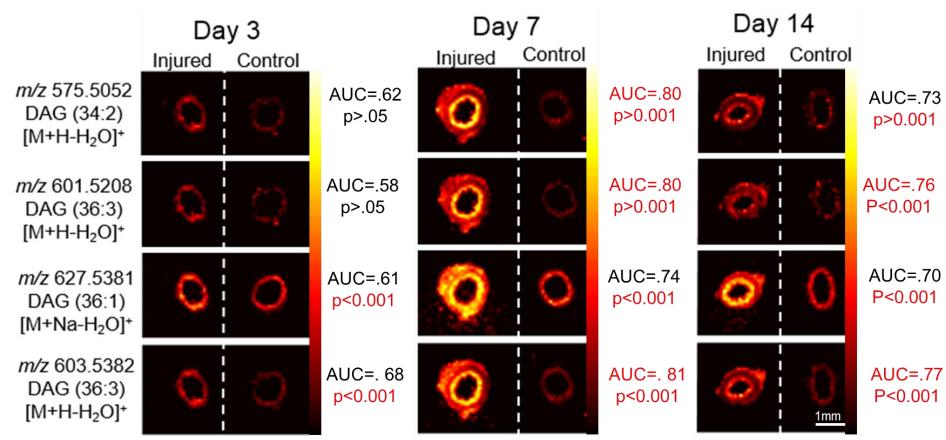


Jill Johnson



Diacylglycerols Upregulation: Statistics



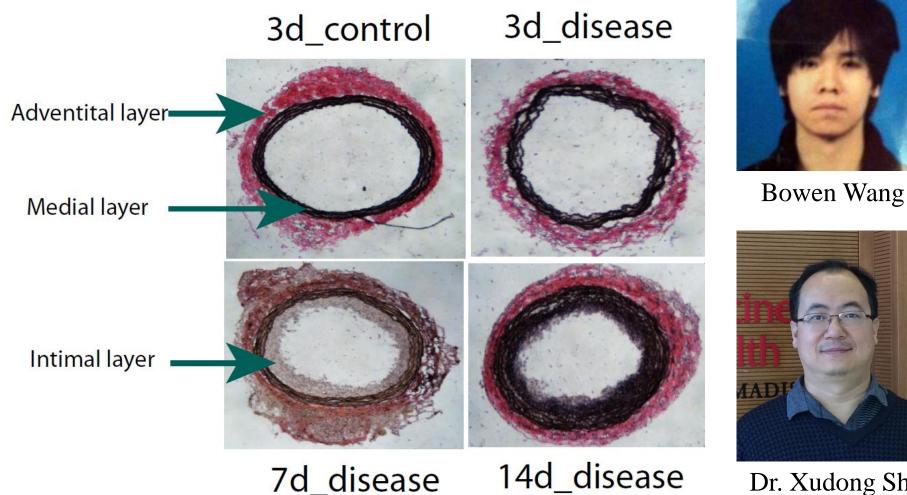


Mass Spectrometric Imaging Reveals Temporal and Spatial Dynamics of Bioactive Lipids in Arteries Undergoing Restenosis.

Shi Y, Johnson J, Wang B, Chen B, Fisher GL, Urabe G, Shi X, Kent KC, Guo LW, Li L. *J Proteome Res.* 2019 Apr 5;18(4):1669-1678. doi: 10.1021/acs.jproteome.8b00941. Epub 2019 Mar 11.

Verhoeff-van Gieson Staining

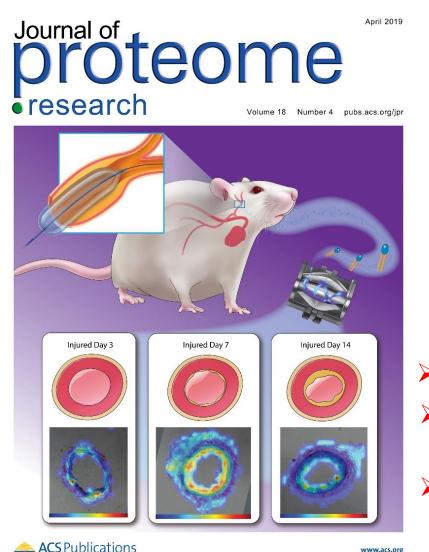


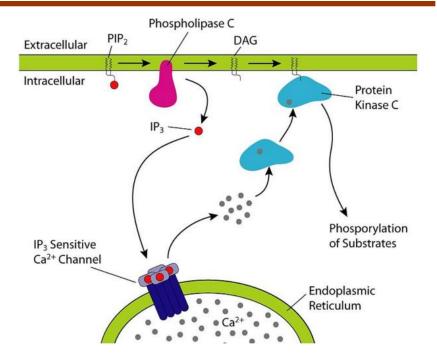


Dr. Xudong Shi

MALDI MSI Reveals Unique Neointimal Distributions of DAGs





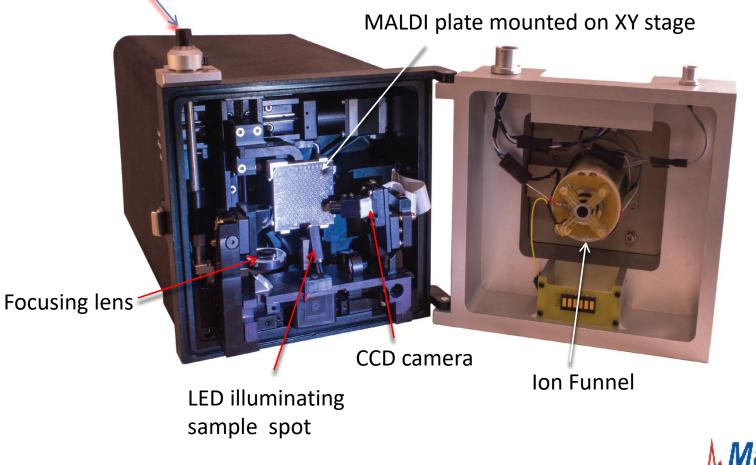


- DAGs were up-regulated during restenosis
- DAG-mediated signal pathway was proven to be involved in the process of restenosis
- LysoPCs are upregulated during the process of restenosis

Shi et al., J Proteome Res (2019).

SubAP-MALDI source

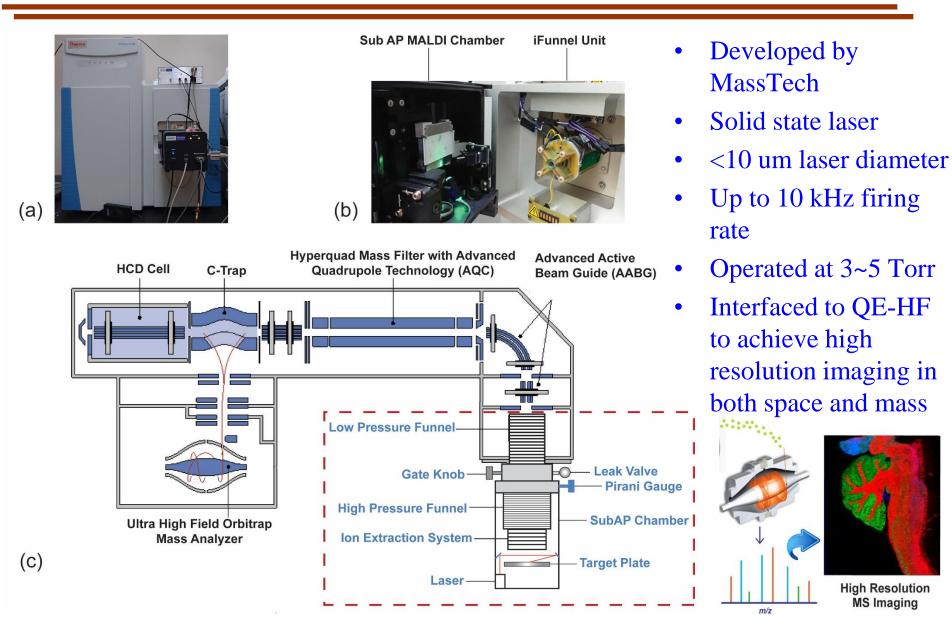
Dial controlling laser spot size by changing a distance between focusing lens and sample plate





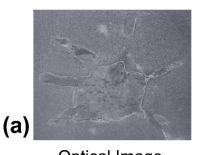
A High Resolution SubAP/MALDI(ng) UHR Source Coupled to a Quadrupole-Orbitrap Platform for MSI



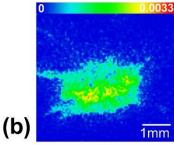


A High Resolution SubAP/MALDI-Q-Orbitrap Platform Enables *In Situ* Analysis of Biomolecules by Negative Mode Ionization and Acquisition

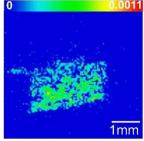




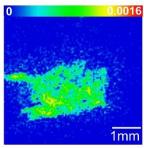
Optical Image



134.0461 ± 5 ppm Adenine - H⁺

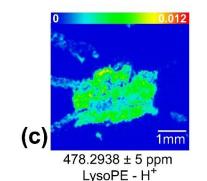


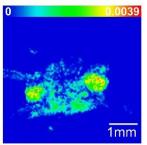
 $152.0706 \pm 5 \text{ ppm}$ Dopamine - H⁺



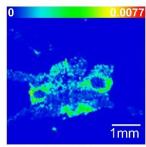
 $217.0975 \pm 5 \text{ ppm}$ N-acetylserotonin - H⁺

SubAP MALDI – QE HF platform used for visualizing various biomolecules, including metabolites, lipids and neuropeptides in negative ionization mode.

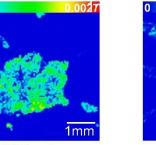




736.4930 ± 5 ppm PE - H⁺

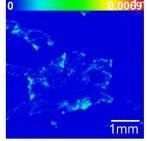


855.5022 ± 5 ppm PI - H⁺

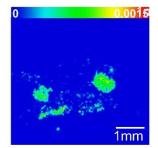


 $597.3051 \pm 5 \text{ ppm}$ YTFGLamide - H⁺

(d)



 $885.5440 \pm 5 \text{ ppm}$ PSLRLRFamide - H⁺



901.4937 \pm 5 ppm LPVYNFGLamide - H₂O - H⁺



ORIGINAL RESEARCH published: 28 August 2018 doi: 10.3389/fpls.2018.01238



Comparison of Vacuum MALDI and AP-MALDI Platforms for the Mass Spectrometry Imaging of Metabolites Involved in Salt Stress in *Medicago truncatula*

Caitlin Keller¹, Junko Maeda², Dhileepkumar Jayaraman³, Sanhita Chakraborty⁴, Michael R. Sussman⁵, Jeanne M. Harris⁴, Jean-Michel Ané^{2,3} and Lingjun Li^{1,6*}

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Received: 17 April 2018 Accepted: 06 August 2018 Published: 28 August 2018 ¹ Department of Chemistry, University of Wisconsin–Madison, Madison, WI, United States, ² Department of Agronomy, University of Wisconsin–Madison, Madison, WI, United States, ³ Department of Bacteriology, University of Wisconsin–Madison, Madison, WI, United States, ⁴ Department of Plant Biology, University of Vermont, Burlington, VT, United States, ⁵ Department of Biochemistry, University of Wisconsin–Madison, Madison, WI, United States, ⁶ School of Pharmacy, University of Wisconsin–Madison, Madison, WI, United States

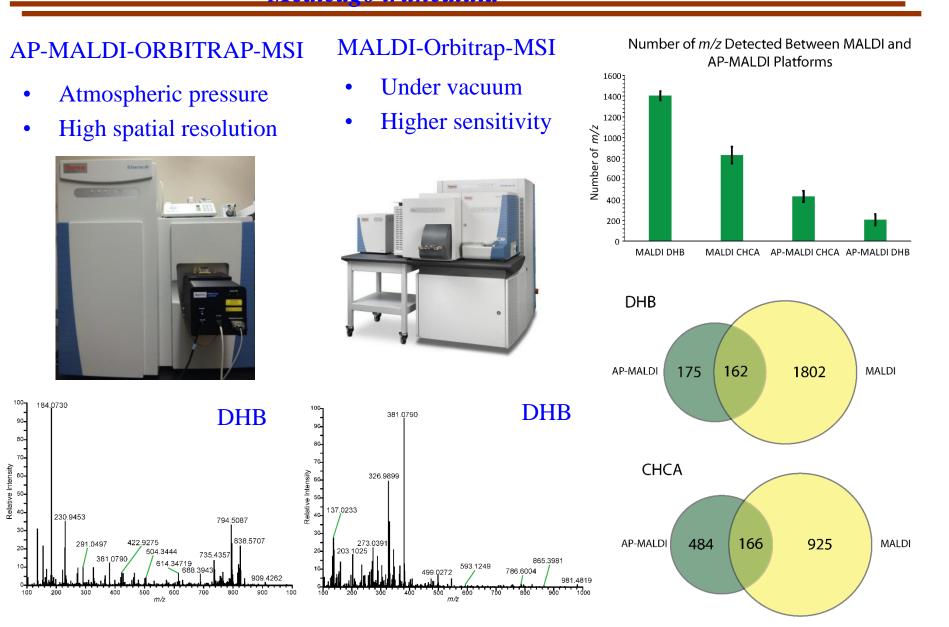
Matrix-assisted laser desorption/ionization-mass spectrometry imaging (MALDI-MSI) is routinely used to determine the spatial distributions of various biomolecules in tissues. Recently, there has been an increased interest in creating higher resolution images using sources with more focused beams. One such source, an atmospheric pressure (AP) MALDI source from MassTech, has a laser capable of reaching spatial resolutions of 10 μm. Here, the AP-MALDI source coupled with a Q Exactive HF Orbitrap platform is compared to the commercial MALDI LTQ Orbitrap XL system using Medicago truncatula root nodules. AP-MALDI parameters, such as the S-lens value, capillary temperature, and spray voltage, were optimized on the Q Exactive-HF platform for optimal detection of plant metabolites. The performance of the two systems was evaluated for sensitivity. spatial resolution, and overall ability to detect plant metabolites. The commercial MALDI LTQ Orbitrap XL was superior regarding the number of compounds detected, as at least two times more m/z were detected compared to the AP-MALDI system. However, although the AP-MALDI source requires a spatial resolution higher than 10 µm to get the best signal, the spatial resolution at 30 μ m is still superior compared to the 75 μ m spatial resolution achieved on the MALDI platform. The AP-MALDI system was also used to investigate the metabolites present in *M. truncatula* roots and root nodules under high salt and low salt conditions. A discriminative analysis with SCiLS software



Dr. Caitlin Keller

A High Resolution AP/MALDI-Q-Orbitrap Platform Enables In Situ Analysis of Metabolites involved in Medicago truncatula

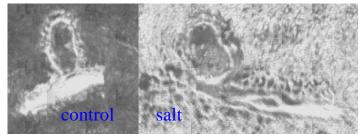




A High Resolution AP/MALDI-Q-Orbitrap Platform Enables *In Situ* Analysis of Metabolites involved in Salt Stress in *Medicago truncatula*



- Salt stress
 - Decreased plant growth
 - Poor development of symbiosis in root-nodule
 - Reduced nitrogen-fixation capacity
- Appearance of salt stress nodules: fewer, smaller, globular, white/brown



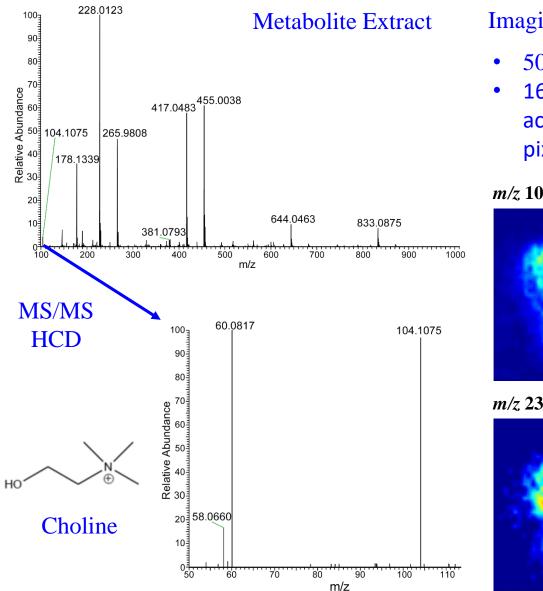
m/*z* 175.1186 +/- 5 ppm; Arginine, -1.81 ppm



m/z; Retention time (min)	Distribution	AUC >0.75 Location	Identification; Adduct Identified	Literature Molecular Weight	Delta ppm
268.1034; 3.55	Control Nodule and Root	Root	Adenosine [M+H] ⁺	267.0968	-2.53
175.1186; 1.04	Salt Nodule	Nodule	Arginine [M+H] ⁺	174.1117	-1.81
965.5076; 20.46	Salt Root and Outer Nodule	Root	Soyasaponin I [M+Na] ⁺	942.5188	-0.44

A High Resolution Sub-AP/MALDI-Q-Orbitrap **Platform Enables Identification and In Situ** Analysis of Metabolites in Medicago Truncatula

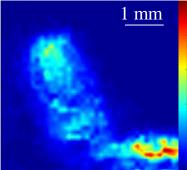




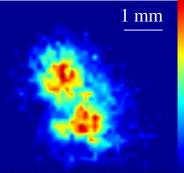
Imaging

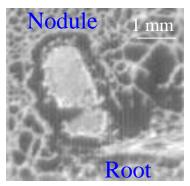
- 50 µm raster
- 16.91 minutes to acquire 2200 pixels

m/z 104.1077 +/- 5 ppm

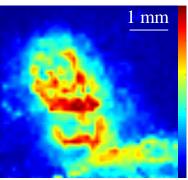


m/z 233.0525 +/- 5 ppm

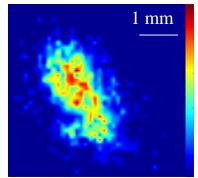




m/z 455.0043 +/- 5 ppm

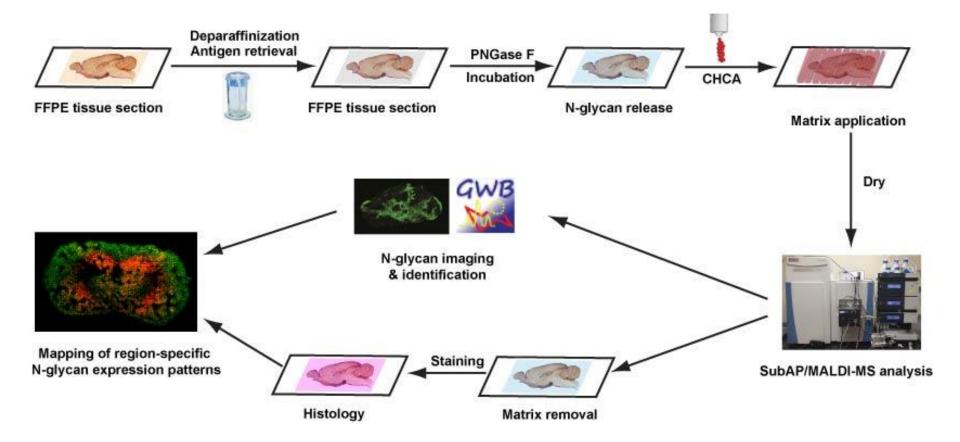


m/z 241.0691 +/- 5 ppm



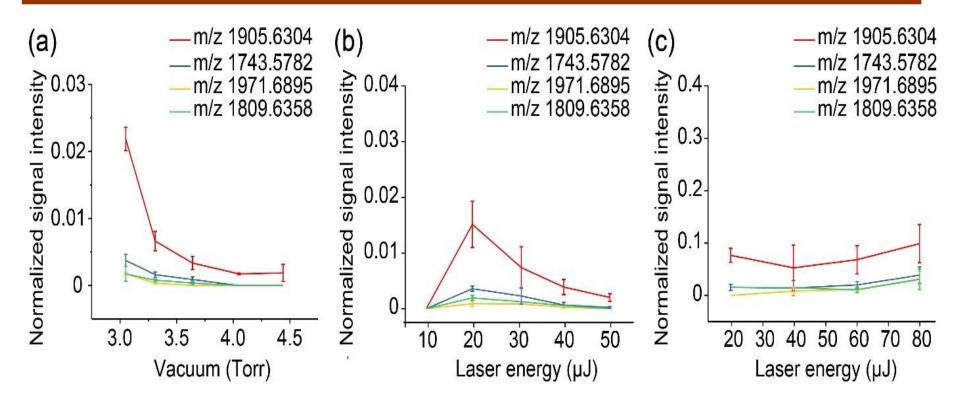
In Situ N-glycan Imaging of Mouse Brain with SubAP/MALDI-Q-Orbitrap Platform





SubAP/MALDI imaging of N-glycans from formalinfixed, paraffin-embedded (FFPE) tissue sections

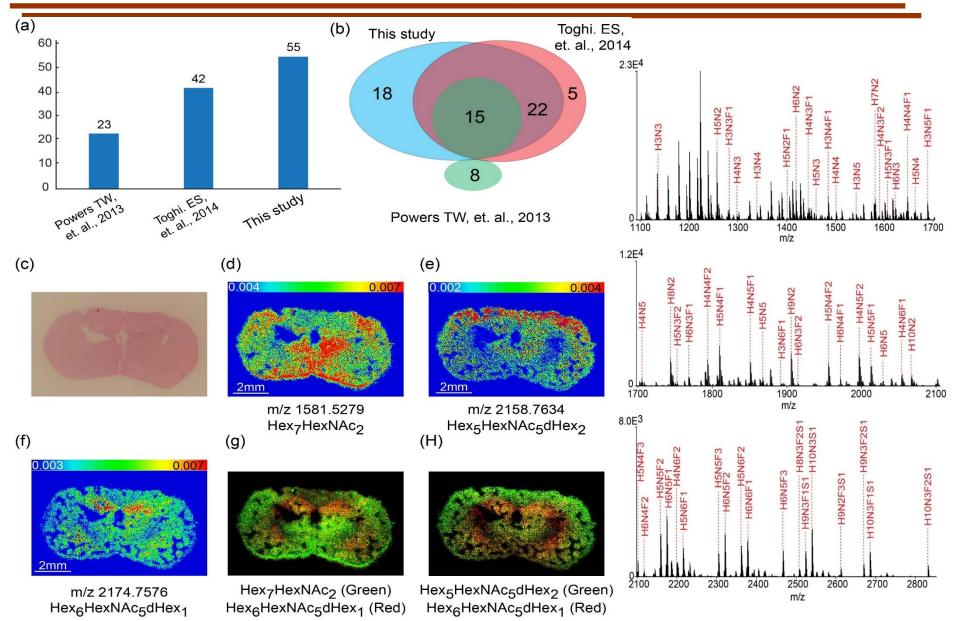
Optimization of the SubAP/MALDI Source Parameters for N-linked Glycan Analysis



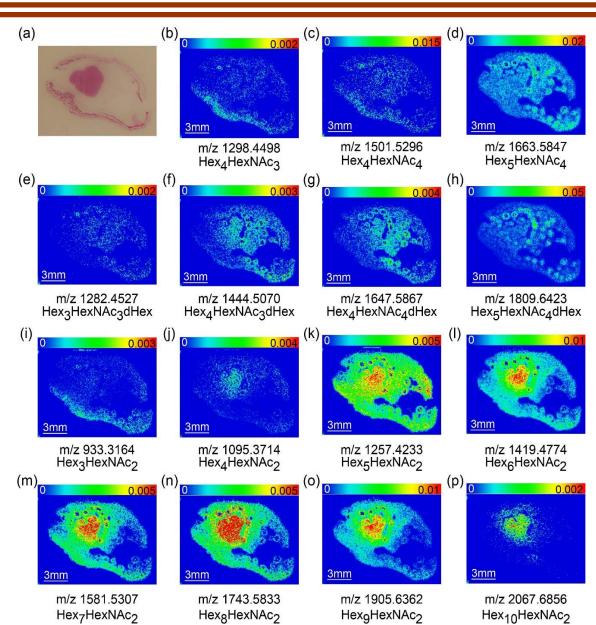
(a) TIC-normalized signal intensities of N-glycans significantly dropped following the decrease of source vacuum; (b) When CHCA used as matrix, laser energy of 20µJ showed the highest TIC-normalized N-glycan signal intensities; (c) TIC-normalized N-glycan signal intensities were independent of laser energy when DHB was used.

In Situ N-glycan Imaging of Mouse Brain with SubAP/MALDI-Q-Orbitrap Platform





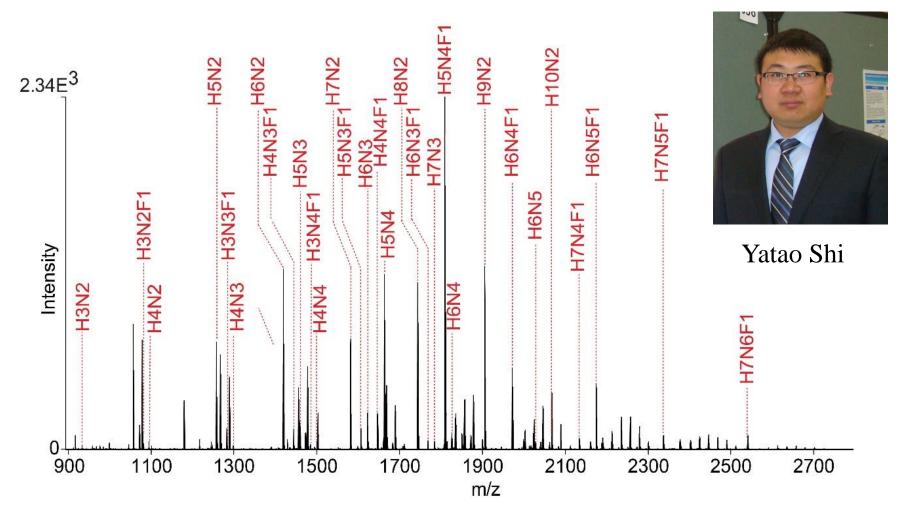
MSI of N-Glycan Analysis Reveals Distinct Distribution Patterns for Ovarian Cancer



Images of N-glycans showing different spatial distribution patterns on FFPE mouse tissue section with ovarian cancer. (a) H&E stained FFPE mouse tissue section with ovarian cancer. (b-h) Complex Nglycans showed similar distribution in cancer area in comparison to peripheral area; (i-p) High mannose Nglycans accumulated in cancer area except Hex₃HexNAc₂

THE UNIVERSITY

N-glycans detected from FFPE mouse tissue section with ovarian cancer

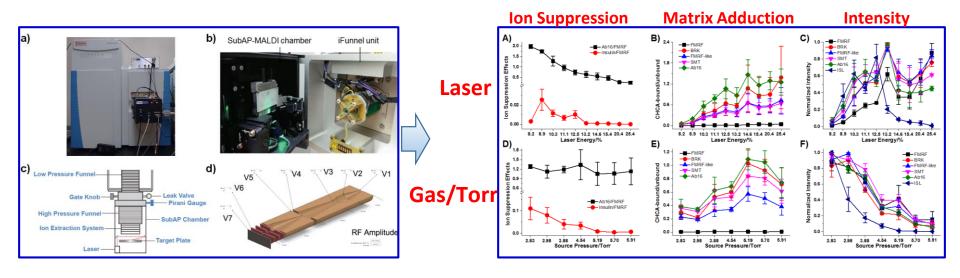


N-glycans detected from FFPE mouse tissue section with ovarian cancer. H: Hexose; N; N-Acetylglucosamine; F: Fucose; S: Sialic acid



AP-MALDI Sensitivity: SubAP + Ion Funnel + Optimization





SubAP-MALDI Platform

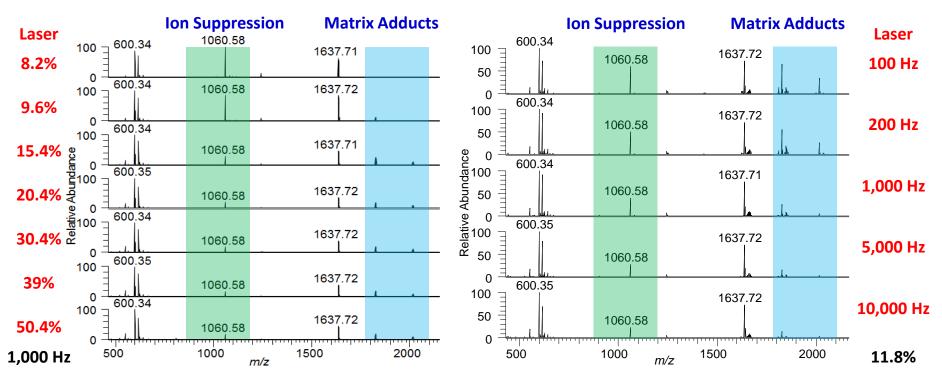
Optimization

- SubAP-MALDI was employed as a model system for AP-MALDI sensitivity study, due to its feasibility in parameter optimization.
- ◆ The sensitivity/performance of SubAP-MALDI system is laser energy- and gas pressure-dependent.
- ◆ In addition, laser firing frequency and ion funnel voltages are other important parameters to optimize.

Li, G., Cao, Q., Liu, Y., DeLaney, K., Tian, Z., Moskovets, E., & Li, L. (2019). Characterizing and alleviating ion suppression effects in atmospheric pressure matrix-assisted laser desorption/ionization. *Rapid Communications in Mass Spectrometry*, 33(4), 327-335.

SubAP-MALDI: Ion Suppression + Matrix Adducts





 Neuropeptide mixtures were used to observe the frequency- and laser energy-dependency of ion suppression effects and matrix adduction effects.

Upon increasing laser energy, both ion suppression effects and matrix adduction increase.

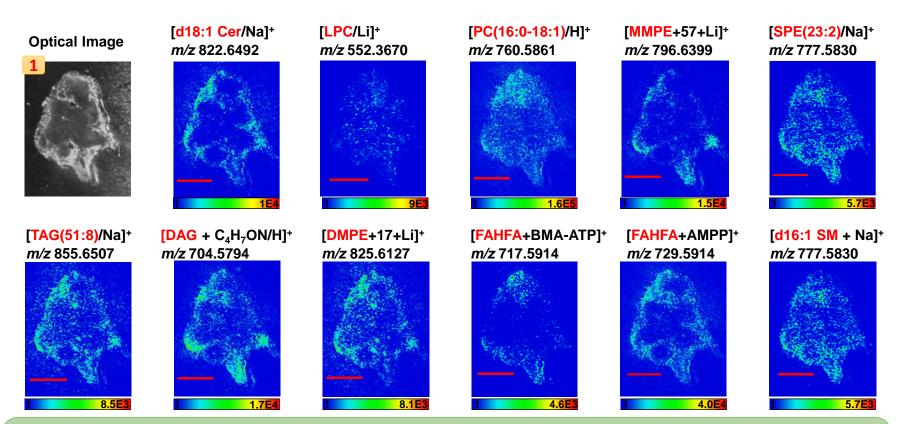
Upon increasing laser frequency, ion suppression increases but matrix adduction decreases.

Optimized laser: frequency of ~1,000 Hz, energy less than ~15% (CHCA).

Li, G., Cao, Q., Liu, Y., DeLaney, K., Tian, Z., Moskovets, E., & Li, L. (2019). Characterizing and alleviating ion suppression effects in atmospheric pressure matrix-assisted laser desorption/ionization. *Rapid Communications in Mass Spectrometry*, 33(4), 327-335.

AP-MALDI imaging: reproducible lipid analysis of crab brain tissue section (#1)

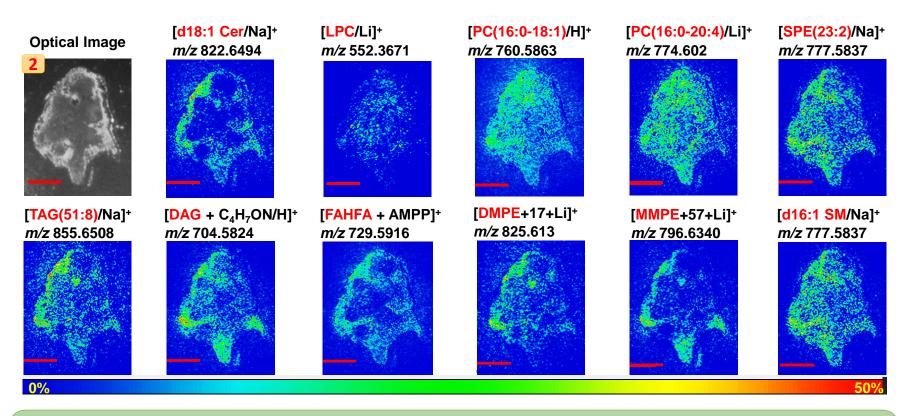




Lipid AP-MALDI-MSI, all ions selected with 10 ppm tolerance. Scale bar, 1 mm. Step size: 30 µm. Images are generated with the normalization to raw data in Thermo ImageQuest. In total, **68 lipids** are identified with accurate mass match, isotopic distribution, charge state comparison and S/N control (>3). CHCA, 20171206

AP-MALDI imaging: reproducible lipid analysis of crab brain tissue section (#2)





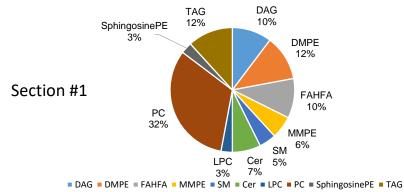
Lipid AP-MALDI-MSI, all ions selected with 10 ppm tolerance. Scale bar, 1 mm. Step size: 30 μ m. Images are generated with the normalization to raw data in Thermo ImageQuest. In total, **77 lipids** are identified with accurate mass match, isotopic distribution, charge state comparison and S/N control (>3). CHCA, 20171206

AP-MALDI: reliable/reproducible lipid imaging of crab brain tissue

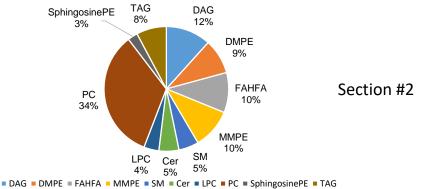


Table 1. Lipid AP-MALDI-MSI analysis of crab brain tissue.											
Tissue Section #	DAG	DMPE	FAHFA	MMPE	SM	Cer	LPC	PC	SphingosinePE	TAG	SUM
S 1	7	8	7	4	3	5	2	22	2	8	68
S2	9	7	8	8	4	4	3	26	2	6	77
in total	9	9	8	8	4	6	3	29	2	8	86

Lipid feature distribution of crab brain via AP-MALDI-MSI



Lipid feature distribution of crab brain via AP-MALDI-MSI



• Both slides share similar lipid features and imaging patterns.

AP-MALDI: Multidimensional, High-

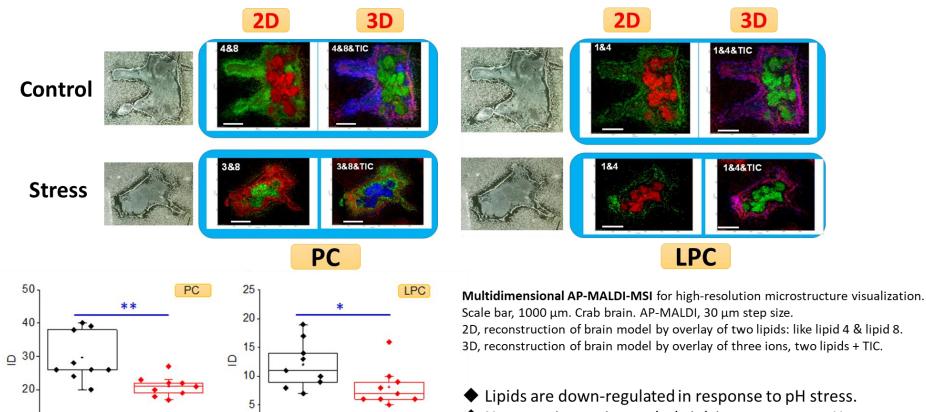


resolution Visualization

184		2	3	4	Species LPC/Na+	lipid features A16:0	PC calculated m/z 504.3424	detected m/z 504.3445	Deita m/z (ppm) 4.07	charge	S/N 104.94
				2	LPC/Li+	LPC18:3	524.3323	524.3348	4.79	1	34.08
	0.005 0.010 0.015	0.0010.0020.0030.0040.0050.006	0.002 0.005 0.010	0.005 0.010 0.015 3	LPC/Li+ LPC/Li+	X20:4 X20:3	550.3479	550.3503 552.3660	4.29	1	118.43
1&4&TIC	5	6	7	4 5	LPC/LI+ LPC/Na+	P20:0	552.3636 558.3894	552.3660	4.36 8.42	1	86.49 145.00
TOLTO TO					LPC/Li+	X22:4	578.3792	578.3815	3.91	1	42.41
And the second	Contract Price and a second			7	LPC/Li+	X22:3	580.3949	580.3971	3.81	1	80.63
199		0.002 0.005 0.008	0.005 0.010 0.015	1							
48.8		2	3	4			PC				
48.8	1	2	3	4	Species	lipid features	calculated m/z	detected m/z			
4&8	1	2	3		PC/H+	lipid features D16:1-16:0/D14:1-18:0	calculated m/z 732.5538	732.5540	0.30	1	402.79
4&8		2	3			lipid features D16:1-16:0/D14:1-18:0 D16:0-16:0	calculated m/z 732.5538 734.5694	732.5540 734.5686	0.30		402.79 281.44
48.8				3	PC/H+ PC/H+ PC/Li+ PC/H+	lipid features D16:1-16:0/D14:1-18:0 D16:0-16:0 P16:0-18:1/A16:0-18:2 8:0/P18:0-16:0/A18:1-16:0/A11	calculated m/z 732.5538 734.5694 746.5670 746.6058	732.5540 734.5686 746.5691 746.6060	0.30	1	402.79 281.44 131.22 145.54
		Street and a second sec		3 0.005 0.010 0.015 0.020 4	PC/H+ PC/H+ PC/Li+ PC/H+ PC/H+	lipid features D16:1-16:0/D14:1-18:0 D16:0-16:0 P16:0-18:1/A16:0-18:2	calculated m/z 732.5538 734.5694 746.5670	732.5540 734.5686 746.5691	0.30 1.13 2.76	1 1 1	402.79 281.44 131.22
4&8 4&8 4&8&TIC	1 0.01 0.02 0.03 0.04 0.05 0.06 0.07 5	2 0.01 0.02 0.03 0.04 0.05 6		9 0.005 0.010 0.015 0.020 4	PC/H+ PC/H+ PC/Li+ PC/H+ PC/H+ PC/H+	lipid features D16:1-16:0/D14:1-18:0 D16:0-18:0 P16:0-18:1/A16:0-18:2 8:0/P18:0-16:0/A18:1-16:0/A10 D16:0-18:1	calculated m/z 732.5538 734.5694 746.5670 746.6058 758.5694 760.5851	732.5540 734.5686 746.5691 746.6060 758.5694 760.5846	0.30 1.13 2.76 0.24 0.04 0.63	1 1 1 1	402.79 281.44 131.22 145.54 239.56 2241.00
		Street and a second sec		3 0.005 0.010 0.015 0.020 4 5 6 7	PC/H+ PC/Li+ PC/Li+ PC/H+ PC/H+ PC/H+	lipid features D16:1-16:0/D14:1-18:0 D16:0-16:0 P16:0-18:1/A16:0-18:2 8:0/P18:0-16:0/A18:1-16:0/A1 D16:0-18:2 D16:0-18:2 D16:0-18:2 D16:0-18:2	calculated m/z 732.5538 734.5694 746.5670 746.6058 758.5694 760.5851 786.6007	732.5540 734.5686 746.5691 746.6060 758.5694 760.5846 786.6006	0.30 1.13 2.76 0.24 0.04 0.63 0.17	1 1 1 1 1 1 1 1	402.79 281.44 131.22 145.54 239.56 2241.00 471.26
		Street and a second sec		3 0.005 0.010 0.015 0.020 4 5 6	PC/H+ PC/H+ PC/Li+ PC/H+ PC/H+ PC/H+	lipid features D16:1-16:0/D14:1-18:0 D16:0-18:0 P16:0-18:1/A16:0-18:2 8:0/P18:0-16:0/A18:1-16:0/A10 D16:0-18:1	calculated m/z 732.5538 734.5694 746.5670 746.6058 758.5694 760.5851	732.5540 734.5686 746.5691 746.6060 758.5694 760.5846	0.30 1.13 2.76 0.24 0.04 0.63	1 1 1 1 1 1	402.79 281.44 131.22 145.54 239.56 2241.00

AP-MALDI: Multidimensional Visualization (Control vs. pH Stress)





pH stress

Statistical comparisons are performed using student's *t*-tests; *P < 0.05, **P< 0.01, ***P < 0.001, n.s., not significant. All error bars denote SD; n = 9.

Control

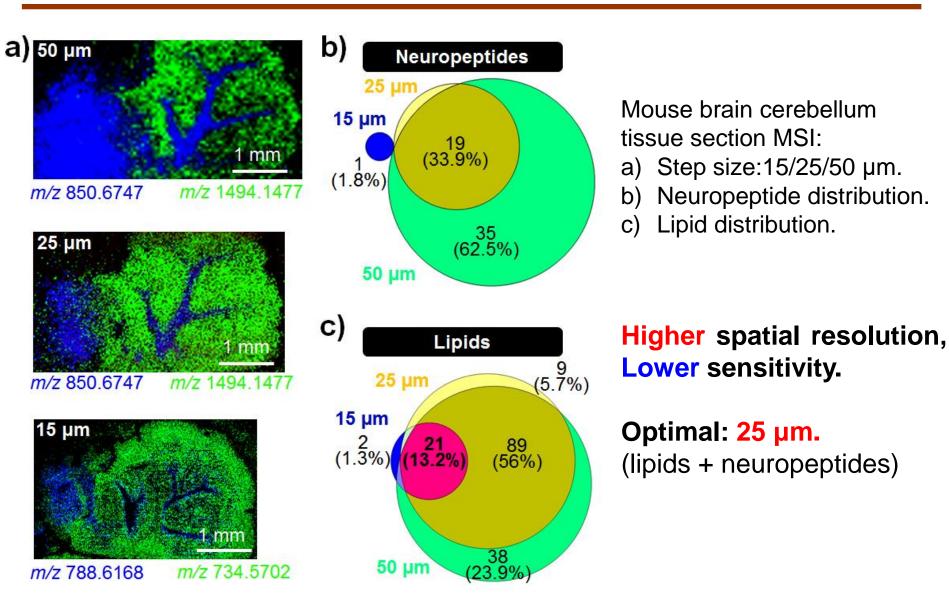
pH stress

Control

Lipids are down-regulated in response to pH stress. Neurons, just as imaged, shrink in response to pH stress.

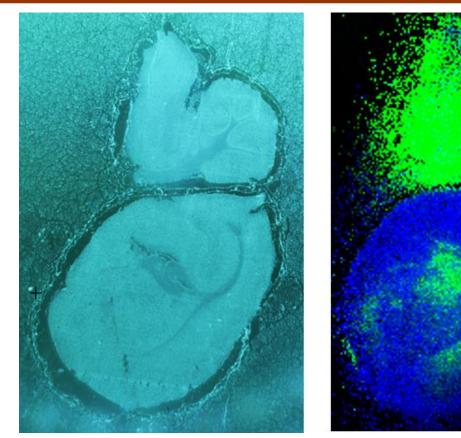
High-resolution SubAP-MALDI-MSI Spatial Resolution & Sensitivity

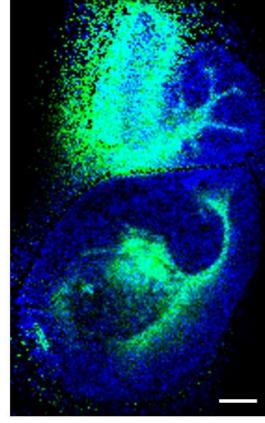




High-resolution SubAP-MALDI-MSI Mass Resolution & Sensitivity







Optical image

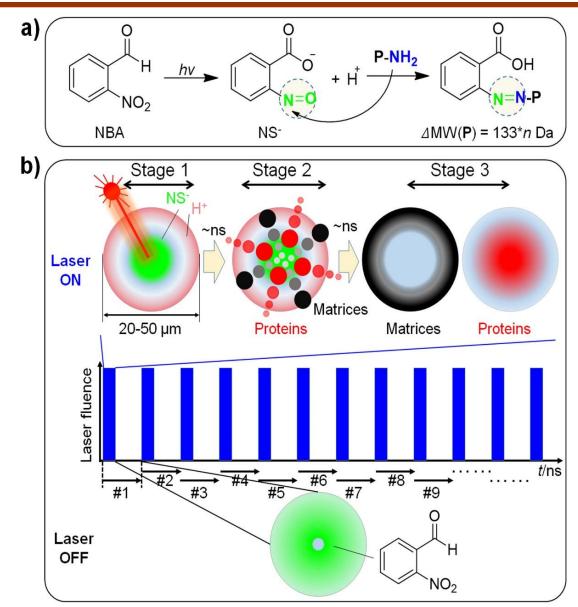
TAG(52:9)/Na+ Lactosyle Ceramide(16:0)/Li+ *m/z* 867.6530 vs 867.6239 LFDDFLRFamide/NH4+ [MMPE(38:4)+70+Li]+ *m/z* 1088.59 vs 822.647

High mass resolution

neuropeptides+lipids

Nanosecond Photochemical Reaction (nsPCR) Enables On-demand Matrix Removal





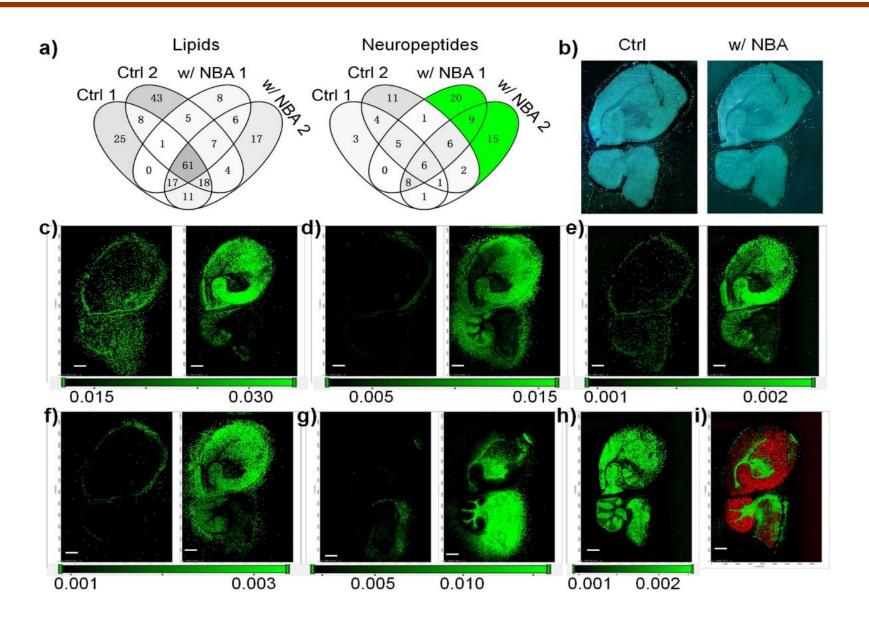


Dr. Gongyu Li

a) Nanosecond
photochemistry on NBA.
creating reactive NS⁻ for
localized micro-electric field.
b) On-demand three-stage
matrix removal regulated by
laser ON/OFF switch.

Enhanced Neuropeptide Identification and Visualization via nsPCR

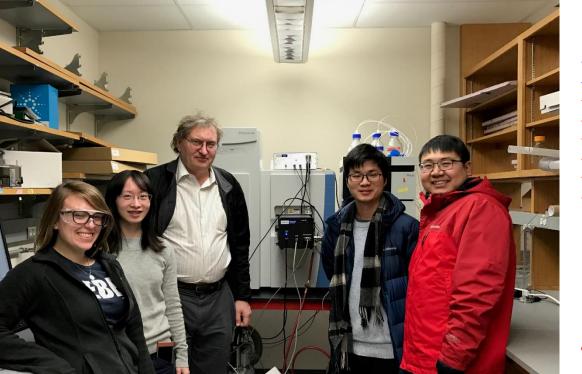




Take Home Messages...

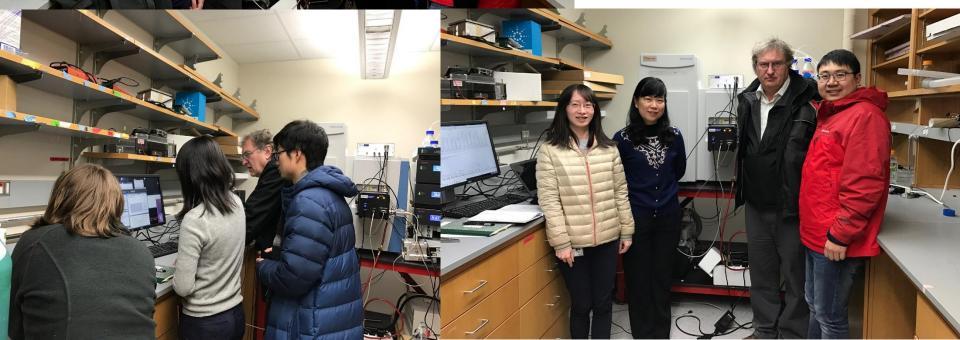


- LSI/MAIV-MS combines the benefit of MALDI and ESI to achieve expanded mass range, improved MS/MS efficiency, MS imaging capability and labile PTM protein analysis.
- Novel combination of multiplexed MSI with DDA on a MALDI Orbitrap platform enables enhanced in situ neuropeptide identification.
- AP/MALDI-Q-Orbitrap platform enables high resolution MSI in mass and space by multi-mode ionization and acquisition
- SubAP/MALDI-Q-Orbitrap platform provides promising solution to combine high spatial and mass spectral resolution with sensitivity for MSI of diverse biomolecules



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Special thanks to Thermo Fisher Scientific John Butler





Acknowledgments



The Lingjun Li Research Group at UW-Madison

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Dr. Erin Gemperline Dr. Zhidan Liang Dr. Jingxin Wang Dr. Shan Jiang Dr. Chuanzi Ouyang Dr. Chenxi Yang Mr. Kankai Chen Prof. Wei Wang Prof. Yan Liu Dr. Matt Glover Dr. Bingming Chen **Collaborators** Dr. Eugene Moskovets (MassTech)

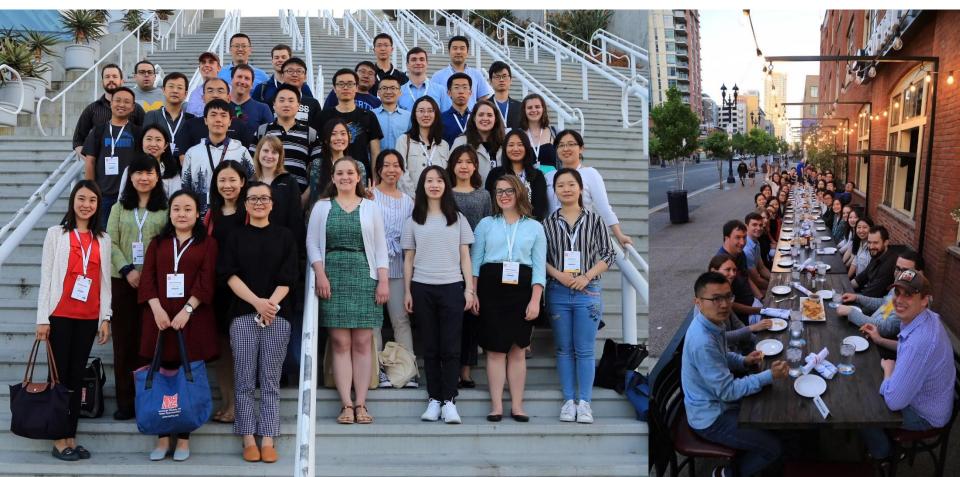


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UW Graduate School, School of Pharmacy, WARF **UW ICTR**, Wisconsin IEDR Program NSF CAREER Award (CHE-0449991, CHE-0957784, CHE-1413596) NIH-NIDDK (1R01DK071801) NIH-NIGMS (P41GM108538) NIH-NIDA (R21 DA038973) NIH-NCRR (S10RR029531) NIH NIA (R21AG055377, R01AG052324) NIH NIMH (R56MH110215) WMCP Alzheimer's Disease Pilot Grant Alfred P. Sloan Research Foundation Vilas Associates Program **Romnes Fellowship program**

The Lingjun Li Research Group Wisconsin

The Lab started in 2003; Successfully trained and graduated 43 Ph.D. students; Currently training 24 grad students; 5 postdocs; 6 undergrads; 1 HS





Organizers

Julia Laskin Purdue University

Lingjun Li University of Wisconsin-Madison

Jeffrey Spraggins Vanderbilt University

35THASILOMAR CONFERENCE Mass Spectrometry Imaging: New Developments and Applications

October 11 – 15, 2019 Asilomar Conference Center • Pacific Grove, CA



Sponsored by American Society for Mass Spectrometry

Conference Organizers

Julia Laskin Purdue University

Lingjun Li University of Wisconsin-Madison

Jeffrey Spraggins Vanderbilt University

IMPORTANT DEADLINES

August 9 Travel stipend application for students and post-docs

September 6 Abstract submissions for contributed posters and hot topic talks

September 10 Room reservations at Asilomar

September 13 Conference Registration



35th Asilomar Conference on Mass Spectrometry

Mass Spectrometry Imaging New Developments and Applications

October 11 - 15, 2019 ASILOMAR CONFERENCE CENTER, PACIFIC GROVE, CALIFORNIA

Mass spectrometry imaging is a vibrant, rapidly developing area of research that attracts researchers from numerous fields including instrumentation development, drug discovery, biotechnology, clinical research, forensics, and beyond. The 2019 ASMS Asilomar conference on mass spectrometry imaging is timely as there will be discussion on the progress made over the last decade. This conference will bring together researchers from multiple disciplines to discuss key challenges, innovative developments, and emerging applications in mass spectrometry imaging.

Detailed program at www.asms.org/asilomar-conference/program.

INVITED SPEAKERS

The program concludes with an after-dinner talk by Richard Caprioli (Vanderbilt University).

Nathalie Agar (Brigham and Women's Hospital, Harvard Medical School)

Theodore Alexandrov (EMBL)

Per Andren (Uppsala University)

Josephine Bunch (The National Physical Laboratory, UK) Zongwei Cai (Hong Kong Baptist University)

Pierre Chaurand (University of Montreal)

- Bingming Chen (Merck)
- Pieter Dorrestein (University of California, San Diego)
- Richard R. Drake (Medical University of South Carolina) Livia Eberlin (University of Texas, Austin)

Ron Heeren (Maastricht University)

Amanda Hummon (The Ohio State University)

Ryan Kelly (Brigham Young University) Ingela Lanekoff (Uppsala University) Young-Jin Lee (Iowa State University) Martina Marchetti-Deschmann (TU Wien) David Muddiman (North Carolina State University)

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Olga Vitek (Northeastern University) Zhibo Yang (University of Oklahoma)

PROGRAM HIGHLIGHTS AND SPECIAL FEATURES Pre-conference workshop hosted by Imaging Mass Spectrometry Society (IMSS)

Posters and Hot Topic short talks selected from submitted abstracts.

Go to www.asms.org to register, apply for stipend, submit an abstract, or reserve a room at Asilomar.