

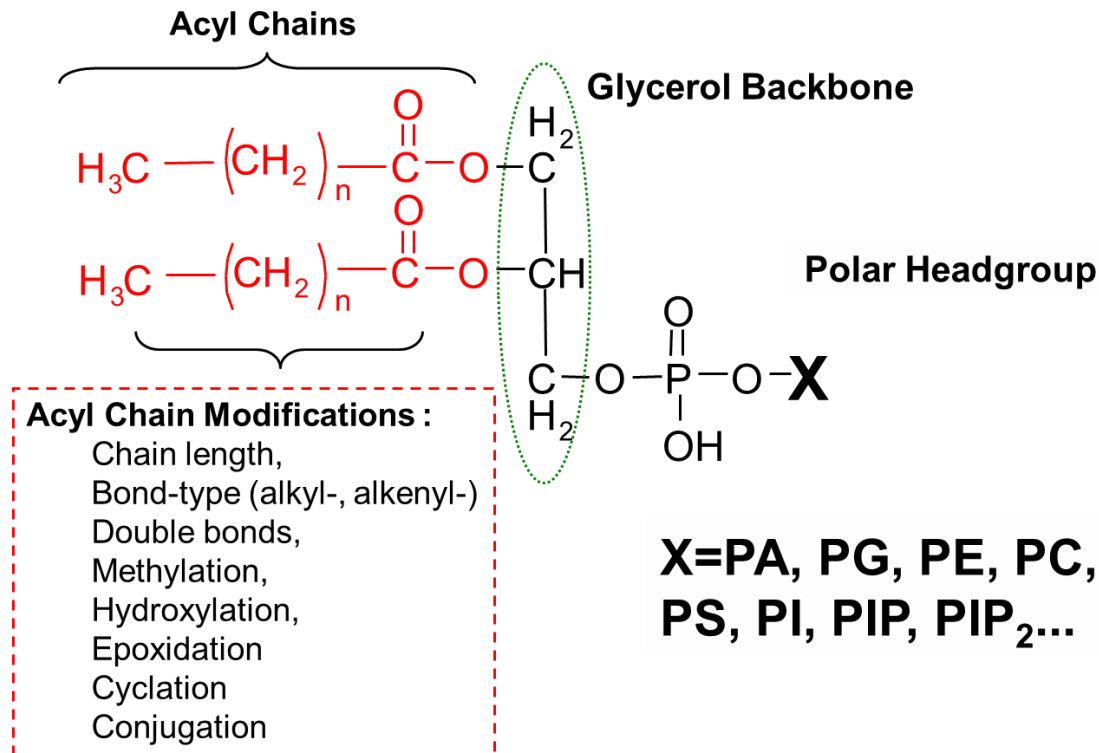


Electron activated dissociation (EAD) for lipidomics

Using the ZenoTOF 7600 system

The challenge of structural diversity

STRUCTURAL DETAILS OF GLYCEROPHOSPHOLIPIDS



- The potential number of unique glycerophospholipids is > 12,000
- Fatty acid modifications increases this number

Complexity as a function of specificity: PE 36:1

TRANSLATION OF SUM COMPOSITION TO SPECIFIC LIPID MOLECULAR SPECIES

Class Level	Sum-Composition Level	Fatty Acid Level	Positional Isomer Level	Double Bond Position(s)	Cis/Trans
PE	PE 36:1	PE(14:0_22:1)	PE(14:0/22:1)	1	2
		PE(14:1_22:0)	PE(22:1/14:0)	1	2
		PE(16:0_20:1)	PE(14:1/22:0)	3 - ($\Delta 8$, $\Delta 9$, $\Delta 11$)	6
		PE(16:1_20:0)	PE(22:0/14:1)	3 - ($\Delta 8$, $\Delta 9$, $\Delta 11$)	6
		PE(18:0_18:1)	PE(16:0/20:1)	4 - ($\Delta 13$, $\Delta 11$, $\Delta 9$, $\Delta 8$)	8
			PE(20:1/16:0)	4 - ($\Delta 13$, $\Delta 11$, $\Delta 9$, $\Delta 8$)	8
			PE(16:1/20:0)	2 - ($\Delta 9$, $\Delta 6$)	4
			PE(20:0/16:1)	2 - ($\Delta 9$, $\Delta 6$)	4
			PE(18:0/18:1)	4 - ($\Delta 12$, $\Delta 11$, $\Delta 9$, $\Delta 7$)	8
			PE(18:1/18:0)	4 - ($\Delta 12$, $\Delta 11$, $\Delta 9$, $\Delta 7$)	8

Possibilities:

1

5

10

28

56

The Challenge of specificity

THE MANY LAYERS OF LIPID STRUCTURAL SPECIFICITY

Increasing specificity

Lipid class: PC, SM, TAG, etc.

- TLC, NMR, MS

Sum composition: PE 36:1

- Shotgun, IDA/DDA (via infusion or by LC MS/MS)

Fatty acid identification: PE
(16:0_20:1); (18:0_18:1);
(14:0_22:1); etc.

- LC-MS/MS, MS/MS^{ALL}, IDA/DDA

Fatty acid position:
PE(16:0/20:1)

- DMS (SelexION® Technology),
PLA₂

Double bond position: PE (16:0/20:1 Δ 11)

- OzID, Paternò-Büchi Rxn, Hv-PD

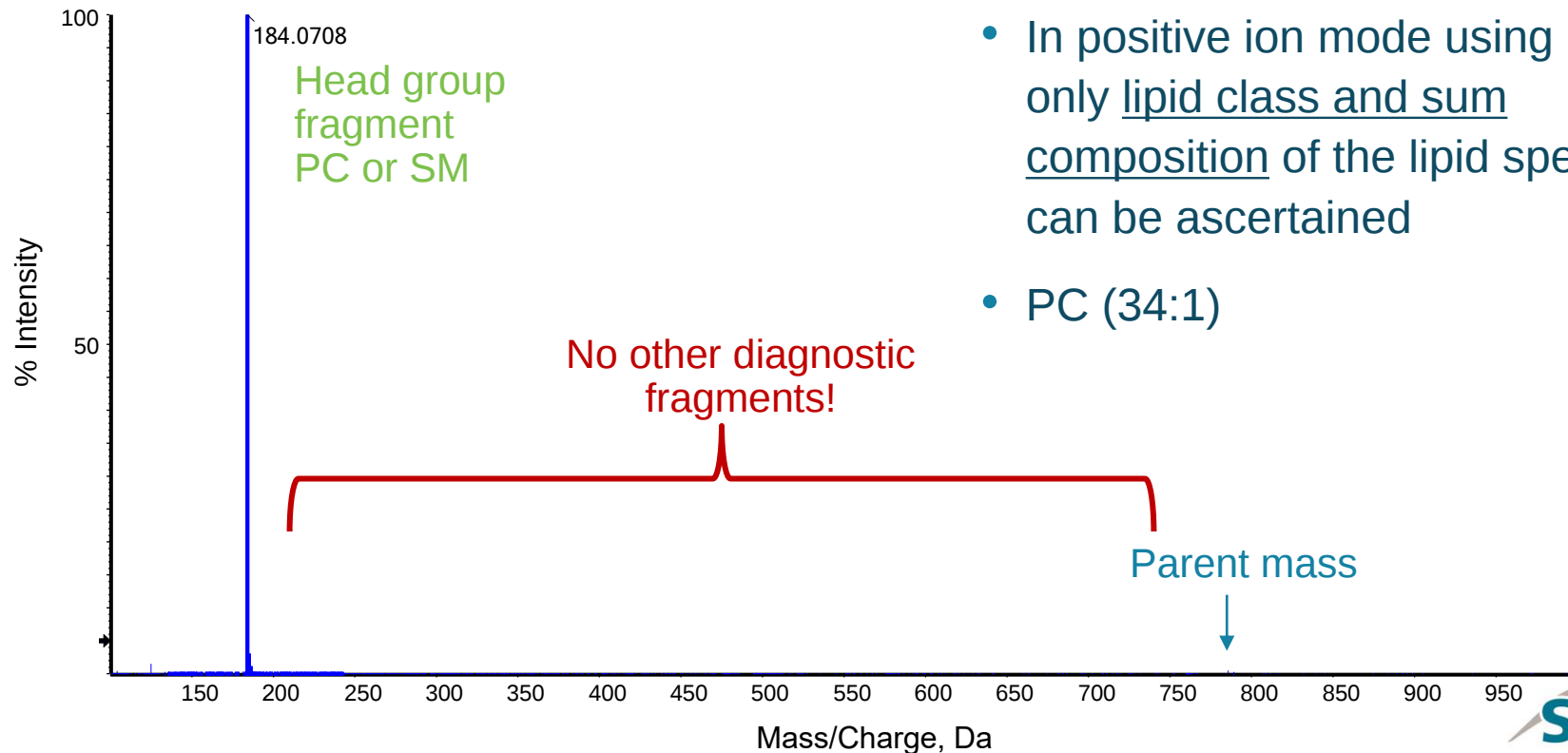
Stereochemistry: PE (16:0/20:1(11Z))

- GC-MS/MS, HR-NMR, complex LC-MS/MS techniques

Currently, no single commercial technology can fully characterize a lipid

Collision induced dissociation for lipidomics

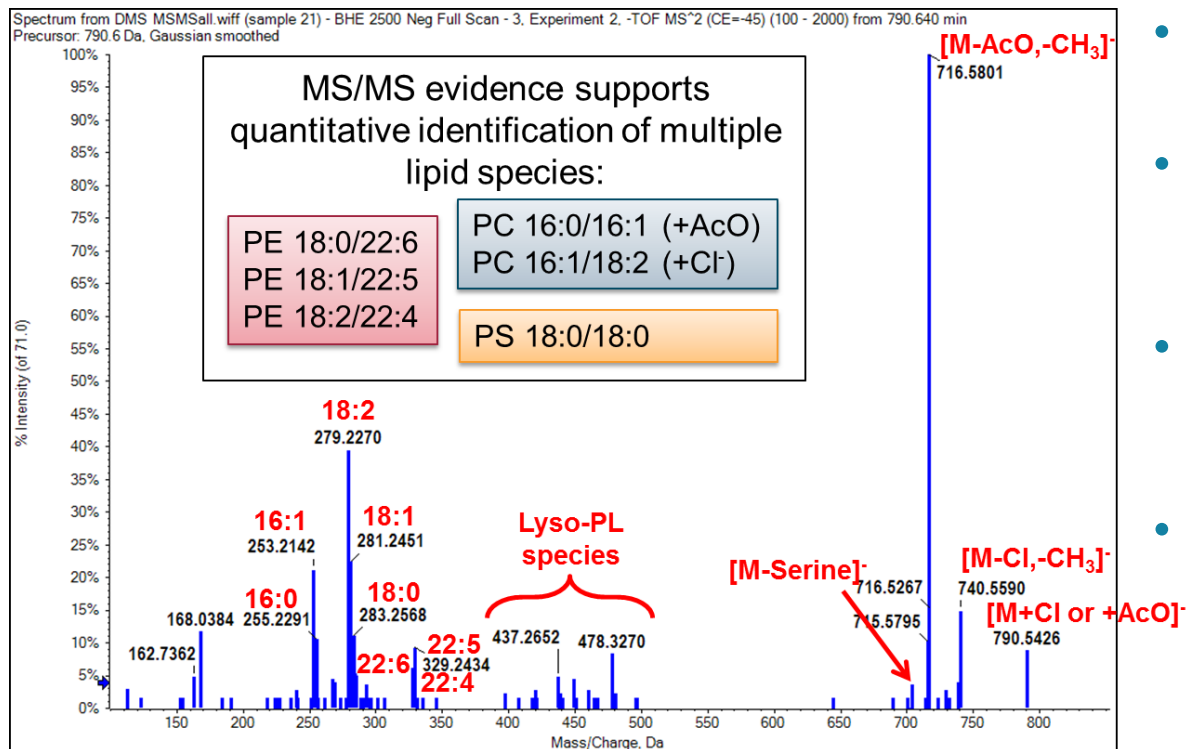
IDA SPECTRUM OF 788.6185



- In positive ion mode using CID, only lipid class and sum composition of the lipid species can be ascertained
- PC (34:1)

Example of isobaric interference in infusion-based lipidomics

COMPLICATED INTERPRETATION

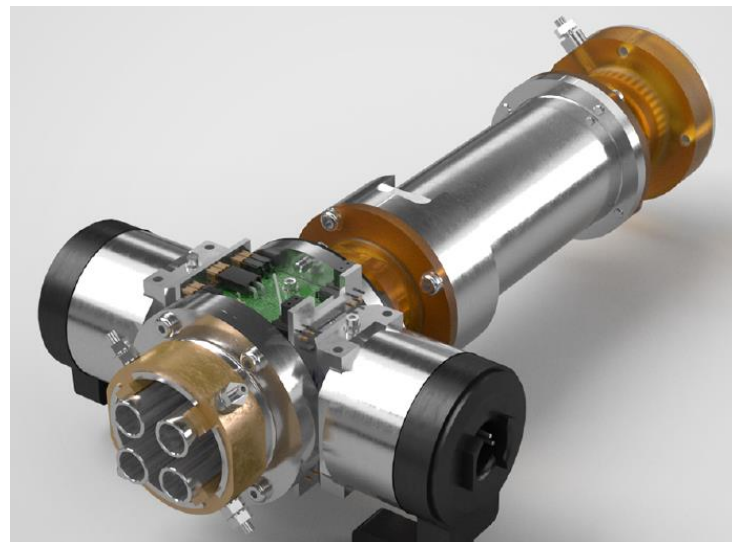


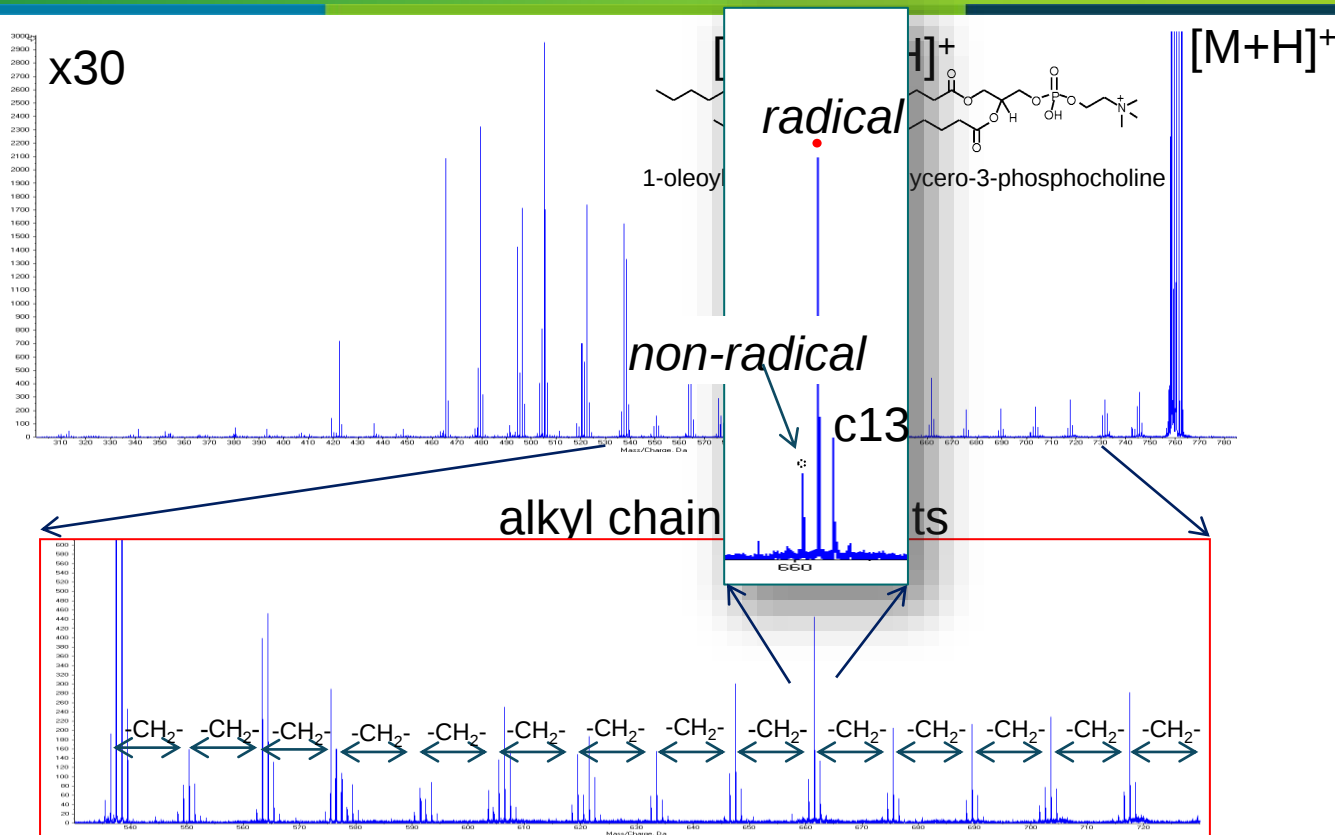
- Many lipids share the same precursor mass
- Many of those same precursors, share the same fragments
- Careful data analysis is needed to successfully interpret shotgun data
- Quantification strategies must accommodate shared fragment ions

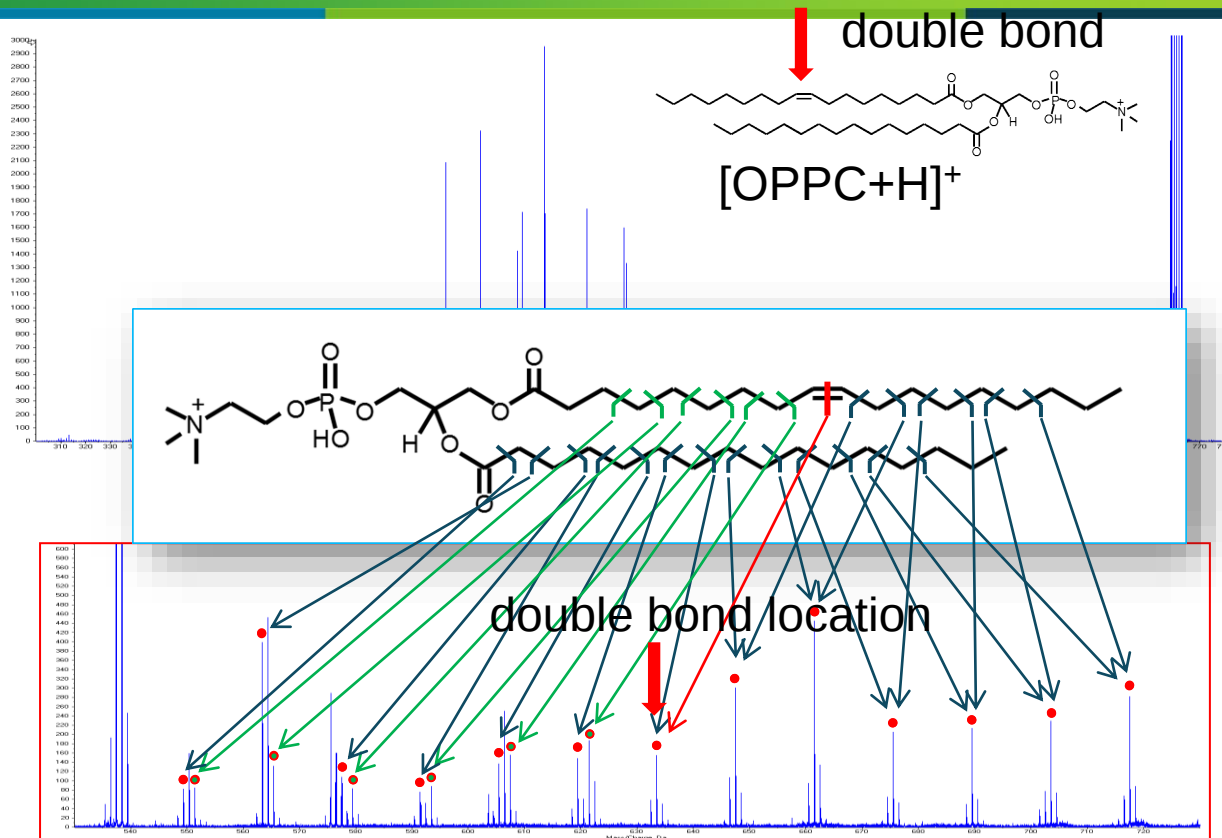
Characterization of lipid species



- EAD kinetic energy can be tuned depending on analyte type
- EAD fragmentation is reproducible at a quantitative level
- Fast fragmentation and acquisition
 - Electron irradiation times ~ 10-30 msec
 - System can do DDA on LC time scale up to 20 Hz
 - Maintaining spectral resolution of 30,000
- EAD is optimized to limit secondary fragmentation (unless desired)
- EAD does not require further activation of charged reduced species by CID, but workflow is possible





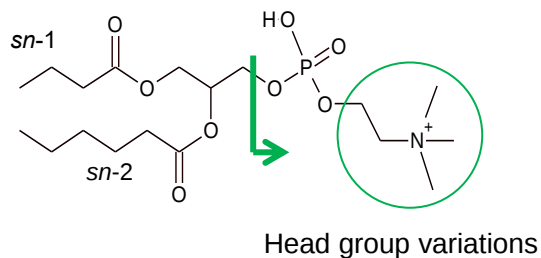


FRAGMENTATION PATTERNS

- EAD produces diagnostic fragments of:

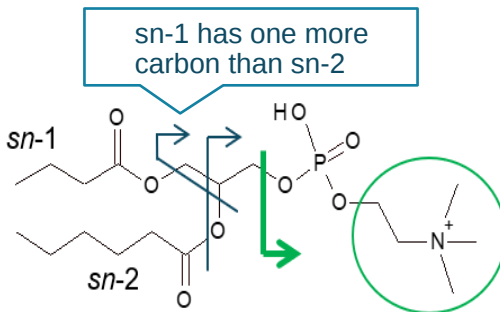
- Head group

- PC (SM), PE, PS, PI, PA, PG



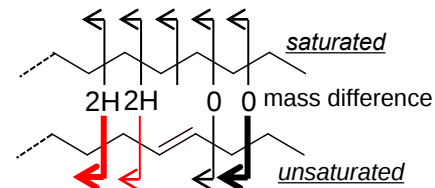
Backbone (glycerol/sphingoid)

- Regioisomerism (sn-1, sn-2, etc.)



Chain structure

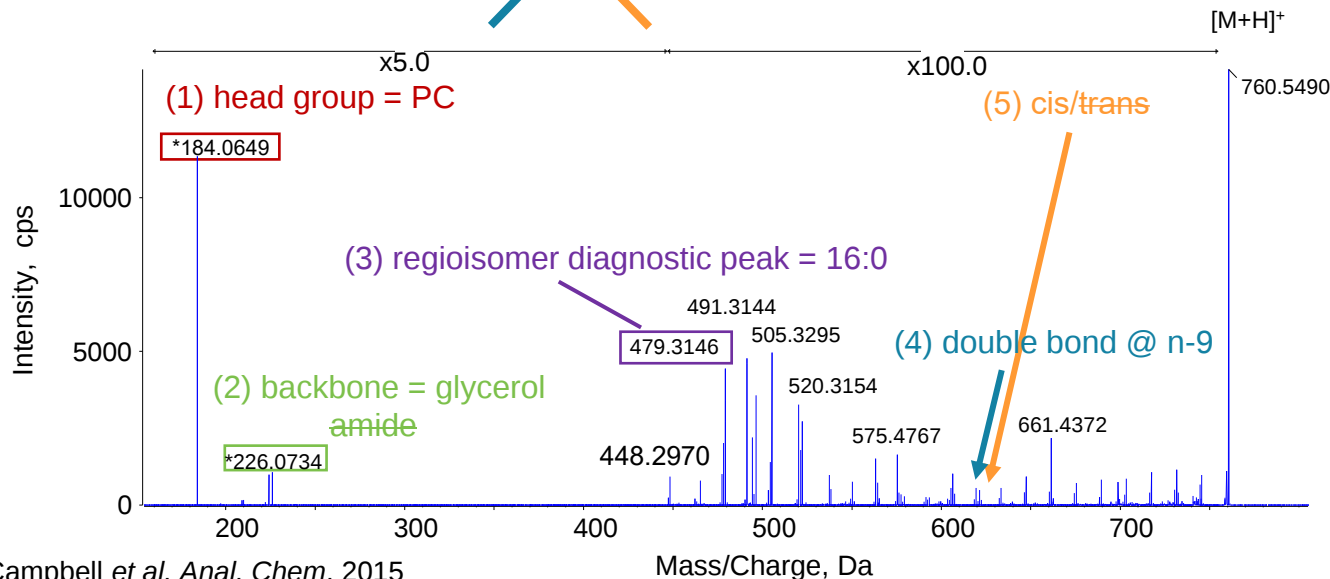
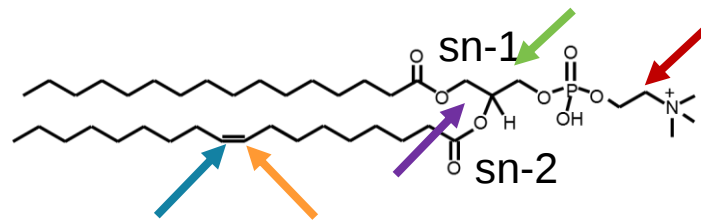
- Length and double bond positions
- Double bond stereochemistry



WITH ZenoTOF 7600 SYSTEM

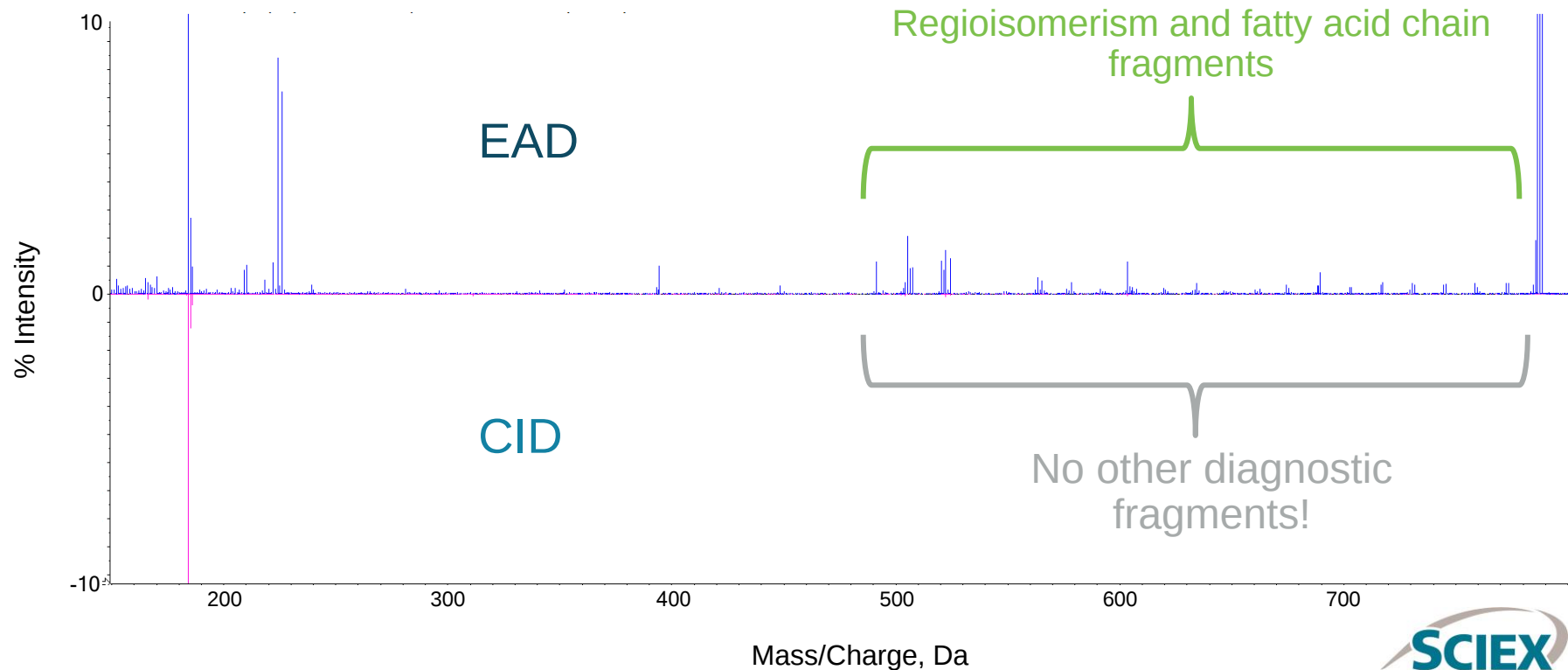
- Electron activated dissociation (EAD) can provide:
 - Structural elucidation of lipid species within one LC-MS/MS analysis
 - Lipid class
 - Fatty acid identification
 - Fatty acid position
 - Double bond position
 - Double bond stereochemistry

single experiment → *de novo* analysis → PC 16:0 / 18:1(n-9:cis)



Campbell et al. Anal. Chem. 2015

TIC OF 788.6185





SCIEX OS SOFTWARE 2.0

▼ Experiment IDA

Polarity Positive V Spray voltage 5500 V

TOF MS

TOF start mass 400 Da Declustering potential 80 V Collision energy 10 V

TOF stop mass 1000 Da DP spread 0 V CE spread 0 V

Accumulation time 0.25 s

IDA Criteria Peptide

Maximum candidate ions 5

Intensity threshold exceeds 100 cps

☒ Dynamic background subtraction

☐ Dynamic CE for MS/MS

☒ Exclude former candidate ions

☐ Charge state 1

For 6 s to 5

After 2 occurrences Isotope to select Monoisoto...

☐ Dynamic ETC for MS/MS

► Advanced Criteria

TOF MSMS

Fragmentation mode EAD

TOF start mass 80 Da Precursor ion 830 Da Q1 resolution Unit

TOF stop mass 1000 Da Declustering potential 50 V Collision energy 12 V

Accumulation time 0.25 s DP spread 0 V CE spread 0 V

Electron KE 12 eV Zeno pulsing ☒ Electron beam current 9000 nA

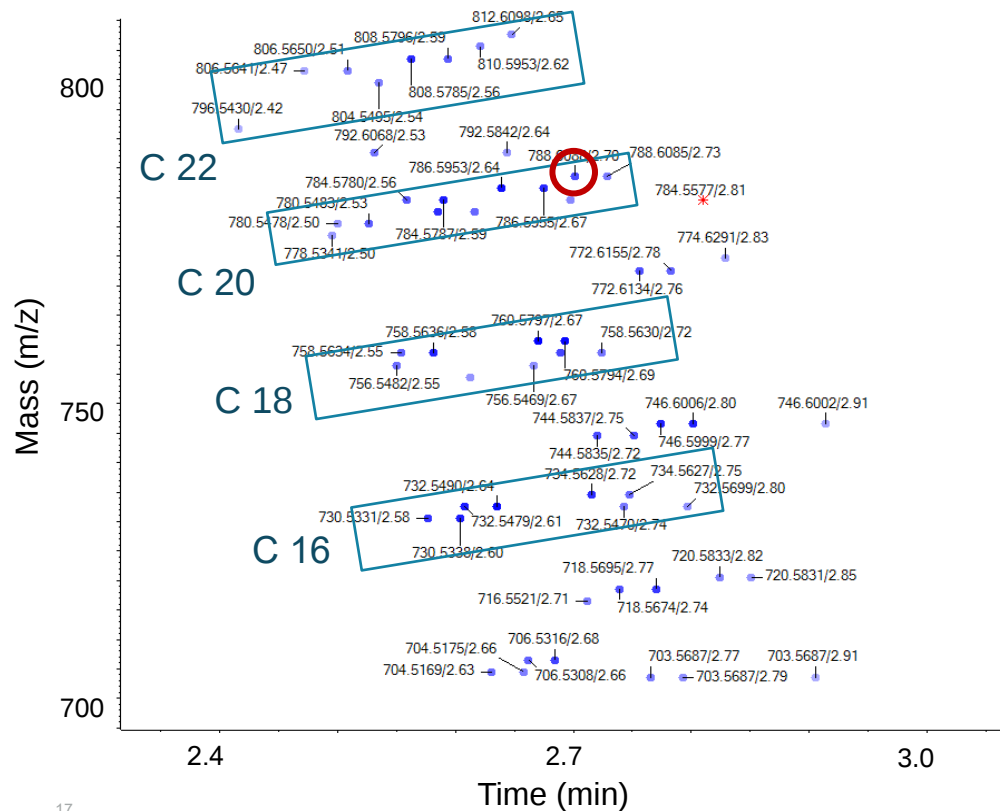
ETC 100 %

- IDA acquisition
- EAD fragmentation with high kinetic energy – 12 eV
- Pulsing with Zeno trap ON
- Current of 9000 nA

C2C12 MYOTUBES

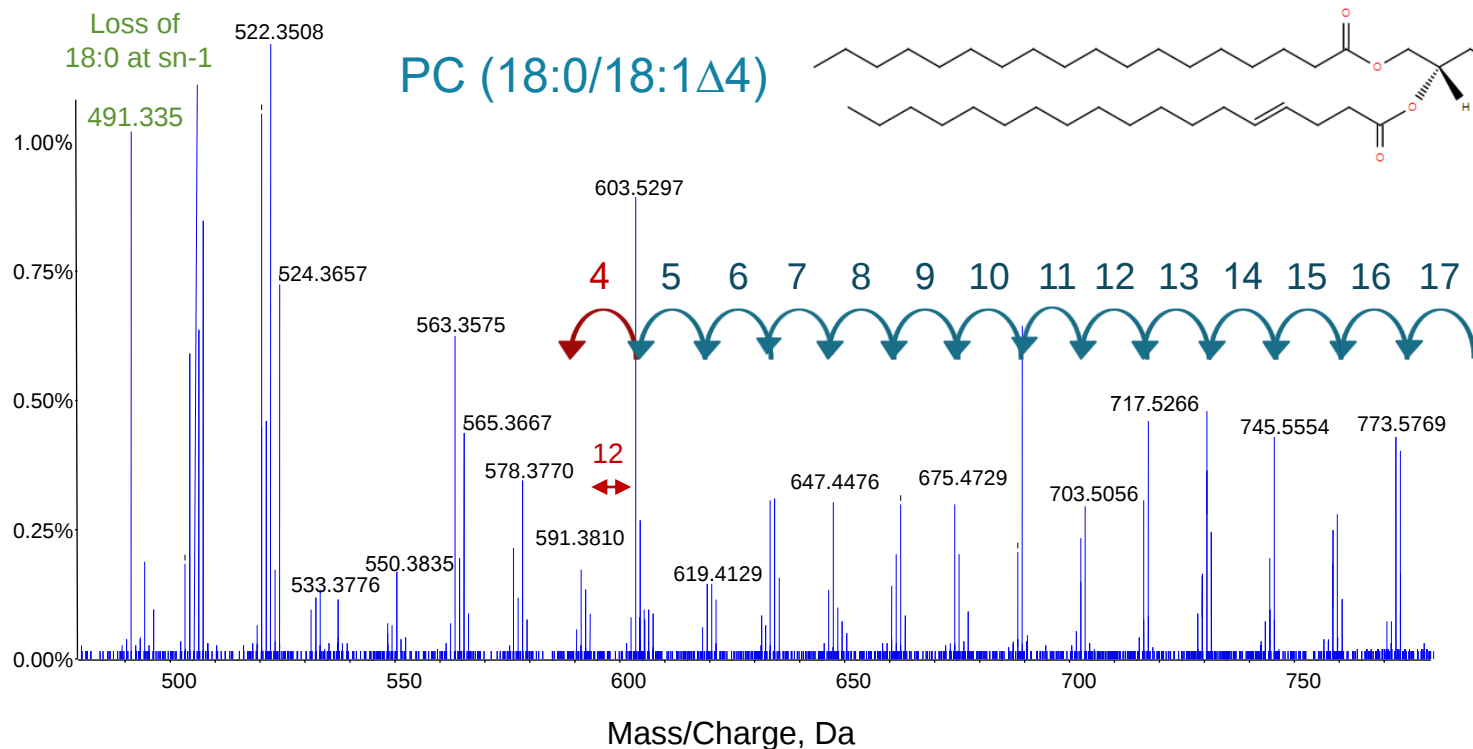
- Collaboration with Dr. Katsu Fenai's group at U. Utah
- Separation achieved using Phenomenex Cyano column (P/N:00D-4254-Y0)
 - Normal phase chromatography for class-based separation
- Cells extracted using modified LLE: 3-phase extraction
- Data collected using LC-based data dependent acquisition

IDA EXPLORER - FATTY ACID CHARACTERIZATION ON LC TIME FRAME

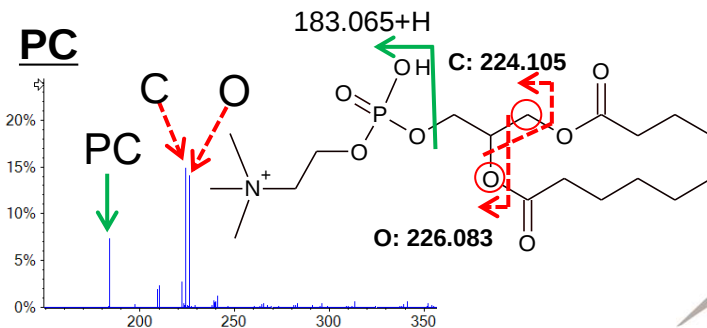
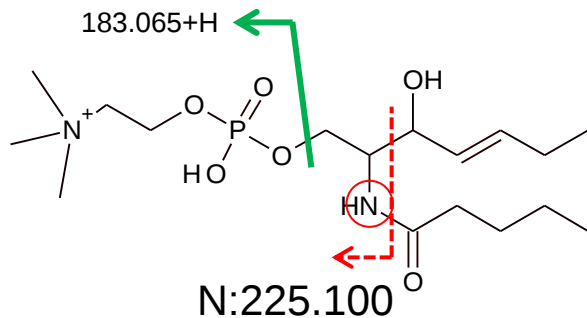
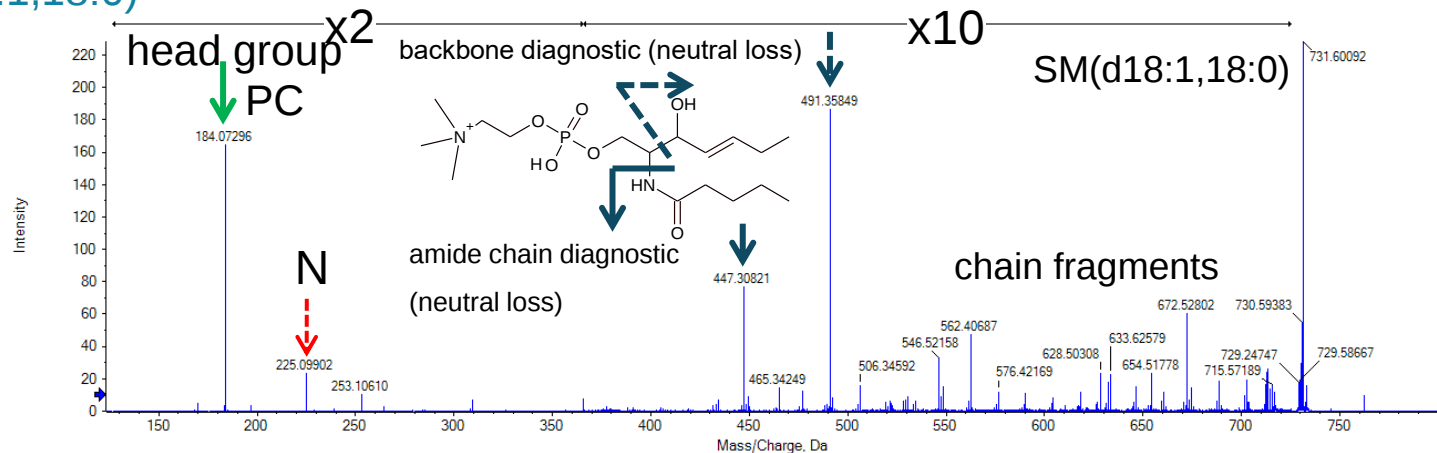


- Lipids extracted from C2C12 myotubes
- Lipids with different chain lengths appear as ladders increasing in mass (blue boxes)
- Unsaturated lipids for each chain length elute over time on normal phase chromatography
- Red circle indicates the lipid shown on next slide

EIEIO SPECTRUM OF 788.6185 (PC) – COLLECTED BY DATA DEPENDENT LC-MS

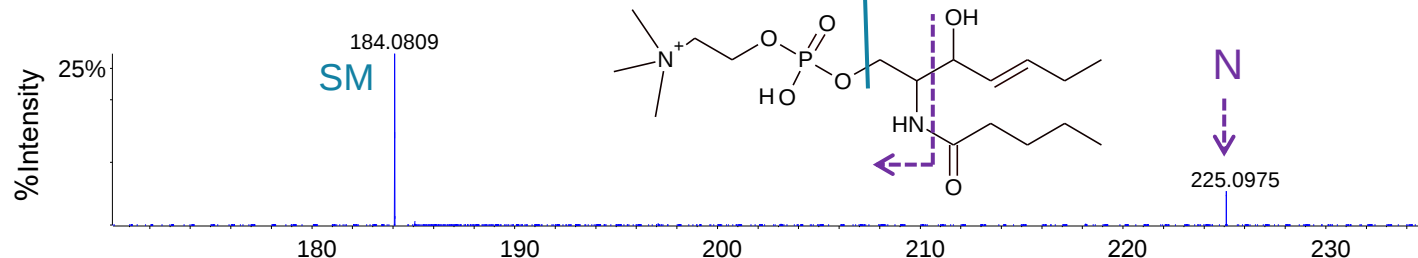


SM(d18:1,18:0)

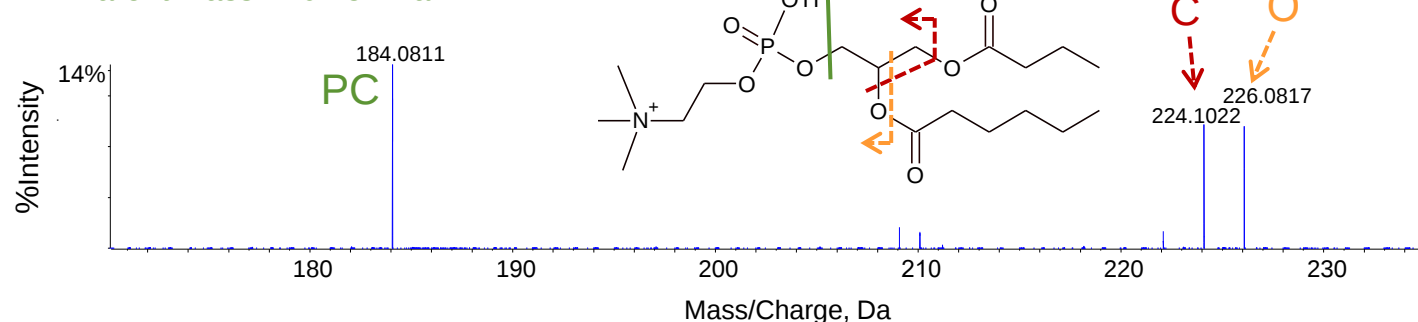


DIAGNOSTIC BACKBONES BY EAD MS/MS

Parent mass - 703.57 Da

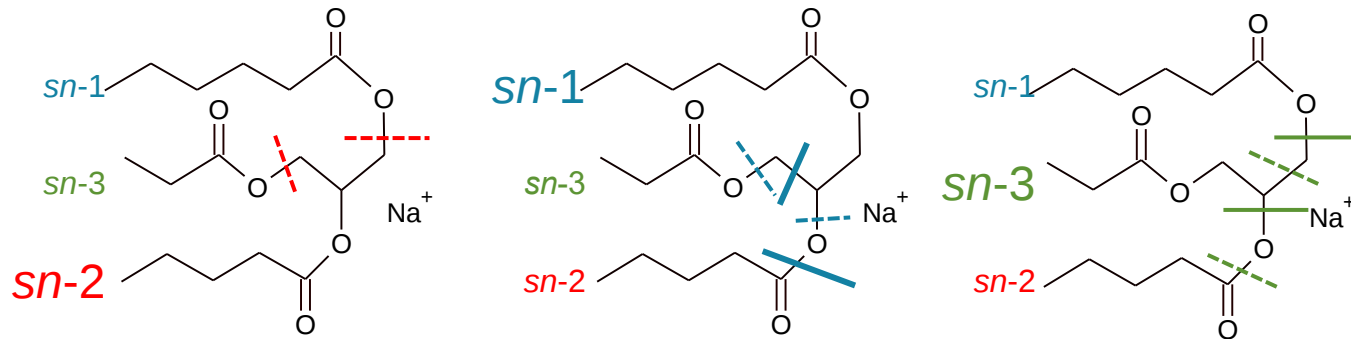
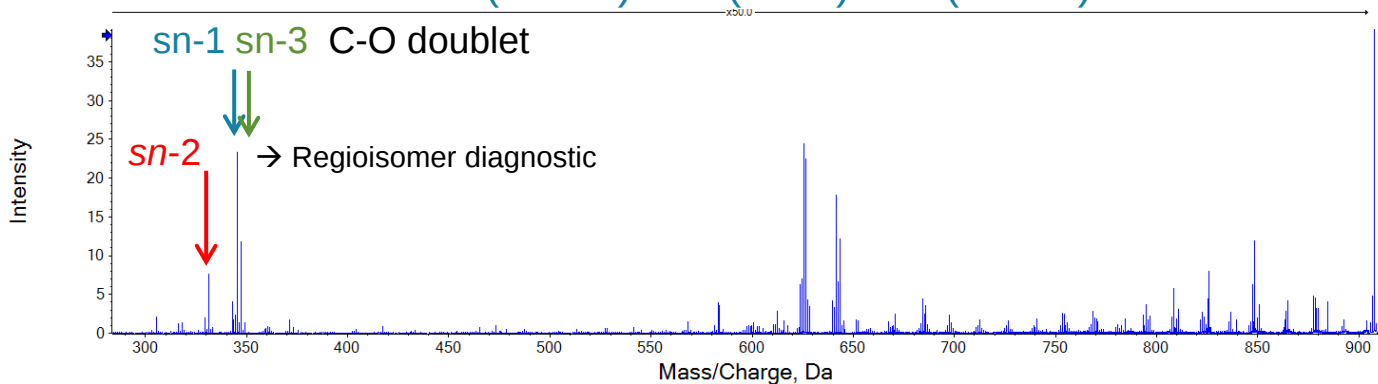


Parent mass - 704.52 Da



- Sphingomyelins vs. phosphatidylcholine
- PC head group at m/z 184
- Fragment ions containing either nitrogen (m/z 225) or carbon and oxygen (m/z 224 and 226) to distinguish SM from PC

EAD MS/MS - TAG 18:1(N-12Z)/18:1(N-9Z)/18:1(N-12Z)



- sn-2 attachment point can be differentiated from the sn-1 position **or** sn-3 position through examination of the dual chain loss fragment ions

Phospholipids

	class	double bond locations	
		protonated	sodiated
PC	✓	✓✓✓	✓
PE	✓	✓	✓
PS	✓	✓	✓
PA	✓	x	✓
PG	✓	x	✓
PI	✓	x	✓

including plasmalogens and ethers

Other adducts can be formed
and detected using EIEIO

Spingolipids

	class	double bond locations	
		protonated	sodiated
Cer	✓	✓	✓
HexCer	✓	✓	✓✓
LacCer	✓	✓	✓
SM	✓	✓✓	✓

including hydroxy

Acylglycerols

	class	double bond locations	
		protonated	sodiated
DG	x	x	✓
MGDG	✓	x	✓
TG	✓	x	✓✓

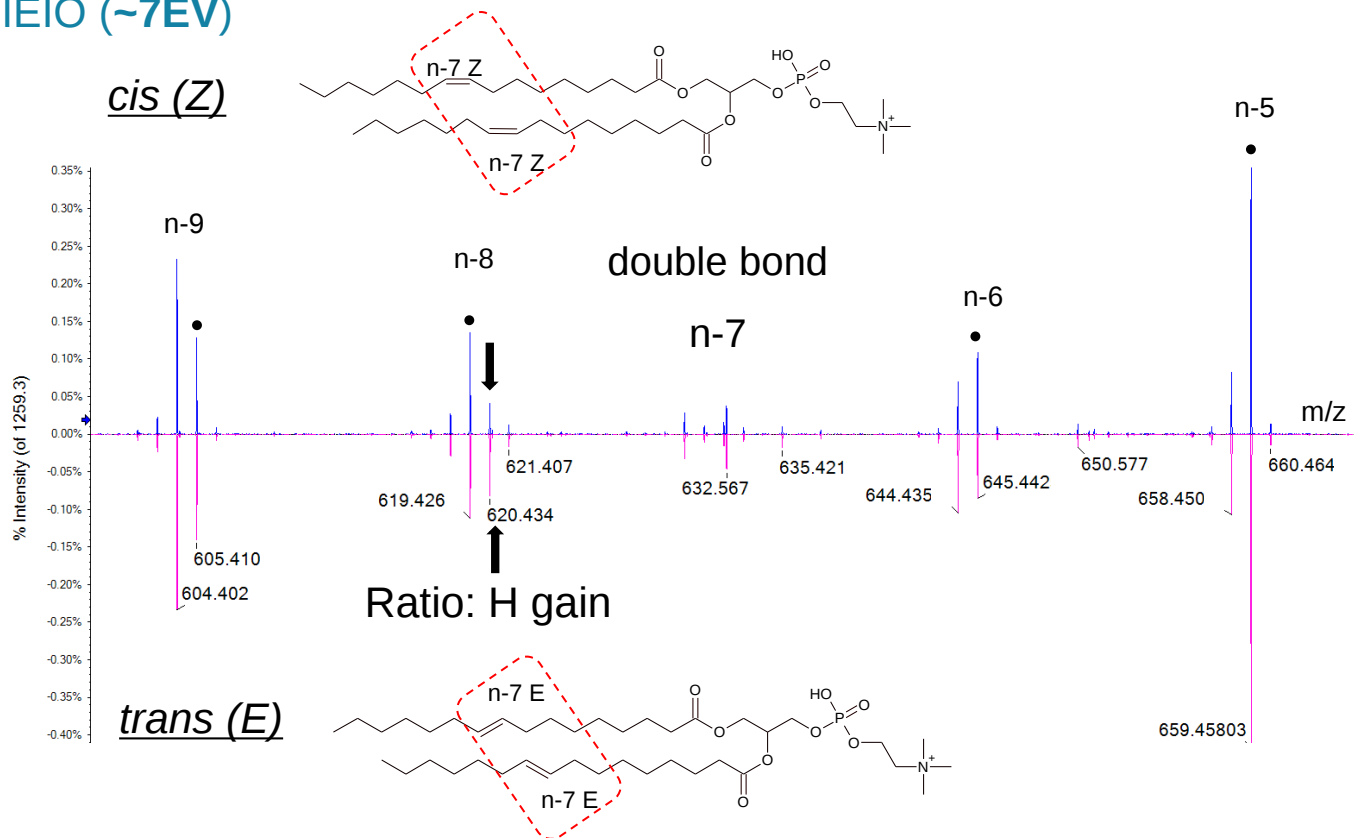
Double bond stereochemistry

CIS/TRANS



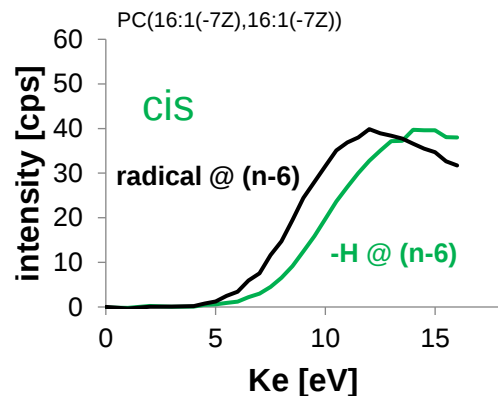
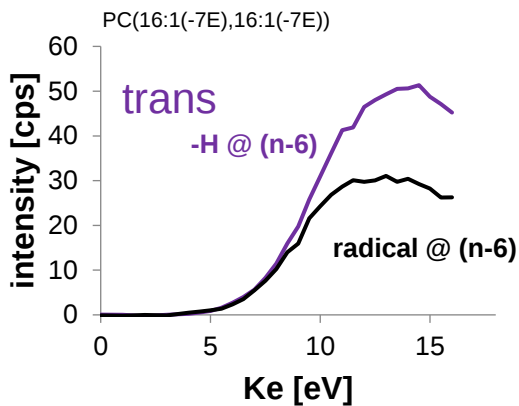
Finding cis/trans difference

EIEIO (~7EV)



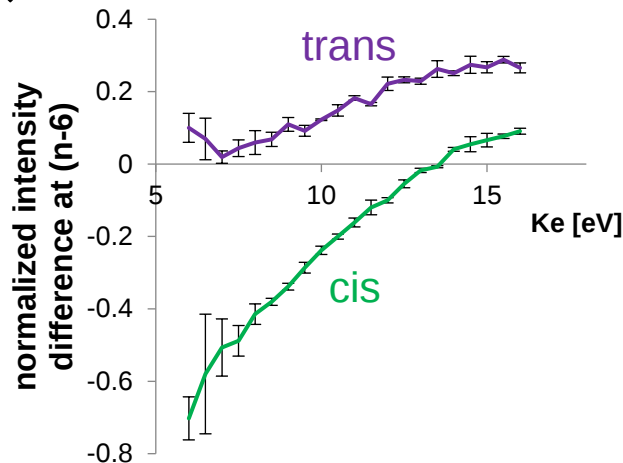
Biological significance:

- Nutrition
- Food adulteration
- Biomarker research
- Membrane fluidity
- Lipid biological function

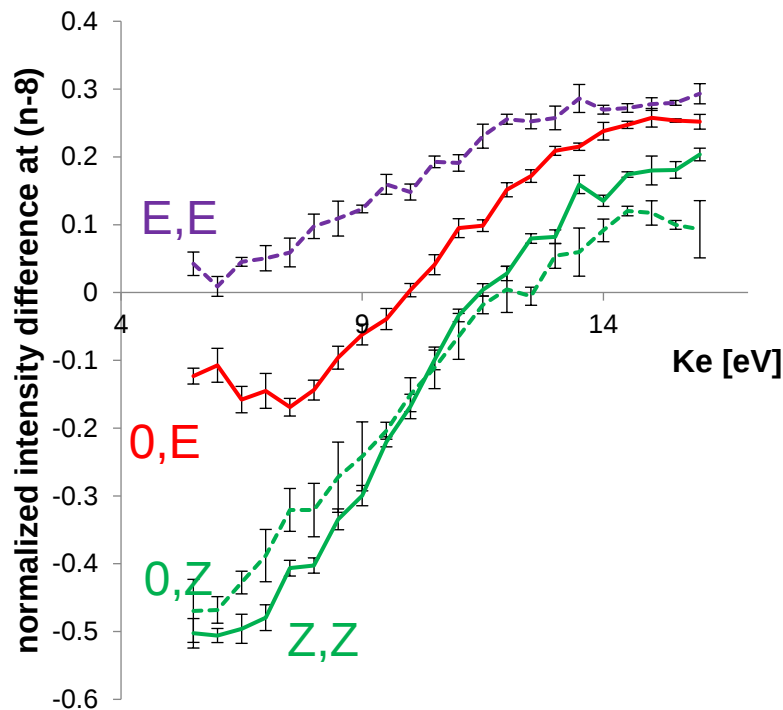


normalized intensity difference

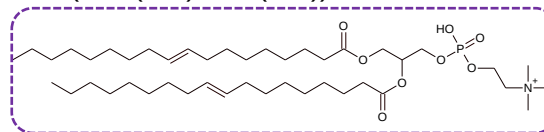
$$D = \frac{[\text{H loss}] - [\text{radical}]}{[\text{H loss}] + [\text{radical}]}$$



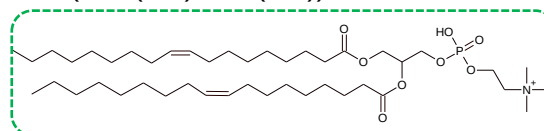
D indicates trans/cis difference significantly



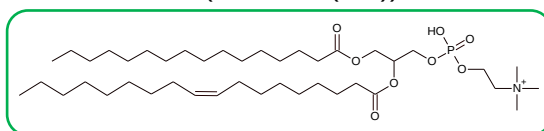
PC(18:1(-9E),18:1(-9E))



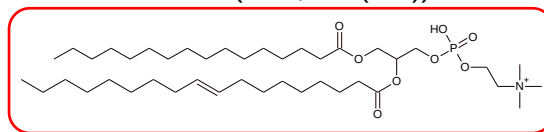
PC(18:1(-9Z),18:1(-9Z))



cis-POPC: PC(16:0,18:1(-9Z))



trans-POPC: PC(16:0,18:1(-9E))



NEAR COMPLETE LIPID CHARACTERIZATION IN ONE EXPERIMENT

- EIEIO for lipids is a powerful tool for characterization
 - In one LC-MS data dependent acquisition:
 - Lipid class
 - Fatty acid identification
 - Fatty acid position
 - Double bond position
 - Double bond stereochemistry



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