OMICS and Precision Medicine - Full Workflows for Lipidomics and Metabolic Profiling

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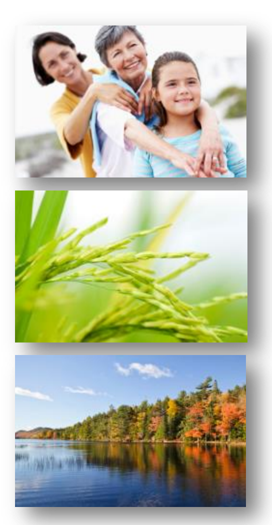
Account Manager TN & MS

The Promise of Quantitative Systems Biology

- **Human Health**
  - Biomarkers will help monitor wellness, detect early disease, monitor disease progression, and stratify patients for more tailored care.
- **Agriculture and Food**
  - Bioengineering of key crops will enable the optimization of production, nutrition, taste, durability, and resistance to infectious agents.
- **Energy and Environment**
  - Bioengineering based on a systems level knowledge for the development of alternative bioenergy sources and improved carbon sequestration.



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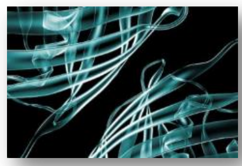
The Challenges in Systems Biology

Today's biomarker discovery	Tomorrow's personalized medicine
Omics data are information rich and context dependent	NEED to compare complex biological results from diverse technologies
Vast amounts of omics data are generated by different labs	NEED to integrated environment to combine, compare, and share results



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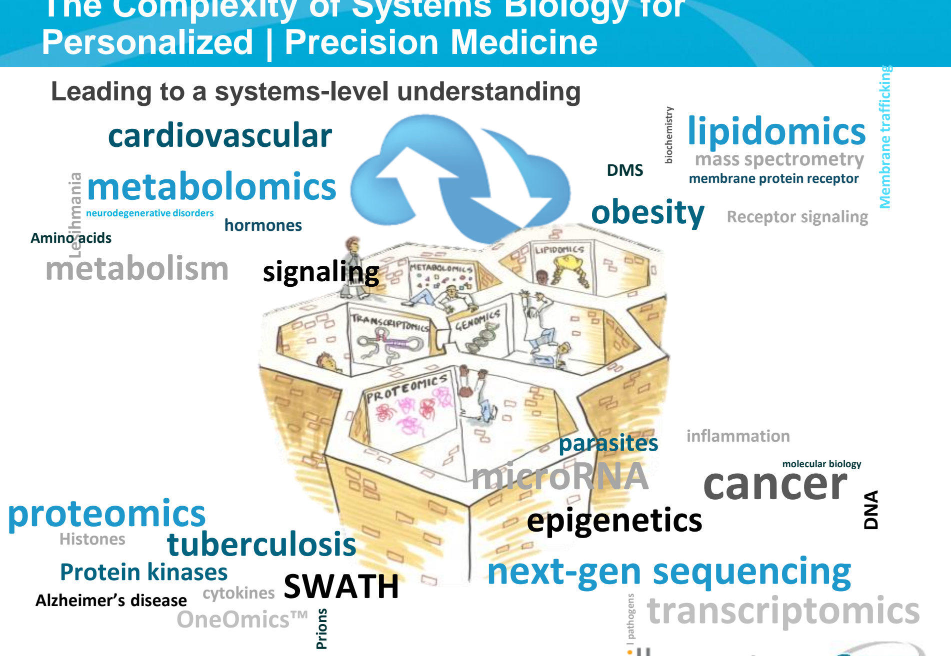
The Complexity of Systems Biology for Personalized | Precision Medicine



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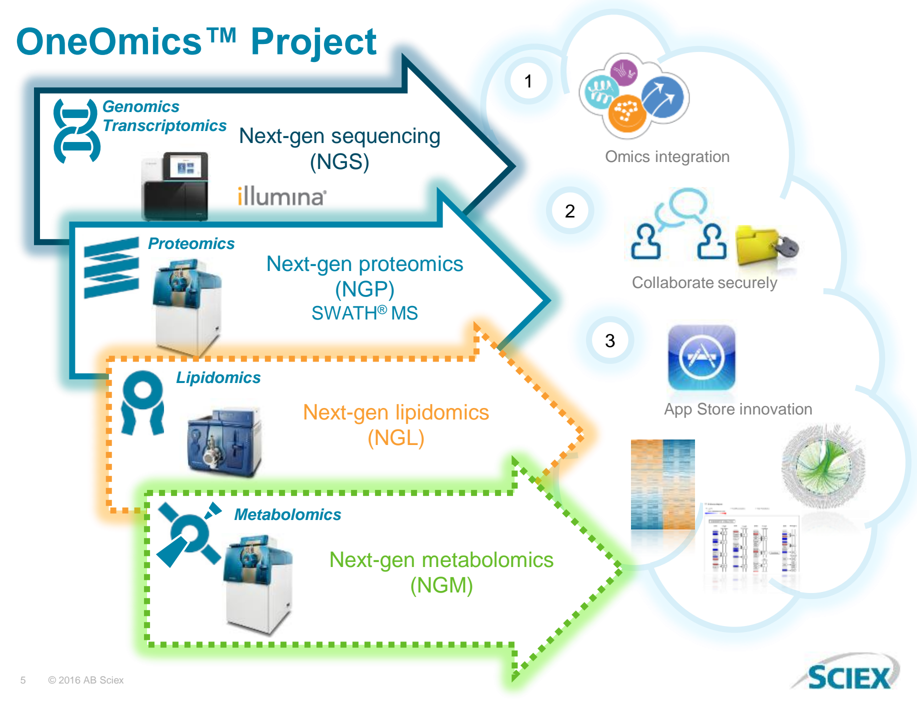
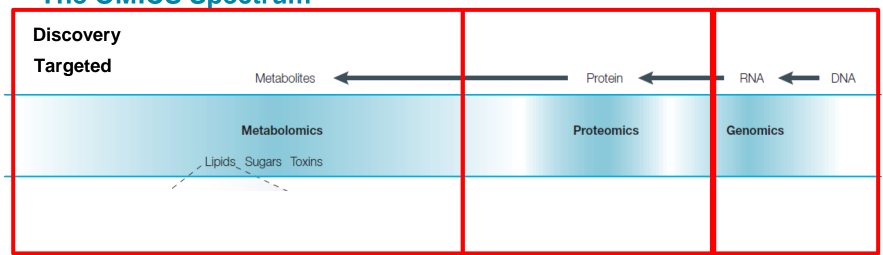


OMICS Technologies

The OMICS Spectrum



Wenk et al. Nature 2005

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OMICS Technologies

The OMICS Spectrum

Metabolites ← Protein ← RNA ← DNA

Metabolomics | Proteomics | Genomics

Lipids Sugars Toxins

Lipidomics

B

Tissues and cells → (Lipid isolation, a) → Lipid extract → (Lipid analysis, b) → Lipid profile → (Pathway analysis, c) → Candidate enzyme/ protein → (d) → Responsible enzymes/ proteins → (e) → Genetic basis

Wenk et al. Nature 2005

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SCIEX Metabolomics Portfolio

Discovery | **Translation/Validation** | **Clinical Utilization**

Global Untargeted Screening

- 1000's of *features* in 10's of samples
- SWATH® / IDA Acquisition
- Brings data analysis from weeks to days

Global Targeted Screening

- Profile over 500 known *metabolites* in 10's of samples
- SWATH® / IDA Acquisition
- SCIEX Accurate Mass Spectral Library: processing to visualization in minutes

Targeted Profiling

- 100s of putative biomarkers on 100-1000s of samples
- QTRAP® Systems: Industry standard robustness
- Kits / reagents / existing methods:
  - aTRAQ™ Reagent for AAA
  - Amplifex reagents for enhanced sensitivity
  - MRM assays for Vitamin D, Hormones/Steroids

Validated Assays

- 10s of biomarkers and 100,000s of samples/yr.
- SCIEX Triple Quad™ 4500 MD
- MultiQuant™ Software MD
- Cliquid™ Software MD

Putative biomarkers → # Samples

Applications
FluxOMICS and Pathways

Targeted Metabolomics - FluxOMICS

Quantitative and Qualitative Metabolomics for the Investigation of Intracellular Metabolism

Targeted Analysis on the QTRAP® 5500 System and Reverse-Phase Ion-Pairing Chromatography

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[1]Department of Bioengineering, University of California, San Diego, CA, USA, [2]SCIEX, USA

Liquid chromatography-mass spectrometry (LC-MS) provides a powerful analytical tool for understanding and monitoring intracellular metabolism by measuring the metabolome. The study of intracellular metabolism of model organisms, such as *E. coli*, is vital to further our biochemical knowledge[1], to develop new pharmaceuticals that target harmful pathogens[2], and to improve industrial applications that aim to metabolically engineer bacteria in order to produce commodity chemicals from renewable resources[3]. Paramount to these endeavors is the ability to reliably and accurately measure the intracellular metabolome. For microorganisms, the compounds of most interest comprise intermediates of high flux pathways such as glycolysis, the pentose phosphate pathway, the citric acid cycle, amino acid metabolism, as well as energy and redox cofactors such as ATP and NADH (Figure 1). By measuring the absolute metabolite levels of such compounds, one is able to calculate reaction and pathway thermodynamics[4] and infer *in vivo* enzyme kinetics[5]. In addition, when microorganisms are grown on a specifically chosen labeled substrate (e.g. 1-^{13}C glucose) during a metabolic labeling experiment, the isotopomer distribution of intracellular compounds can be used to calculate the absolute flux through specific reactions of interest[6].

In this work, the QTRAP® 5500 system (a hybrid triple quadrupole linear ion trap mass spectrometer) was used to implement both quantitative and qualitative workflows aimed at measuring anionic and polar compounds of intracellular metabolism.

Key Features of the QTRAP® 5500 System for Qualitative and Quantitative Metabolomics

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Targeted Metabolomics - FluxOMICS

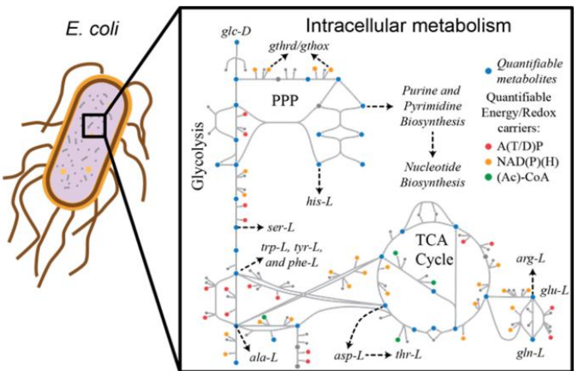

Figure 1. Metabolomics of Intracellular Pathways for Investigations into the Biochemistry of Microorganisms. High flux pathways such as those shown are key to generating a biological picture and targeted metabolomics strategies provide a robust quantitative strategy for monitoring changes.

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Targeted Metabolomics - FluxOMICS

Metabolite	Q1	Q3	RT	DP	EP	CE	CXP	MS Window	Quantifier
L-Arginine-UC13	179	136	0.7	-125.3	-10	-19.1	-6.9	30	1
L-Arginine	173	131	0.7	-125.3	-10	-19.1	-6.9	30	1
L-Ornithine-UC13	136	89	0.7	-61.8	-10	-17.4	-7.9	30	1
L-Ornithine	131	85	0.7	-61.8	-10	-17.4	-7.9	30	1
L-Asparagine-UC13	135	118	0.92	-89.7	-10	-16.1	-7	30	1
L-Asparagine	131	114	0.92	-89.7	-10	-16.1	-7	30	1
L-Asparagine	131	95	0.92	-51	-10	-17.1	-11.3	30	2
L-Serine-UC13	107	76	0.92	-72.8	-10	-15.9	-8.7	30	1
L-Serine	104	74	0.92	-72.8	-10	-15.9	-8.7	30	1
L-Serine	104	42	0.92	-73.9	-10	-18.7	-12.2	30	2
L-Citrulline-UC13	180	136	0.93	-76.4	-10	-19.1	-6.4	30	1
L-Citrulline	174	131	0.93	-76.4	-10	-19.1	-6.4	30	1
L-Glutamine-UC13	150	132	0.93	-19.9	-10	-13.3	-17.7	30	1
L-Glutamine	145	127	0.93	-19.9	-10	-13.3	-17.7	30	1
L-Glutamine	145	101	0.93	-20.2	-10	-14.3	-6.8	30	2
Hexose_Pool_fru_glc-D-UC13	185	61	0.94	-36.2	-10	-23.1	-5.8	30	1
Hexose_Pool_fru_glc-D	179	59	0.94	-36.2	-10	-23.1	-5.8	30	1
Hexose_Pool_fru_glc-D	179	89	0.94	-37.4	-10	-12.9	-6.7	30	2
L-Cystine-UC13	245	123	0.94	-59.7	-10	-17	-14.8	30	1
L-Cystine	239	120	0.94	-59.7	-10	-17	-14.8	30	1
L-Threonine-UC13	122	76	0.94	-46.5	-10	-14.2	-6.7	30	1
L-Threonine	118	74	0.94	-46.5	-10	-14.2	-6.7	30	1
L-Alanine-UC13	91	46	0.95	-14.2	-10	-19.9	-14	30	1
L-Alanine	88	45	0.95	-14.2	-10	-19.9	-14	30	1
L-Alanine	88	42	0.95	-11.2	-10	-19.2	-17	30	2
Cytidine-UC13	251	113	1.15	-100	-4	-16.1	-5.2	30	1
Cytidine	242	109	1.15	-100	-4	-16.1	-5.2	30	1
L-Histidine-UC13	160	143	1.15	-56.7	-10	-18.8	-14.8	30	1
L-Histidine	154	137	1.15	-56.7	-10	-18.8	-14.8	30	1
L-Histidine	154	93	1.15	-57.6	-10	-22.8	-9	30	2
Uracil-UC13	115	43	1.15	-100	-10	-26	-7	30	1
Uracil	111	42	1.15	-100	-10	-26	-7	30	1
5-Aminoimidazole-4-carboxamide riboside-UC13	266	129	1.2	-100	-10	-22	-9	30	1

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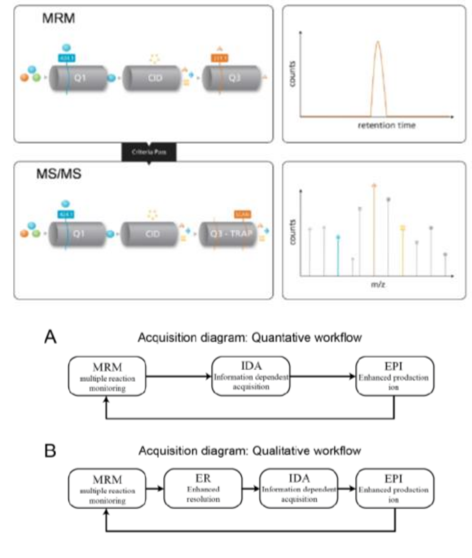
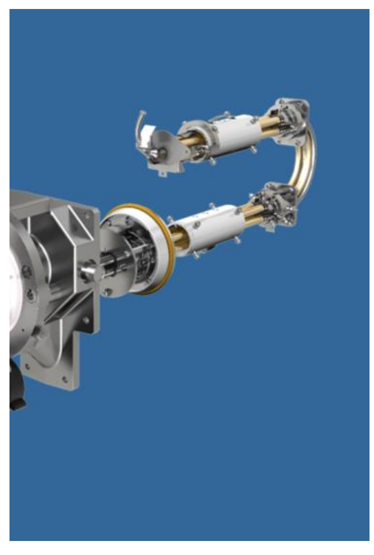
Targeted Metabolomics - FluxOMICS





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Targeted Metabolomics - FluxOMICS

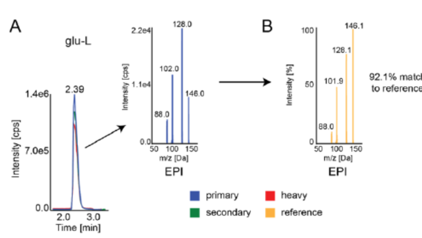

Figure 3. Simultaneous Quantitative Analysis with Qualitative Confirmation of L-Glutamate using the QTRAP® 5500 System. A) The primary and secondary transitions (blue and green) for glu-L are monitored, along with the uniformly heavy carbon labeled analog (red). A full scan MS/MS spectrum (EPI scan) is triggered when the primary and secondary transitions reach a predefined threshold. B) To confirm the identity of the MRM signal, the MS/MS was matched with a greater than 90% match to the reference spectrum (taken for pure standards for glutamate).

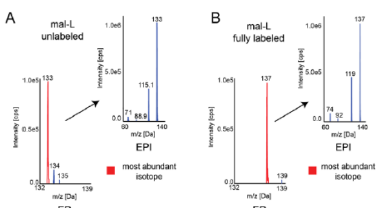

Figure 4. Qualitative Method for Characterizing the Isotopomers, Enabled by the QTRAP 5500® System. The advantage of the qualitative method is highlighted here in this example measuring unlabeled and fully labeled malic acid (mal-L) in E. *coli*. Several transitions corresponding to the isotopomer distribution are monitored per compound. An Enhanced Resolution (ER) scan is triggered when one of the isotopomer transitions reaches a predefined threshold and provides MS and isotope ratio information. An EPI scan is also triggered and provides information regarding the location of the heavy label (if present).

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Targeted Metabolomics - FluxOMICS

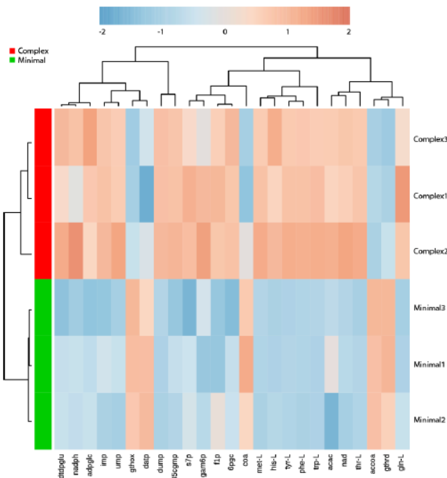

Figure 6. Heat Map of Absolute Metabolite Level Differences Between *E. coli* Grown in Minimal Media and Complex Media. The top 25 most significant metabolites (x-axis) are clustered (Pearson's R, complete linkage) according their significance and fold-change (Students t-test). The media conditions (y-axis) are clustered (Pearson's R, complete linkage) according to similarity in metabolite level of the top 25 most significant metabolite changes.

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The Lipidyzer™ Platform: A Revolutionary Tool for Understanding the Role of Lipids in Disease

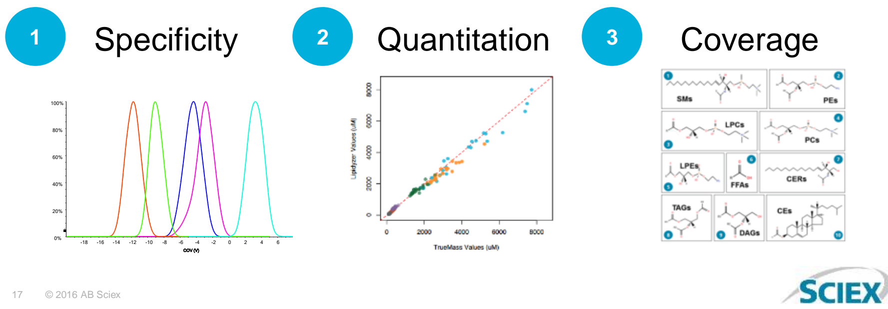
For Research Use Only. Not for use in diagnostic procedures. RUO-MKT-11-4185-A

Industrializing Lipidomics

Lipidyzer™ Platform

- Robust MS System
- Class separation using DMS
- Unique internal standard strategy with validated kits
- Data Visualization including heat maps, box & whisker plots, etc

Lipidyzer™ Platform



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Demonstrating the Power of Lipidyzer™ Platform

Benefits

- Specificity – Differential Mobility Spectrometry (DMS)
- Eliminating Quantitative Bias – Novel Internal Standards
- Coverage – Complex Lipid Metabolism
- Sensitivity and Precision - Assay
- Robustness – Assay and Platform
- Ease of Use - Platform

- Samples Sets used for Biological Validation

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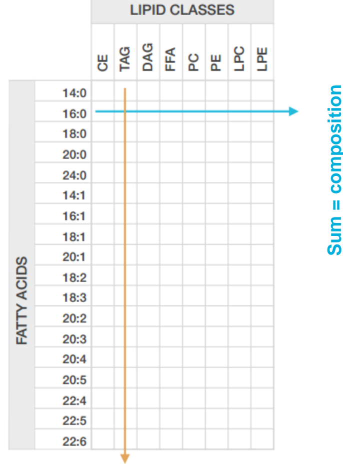
SCIEX

Complex Lipids are like a Matrix

- Lipid are present in classes that have concentrations and compositions (important for level of metabolism)
  - Concentration = sum of the FAs for any given class (column)
  - Composition = relative abundances of each FA (or species) across many classes (rows)



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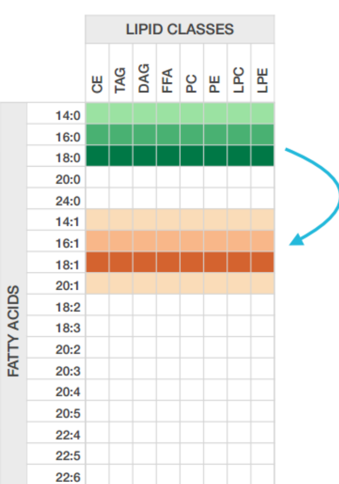
SCIEX

Complex Lipids are like a Matrix

- Lipid are present in classes that have concentrations and compositions (important for level of metabolism)
  - Concentration = sum of the FAs for any given class (column)
  - Composition = relative abundances of each FA (or species) across many classes (rows)
- When FA metabolism is altered there is the ability to change FA composition of all classes



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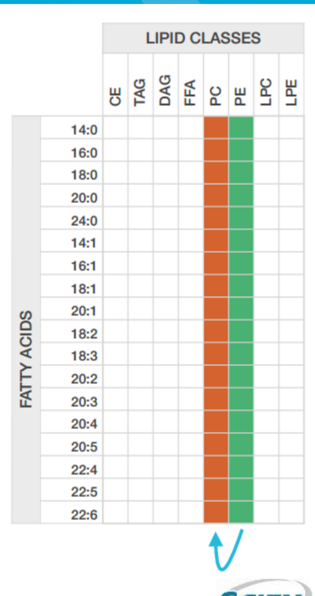
Complex Lipids are like a Matrix

- Lipid are present in classes that have concentrations and compositions (important for level of metabolism)
  - Concentration = sum of the FAs for any given class (column)
  - Composition = relative abundances of each FA (or species) across many classes (rows)
- When FA metabolism is altered there is the ability to change FA composition of all classes
- When lipid class metabolism is altered there is the ability to change all members of the class



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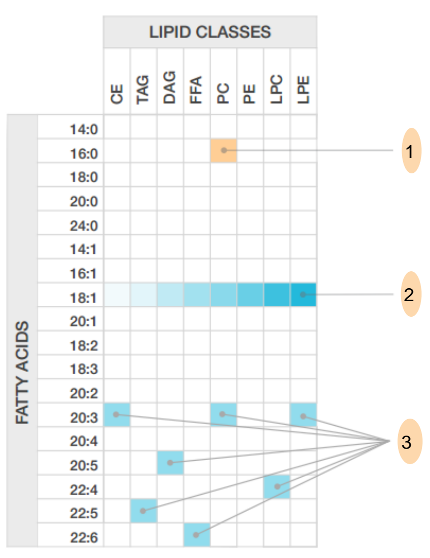
What is needed from a Lipid Platform



1) Specificity
   - A non-specific method (e.g. PC 36:2) does not allow mapping to the elements of the matrix

2) Quantitation
   - A non-quantitative approach does not allow accurate summing of the rows and columns

3) Comprehensive Coverage
   - A partially complete matrix is difficult to interpret

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Broad Range of IS to Normalize Quantitative Data

- Diversity of fatty acid chain lengths and degrees of unsaturation result in differential fragmentation efficiency which impacts quantitation
- Multiple IS that reflect the diversity of lipid molecular species

PHOSPHATIDYLCHOLINE (PC) INTERNAL STANDARD MIX			
STRUCTURE	FATTY ACID	POS	%
	FA16:1 - Palmitoleic acid	sn-2	5
	FA18:1 - Oleic acid	sn-2	20
	FA18:2 - Linoleic acid	sn-2	20
	FA18:3 - α-Linoleic acid	sn-2	5
	FA20:3 - Dihomo-γ-linoleic acid	sn-2	5
	FA20:4 - Arachidonic acid	sn-2	20
	FA20:5 - Eicosapentaenoic acid	sn-2	5
	FA22:4 - Eicosatetraenoic acid	sn-2	5
	FA22:5 - Docosapentaenoic acid	sn-2	5
	FA22:6 - Docosoahexaenoic acid	sn-2	10
	d916:0 - Labeled palmitic acid	sn-1	100

- Each lipid class has multiple internal standards at concentrations that reflect those found in biology

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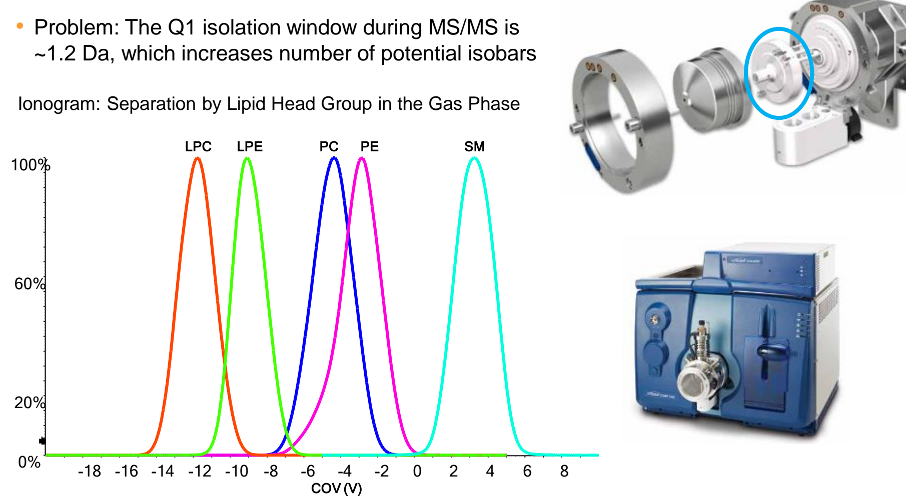
Specificity Offered by SelexION® Technology

Removal of Isobaric Interferences

- Problem: The Q1 isolation window during MS/MS is ~1.2 Da, which increases number of potential isobars

Ionogram: Separation by Lipid Head Group in the Gas Phase



Differential Mobility Spectrometry-Driven Shotgun Lipidomics *Anal. Chem.* 2014. 86. 9662-9669 10.1021/ac5021744

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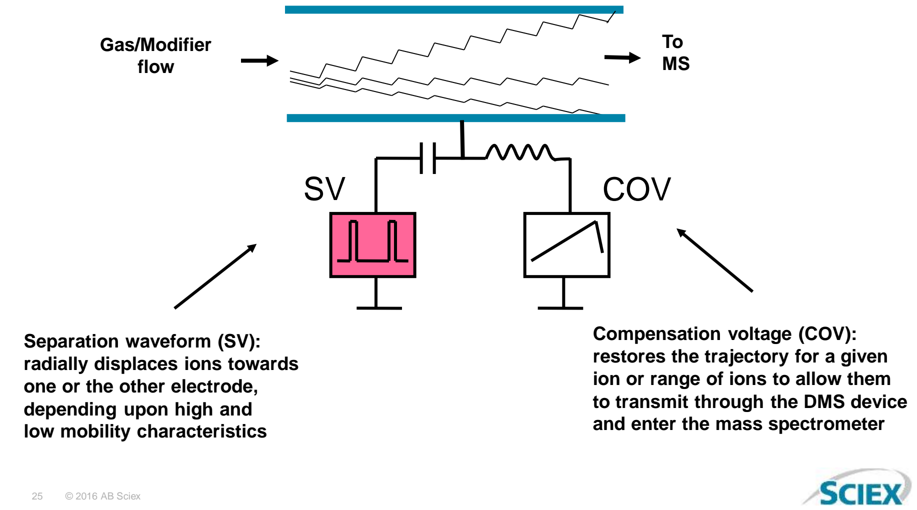
How Does SelexION™ Technology Separate Ions?

Differential Mobility Spectrometry (DMS) separates molecules using planar geometry



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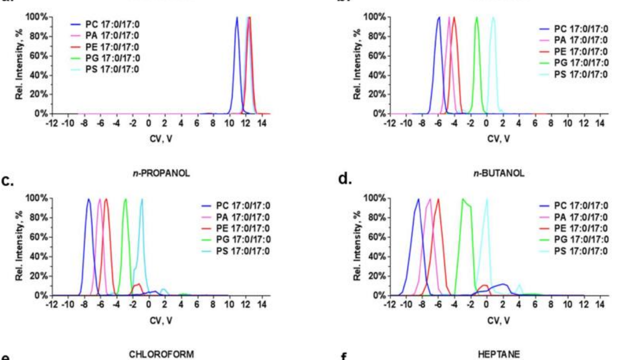
Separation of Lipid Classes Using SelexION™ Technology

Effects of Modifier on COV Values



Differential Mobility Spectrometry-Driven Shotgun Lipidomics

Anal. Chem., In Press DOI: 10.1021/ac5021744

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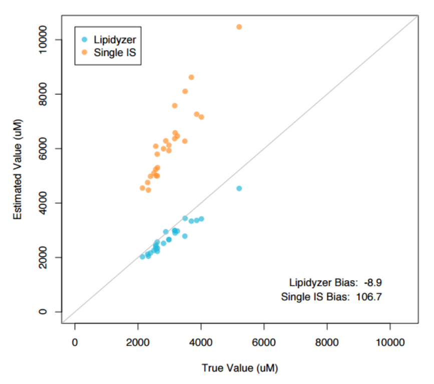
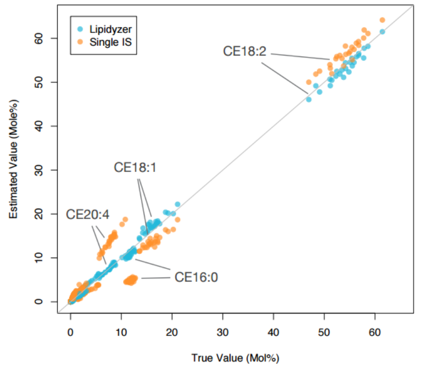
The Lipidyzer Eliminates Quantitative Bias

Multiple internal standards per class provide accurate quantitation

CHOLESTERYL ESTERS (QUANTITATIVE)



CE FATTY ACID COMPOSITION (MOLE%)



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Full Coverage of Complex Lipid Metabolism

Coverage and Depth

- Over 1100 molecular species across 13 lipid classes
- Lipidyzer™ Platform provides 6 measurements:
  1. Lipid Class Concentration
  2. Lipid Species Concentration
  3. Fatty Acid Concentration
  4. Lipid Class Composition
  5. Lipid Species Composition
  6. Fatty Acid Composition

Fraction	Lipid Classes	Number of Species*
Neutral Lipids	Triacylglycerols (TAG)	502
	Diacylglycerols (DAG)	67
	Free Fatty Acids (FFA)	28
	Cholesterol Esters (CE)	34
Polar Lipids	Phosphatidylcholines (PC)	161
	Phosphatidylethanolamines (PE)	233
	Lysophosphatidylcholines (LPC)	28
	Lysophosphatidylethanolamines (LPE)	28
	Sphingomyelins (SM)	16
	Ceramides (CER)	56

*The Ceramides listed above includes the further three classes, DCER, HCER and LCER

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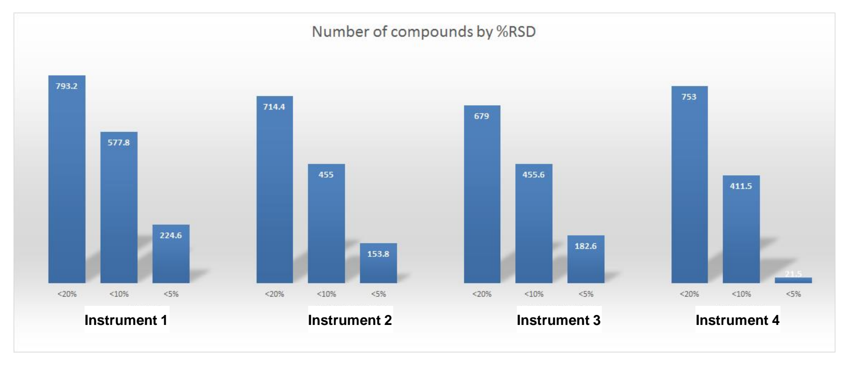
Lipidyzer™ Platform Sensitivity and Precision

5 Day Study

- Validated across 4 instruments and 3 labs the instruments detected similar numbers of lipid species and with similar precision
- >675 lipid species with RSD <20% in this control sample



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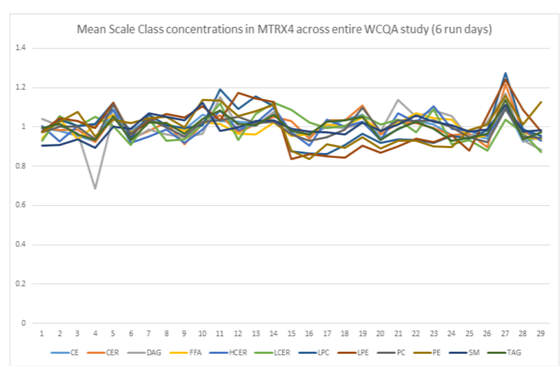
Lipidyzer™ Platform Robustness

Precision: 6 Day Study in Plasma (Total Class Concentration)

- 11/13 Classes <10% RSD over 6 days



Lipid Class	%RSD
Cholesterol esters (CE)	4.7
Ceramides (CER)	6.4
Diacylglycerols (DAG)	9.1
Free Fatty Acids (FFA)	4.5
Hexosylceramides (HCER)	5.8
Lactosylceramides (LCER)	6.9
Lysophosphocholines (LPC)	9.9
Lysophosphoethanolamines (LPE)	10.9
Phosphocholines (PC)	5.1
Phosphoethanolamines (PE)	8.9
Sphingomyelins (SM)	5.4
Triacylglycerols (TAG)	5.1
Dihydroceramides (DCER)	29.5*

*Note: DCERs are present at exceedingly low levels in plasma

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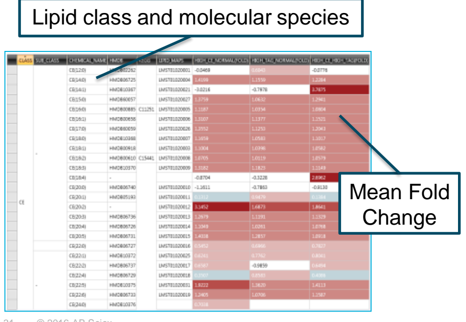
Ease of Use

Lipidomics Workflow Manager Software

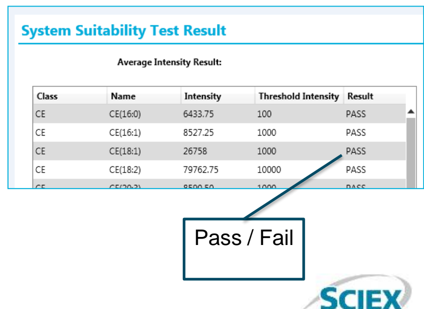
- Automates the entire workflow
  - Kit registration (concentration info)
  - System tuning and testing
  - Experimental design, data collection and processing
- Data Visualization including heat maps, QC charts and quantitative data tables

Lipid class and molecular species



CLASS	SUB_CLASS	CHEMICAL_NAME	HMDB	KEGG	LIPID_MAPS	HIGH_CE_NORMAL(FOLD)	HIGH_TAG_NORMAL(FOLD)	HIGH_CE_HIGH_TAG(FOLD)
CE	-	CE(12:0)	HMDB02262		LMST01020001	-0.0469	0.6043	-0.0778
		CE(14:0)	HMDB06725		LMST01020004	1.4199	1.1559	1.2284
		CE(14:1)	HMDB10367		LMST01020021	-3.0216	-0.7978	3.7875
		CE(15:0)	HMDB60057		LMST01020027	1.3759	1.0632	1.2941
		CE(16:0)	HMDB00885	C11251	LMST01020005	1.1187	1.0354	1.0804
		CE(16:1)	HMDB00658		LMST01020006	1.3107	1.1377	1.1521
		CE(17:0)	HMDB60059		LMST01020026	1.3552	1.1253	1.2043
		CE(18:0)	HMDB10368		LMST01020007	1.1659	1.0583	1.1017
		CE(18:1)	HMDB00918		LMST01020003	1.1004	1.0396	1.0582
		CE(18:2)	HMDB00610	C15441	LMST01020008	1.0705	1.0119	1.0579
		CE(18:3)	HMDB10370		LMST01020009	1.3182	1.1823	1.1149
		CE(18:4)	-			-0.8704	-0.3228	2.6962
		CE(20:0)	HMDB06740		LMST01020010	-1.1611	-0.7863	-0.8130
		CE(20:1)	HMDB05193		LMST01020011	0.1312	0.9479	0.1384
		CE(20:2)	-		LMST01020012	3.1452	1.6873	1.8641
		CE(20:3)	HMDB06736		LMST01020013	1.2679	1.1191	1.1329
		CE(20:4)	HMDB06726		LMST01020014	1.1049	1.0261	1.0768
		CE(20:5)	HMDB06731		LMST01020015	1.4038	1.2857	1.0918
		CE(22:0)	HMDB06727		LMST01020016	0.5452	0.6966	0.7827
	-	CE(22:1)	HMDB10372		LMST01020025	0.6241	0.7762	0.8041
		CE(22:2)	HMDB06737		LMST01020017	0.6587	-0.9859	0.6494
		CE(22:4)	HMDB06729		LMST01020018	0.3507	0.8583	0.4088
		CE(22:5)	HMDB10375		LMST01020031	1.8222	1.3620	1.4113
		CE(22:6)	HMDB06733		LMST01020019	1.2405	1.0706	1.1587
		CE(24:0)	HMDB10376			0.7018		

Mean Fold Change



System Suitability Test Result

Average Intensity Result:

Class	Name	Intensity	Threshold Intensity	Result
CE	CE(16:0)	6433.75	100	PASS
CE	CE(16:1)	8527.25	1000	PASS
CE	CE(18:1)	26758	1000	PASS
CE	CE(18:2)	79762.75	10000	PASS

Pass / Fail

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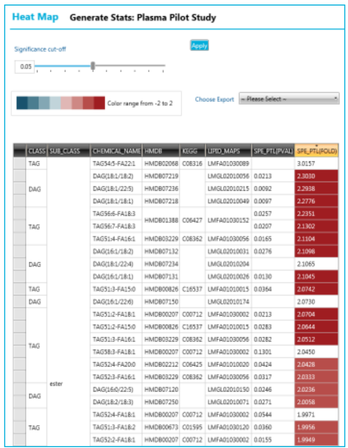
Biological Validation of Lipidyzer™ Platform

Sample Set 1

- Preeclampsia - a leading cause of maternal perinatal morbidity and mortality
  - Shallow invasion of cytotrophoblast (CTB) cells into mother's uterus
  - Failed vascular transformation of the spiral arteries is the hallmark of the placental defects in preeclampsia
  - Response: high blood pressure & proteinuria
- Understand normal CTB development and how this goes awry in preeclampsia
- Pilot study of 12 preterm labor (PTL) vs 12 severe preeclampsia women (SPE).
- Gestational age-matched plasma samples, 25-37 wks
- Validated TAGs and DAGs upregulation in SPE



CLASS	SUB_CLASS	CHEMICAL_NAME	HMDB	KEGG	LIPID_MAPS	SPE_PTL(PVAL)	SPE_PTL(FOLD)
TAG		TAG54:5-FA22:1	HMDB02068	C08316	LMFA01030089		3.0157
DAG		DAG(18:1/18:2)	HMDB07219		LMGL02010056	0.0213	2.3030
		DAG(18:1/22:5)	HMDB07236		LMGL02010215	0.0092	2.2938
		DAG(18:1/18:1)	HMDB07218		LMGL02010049	0.0097	2.2776
TAG		TAG56:6-FA18:3	HMDB01388	C06427	LMFA01030152	0.0257	2.2351
		TAG56:7-FA18:3				0.0207	2.1302
		TAG51:4-FA16:1	HMDB03229	C08362	LMFA01030056	0.0165	2.1104
DAG		DAG(16:1/18:2)	HMDB07132		LMGL02010031	0.0276	2.1098
		DAG(18:1/22:4)	HMDB07234		LMGL02010204		2.1065
		DAG(16:1/18:1)	HMDB07131		LMGL02010026	0.0130	2.1045
TAG		TAG51:3-FA15:0	HMDB00826	C16537	LMFA01010015	0.0364	2.0742
DAG		DAG(16:1/22:6)	HMDB07150		LMGL02010174		2.0730
TAG		TAG51:2-FA18:1	HMDB00207	C00712	LMFA01030002	0.0213	2.0704
		TAG51:2-FA15:0	HMDB00826	C16537	LMFA01010015	0.0283	2.0644
		TAG51:3-FA16:1	HMDB03229	C08362	LMFA01030056	0.0282	2.0512
		TAG58:3-FA18:1	HMDB00207	C00712	LMFA01030002	0.1301	2.0450
		TAG52:4-FA20:0	HMDB02212	C06425	LMFA01010020	0.0424	2.0428
		TAG52:3-FA16:1	HMDB03229	C08362	LMFA01030056	0.0317	2.0333
DAG	ester	DAG(16:0/22:5)	HMDB07120		LMGL02010150	0.0246	2.0236
		DAG(18:2/18:3)	HMDB07250		LMGL02010071	0.0271	2.0058
TAG		TAG52:4-FA18:1	HMDB00207	C00712	LMFA01030002	0.0544	1.9971
		TAG51:3-FA18:2	HMDB00673	C01595	LMFA01030120	0.0360	1.9956
		TAG52:2-FA18:1	HMDB00207	C00712	LMFA01030002	0.0155	1.9949

Professor Katherine Williams & Susan Fisher, Department of Obstetrics, Gynecology, and Reproductive Sciences, University of California San Francisco (UCSF).

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Biological Validation of Lipidyzer™ Platform

Sample Set 2

- Patients with hypertriglyceridemia (high triacylglycerols, TAGs x14), hypercholestberolemics (high cholesteryl esters, CEs x14) and controls (x12)
  - 40 samples total.
- Validated TAG changes with clinical findings
- Validated CE changes with clinical findings

CHEMICAL_NAME	HMDB	KEGG	LIPID_MAPS	HIGH_CE_NORMAL(FOLD)
CE(18:4)	-			5.4032
CE(14:1)	HMDB10367		LMST01020021	4.4896
CE(16:1)	HMDB00658		LMST01020006	3.8689
CE(14:0)	HMDB06725		LMST01020004	3.1034
CE(18:3)	HMDB10370		LMST01020009	2.9469
CE(20:5)	HMDB06731		LMST01020015	2.8251
CE(12:0)	HMDB02262		LMST01020001	2.3344
CE(20:3)	HMDB06736		LMST01020013	2.2789
CE(20:2)			LMST01020012	2.1963

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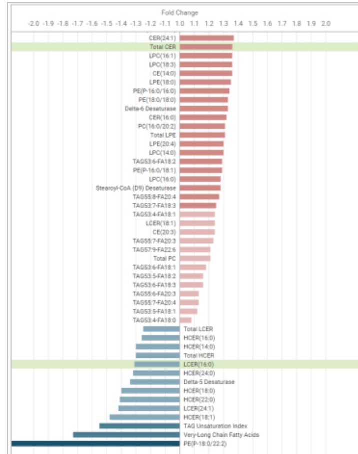
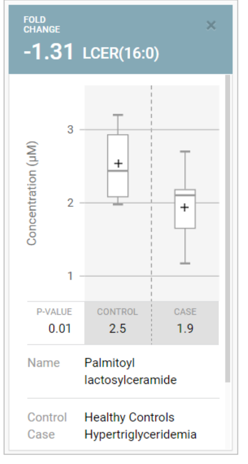
Biological Validation of Lipidyzer™ Platform

Sample Set 2 Continued

- Novel findings in down regulated HCER & LCER highlighting altered glycosphingolipid metabolism





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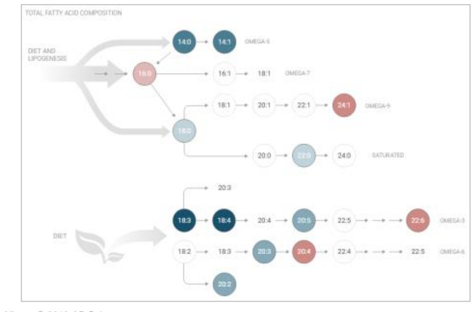
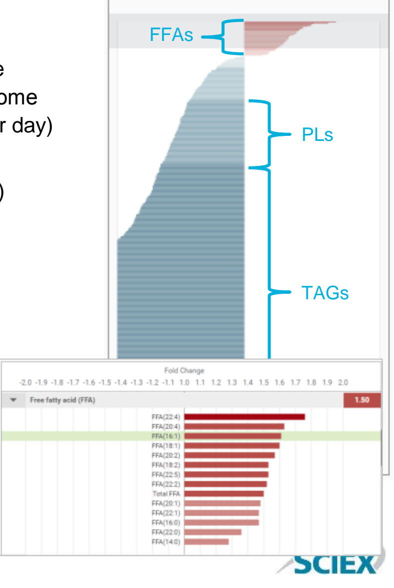
Biological Validation of Lipidyzer

Sample Set 3

- Weight Loss Study
  - Clinical manifestation of inflamed adipose tissue
  - Insulin resistance → leading to metabolic syndrome
  - Calorie-restricted diet over 8 wks (900 kCals per day)
  - Serum taken before and after weight loss
- Decreased lipogenesis (including decreased TAGs)
- Increased FFAs





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Quickest Route to Success

Comparison to a Traditional Discovery Platform

- Lipid changes with age that are prevented by dietary restriction may be responsible for age-related neuronal damages, decreased cognition functions and increased neurological disorders
- Aging Study - Young (10), old (10) and old dietary-restricted (8) mice*
- Discovery data already collected on a QExactive compared to Lipidyzer™ Platform
- QE data collection & processing and 1-2 weeks
- Lipidyzer™ Platform data collection & processing less than 1 day

Identified lipids with non-zero values in more than 50% of the samples

Lipid Class	LC-MS	Lipidyzer
TG	96	226
SM	27	12
SiE	1	0
PS	7	0
PI	15	0
PE	32	30
PC	101	41
LPE	7	5
LPC	34	17
LdMePE	7	0
dMePE	3	0
DG	6	12
ChE	9	24
CerG2GNAc1	1	0
CerG1	3	0
Cer	3	2
FFA	0	26
TOTAL	**351**	**395**

Professor Mike Synder & Kevin Contrepois, Department of Genetics, Stanford

*non-validated matrix

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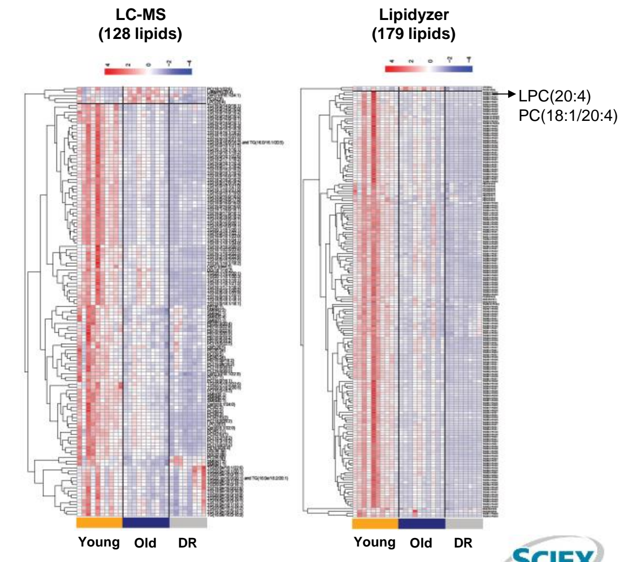
Quickest Route to Success

Significant changes between Young, Old and Calorie Restricted

- Univariate statistical analysis
  - Non-parametric Wilcoxon t test – FDR corrected q value < 0.05
  - Fold change > 1.5

Lipidyzer™ demonstrated:

- Fastest route to successful data ready for interpretation
- Larger number of detected species
- Quantitative data on all species detected
- Allows mapping data to biochemical pathways



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Conclusions

Demonstrating the Power of Lipidyzer™ Platform

- Specificity – Differential Mobility Spectrometry (DMS)
- Eliminating Quantitative Bias – Novel Internal Standards
- Coverage – Over 1100 Molecular Species across 13 lipid classes
- Sensitivity and Precision – Quantitate ~700 species <20%CVs
- Robustness – <10%CVs over 6 days
- Ease of Use – Lipidomics Workflow Manager

- Biological Validation of the Lipidyzer Platform
  - Preeclampsia Pilot Study
  - Hypertriglyceridemia Study
  - Weight Loss Study
  - Aging Pilot Study

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Acknowledgements

SCIEX
- Pauline Vollmerhaus
- Eva Duchoslav
- Paul Baker
- Scott Hamilton
- Marjorie Minkoff
- Larry Campbell
- Yves Le Blanc
- Aaron Hudson
- Mark Cafazzo

METABOLON
- Steve Watkins
- Alex Conner
- Annie Evans
- Richard Robinson
- UyenThao Nguyen
- Joseph Yu
- Luke Miller
- Sarada Tanikella
- Peter Zhu
- Corey DeHaven

Avanti Polar Lipids
- Walt Shaw
- Lisa Connelly

Collaborators
- Katherine Williams &
- Susan Fisher (UCSF)

- Andy Dannenberg (Weill College Medicine)

- Kevin Contrepois &
- Mike Snyder (Stanford)

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