MALDI imaging analysis of the canine heartworm, Dirofilaria immitis, using a timsTOF flex Jeremy Foster,¹ Christopher Taron,¹ and <u>Katherine A. Stumpo^{2,3,4}</u>

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Objectives

- Demonstrate SpatialOMx capabilities of the timsTOF fleX on a complex tissue sample
- Correlate molecular phenotypes across glycomics. lipidomics, and metabolomics imaging experiments

Background

Parasitic nematodes afflict much of the world population and limit agricultural production by infecting livestock and cash crops. The intensity, distribution, and geographic reach of parasitic nematodes is projected to be influenced by global climate change. These diverse species have the potential to further impact crop production rates and expand to new hosts, with impacts on plant and animal life across the planet. A comprehensive understanding of such organisms is critical to best devise strategies to reduce these impacts.

Experimental Methods

- MALDI Imaging experiments performed on fresh frozen canine heartworms, Dirofilaria immitis • <u>Glycomic analysis</u>: tissue embedded in OCT, sectioned at 10 μm thickness and thaw mounted onto conductive IntelliSlides at -19°C. Samples were
- delipidated using standard protocols and digested with PNGaseF, followed by spraying with CHCA matrix • Lipidomic analysis: tissue was embedded in CMC, sectioned at 10 µm thickness, thaw mounted onto IntelliSlides, then sprayed with CHCA.
- Metabolomic analysis: tissue was embedded in CMC, sectioned at 10 µm thickness, thaw mounted onto IntelliSlides, then sprayed with DHAP or norharmane.
- All samples were imaged using a timsTOF fleX at 10 micron lateral spatial resolution in positive or negative ion mode (Bruker Scientific, Billerica, MA). Data analysis was performed using SCiLS lab and MetaboScape (Bruker Scientific, Billerica, MA).



Results



Summary Statements

- MALDI Imaging can be utilized to give multi-omics context to biological samples
- SCiLS Lab and MetaboScape provide comprehensive software solutions for SpatialOMx Imaging
- CCS-aware fragmentation allows for tracking of parent and daughter molecules and extraction of MS/MS information for each mobility separated species
- Key features that are only possible with the timsTOF fleX include: 10 micron lateral spatial resolution, trapped ion mobility separation of isobaric/isomeric species, and MALDI-2 enhancement







			m/z meas.	mSigma 🛛 🛛	ım/z [ppm]	lons	CCS (Å ²)	Name 🔻	Molecular Forr	n Ann	otations	AQ
			278.13622	155.3	5.611	± •	164.4	Thr Thr Gly	C10H19N3O6			
			773.64964	91.6	-4.471	± •	302.1	SM(d16:1/23:0)	C44H89N2O6P		SILC	5
			789.64590	23.5	-2.680	±= =	307.9	SM 39:1;O3	C44H89N2O7P		SI	
			735.50469	294.8	-3.362	± •	281.3	SM 36:7;30	C41H71N2O7P			
			808.52179	363.8	-2.635	± •	298.2	SHexCer 20:2;2	C41H77NO12S			.
			686.41901	216.0	6.753	± •	268.6	SHexCer 13:0;2	C32H63NO12S			<u></u>
			550.27142	168.3	-3.269	± •	237.3	Ser His His Val	C ₂₃ H ₃₅ N ₉ O ₇			
			678.46814	60.9	-3.405	± • •	266.0	PS(P-16:0/13:0)	C35H68NO9P	AL SE		.
			650.40225	208.7	-0.782	± •	258.9	PS(12:0/14:1(9Z))	C32H60NO10P		SIII (III)	.
••• •	10.00		694.46071	20.9	-6.691	± •	270.1	PS 29:0	C35H68NO10P		çill	
36 237			347.13855	133.2	0.531	± •	171.9	Pro Gln Cys	C ₁₃ H ₂₂ N ₄ O ₅ S	SI ISE		
			582.30107	57.2	-4.645	± •	233.0	POB-PS	C ₂₆ H ₄₈ NO ₁₁ P	AL SE		
			808.56950	194.0	-0.409	± •	297.3	PI-Cer(d20:1/16	C42H82NO11P		sill and a second s	
202.7 Sebacic a				709.47869	81.1	-2.246	± • •	281.1 PA 37	Name ▲ Mo 7:5 Cao	lecular Form. H69O8P	Annotations	
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