

UAB
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Knowledge that will change your world

Choosing the metabolomics platform

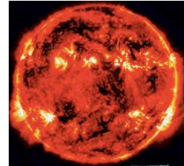
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Targeted
Metabolomics &
Proteomics
Laboratory

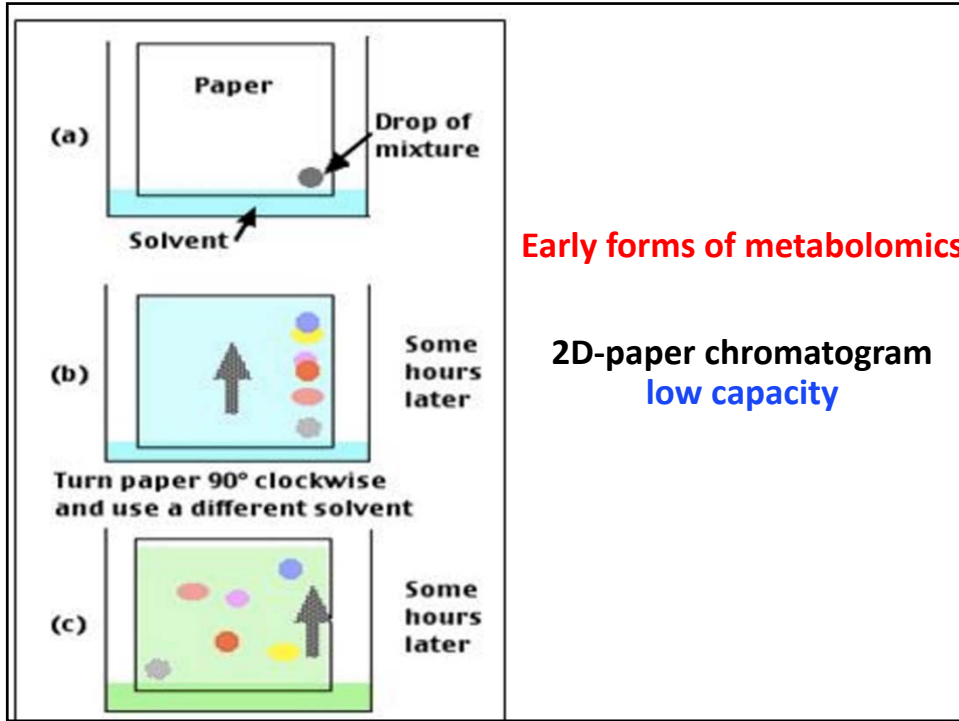
Challenges

- Unlike DNA, RNA and proteins, the metabolome is phenomenally chemically diverse
- Ranges from a gas (H₂) that prevades the universe and is the principal component of the Sun

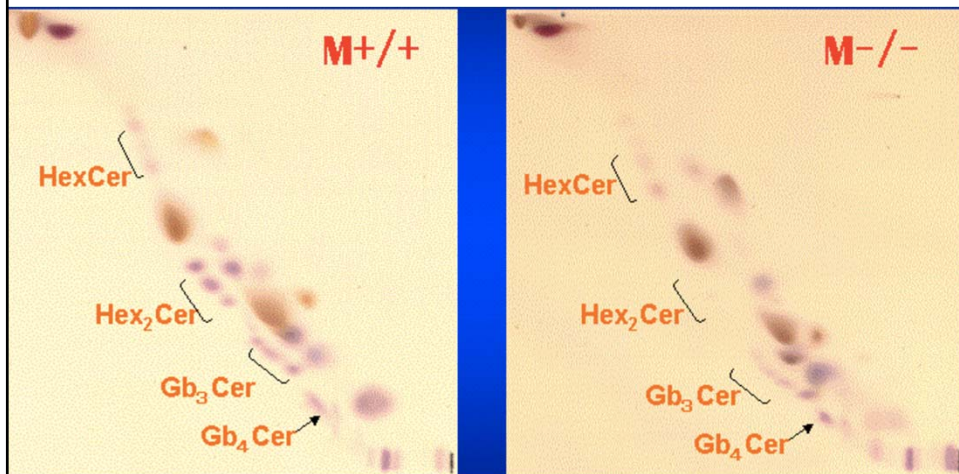
to



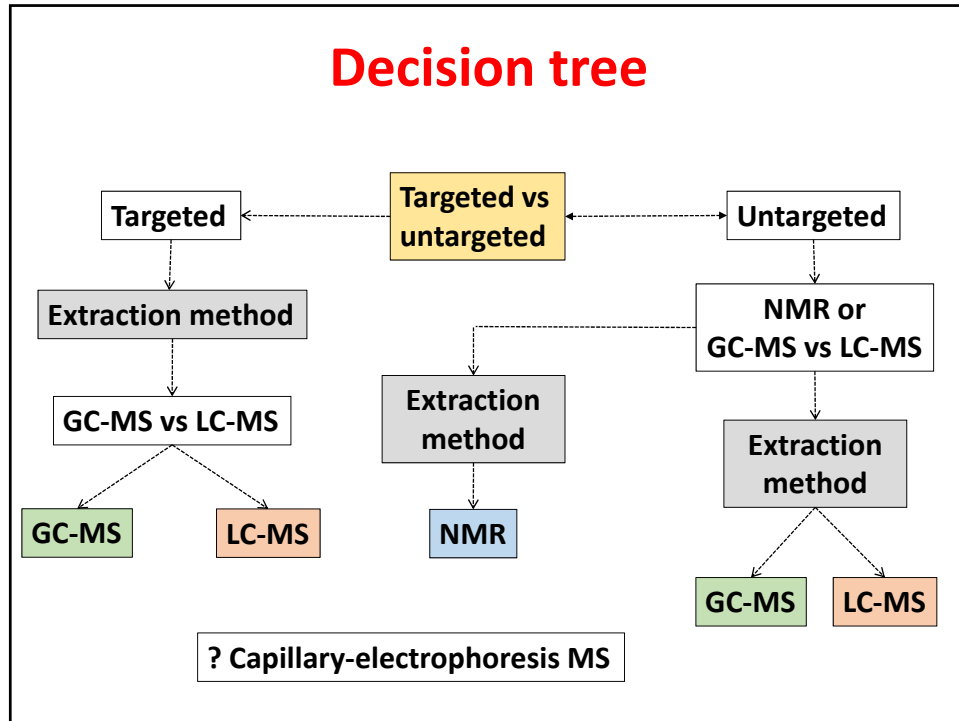
- Earwax (long chain fatty acids, both saturated and unsaturated, alcohols, squalene, and cholesterol)
- No single method of analysis



2D-Thin layer chromatography of lipids
KO of cerebroside sulfatase in kidney



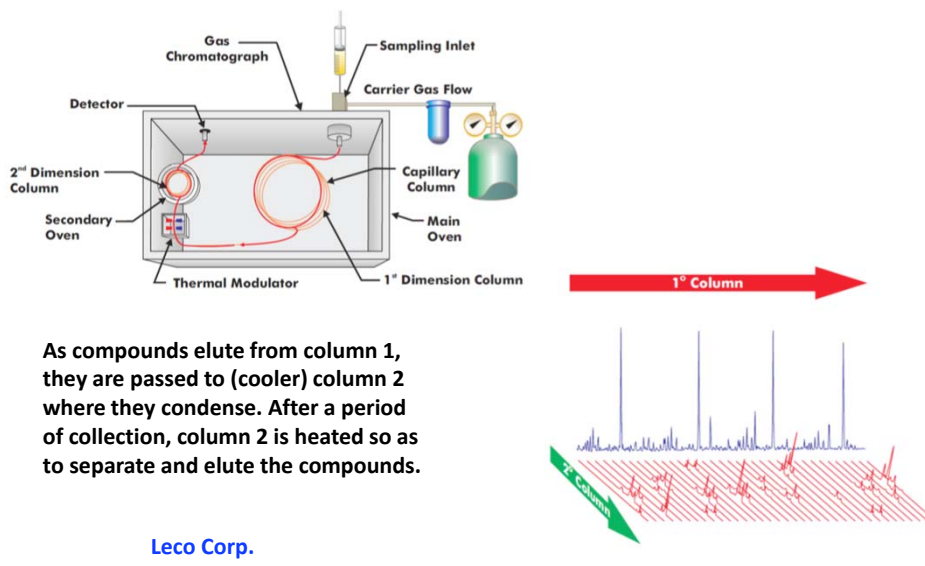
These days can be studied by direct electrospray ionization (DESI)



Metabolomics and GC-MS

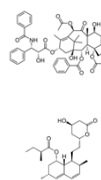
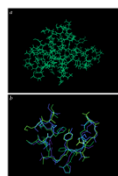
- **PROS**
 - Capillary columns can achieve very high chromatographic resolution
 - Retention times are reproducible
 - Mass spectral libraries are well developed
- **CONS**
 - Not all compounds can be analyzed by GC-MS
 - Although amino acids, sugars, fatty acids, amines and organic acids **can be derivatized**, complex polyphenol glycosides and polar lipids are too unstable, even when derivatized, at the temperatures used to elute them
 - Approximate mass limit of 400 Da

Two dimensional GC to resolve metabolites



Nuclear Magnetic Resonance (NMR) Spectroscopy

- Detects NMR active nuclei
- Robust and highly reproducible
- Non-destructive
- Quantitative
- Used in
 - Structure elucidation
 - Small molecules
 - Macromolecules (DNA, RNA, Proteins)
 - A number of techniques
 - 1D, 2D, 3D
 - Molecular motion and dynamics
- Similar method used in medical Imaging (MRI, fMRI)



from Wimal Pathmasiri

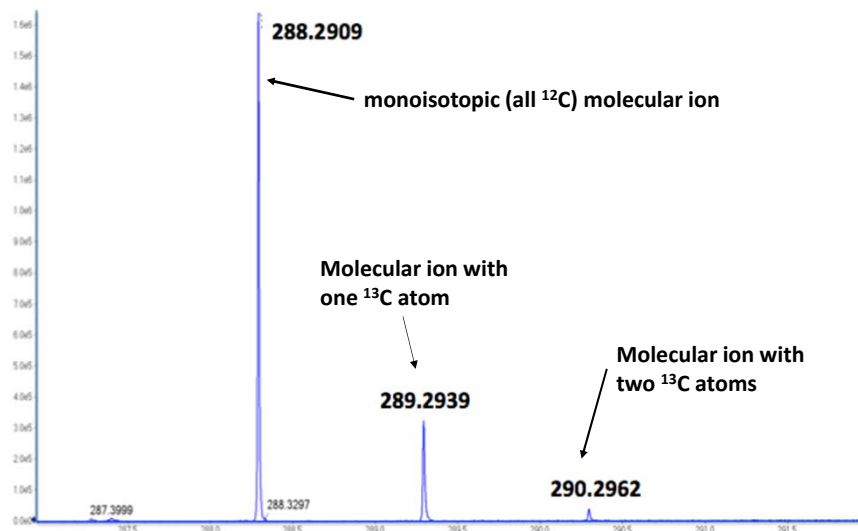
NMR considerations

- **Sample amount:**
 - Typical 600 MHz instrument requires 0.5 ml plasma/serum
 - Higher field instrument and micro coil detector allows use of 0.1 ml
- **Quality control:**
 - In the UK Phenome Center, all samples are analyzed by NMR
 - This allows for detection of outliers
 - Also found that there is a correlation between the NMR spectrum and whether problems occur in LC-MS analysis
 - NMR analysis used to filter out these samples

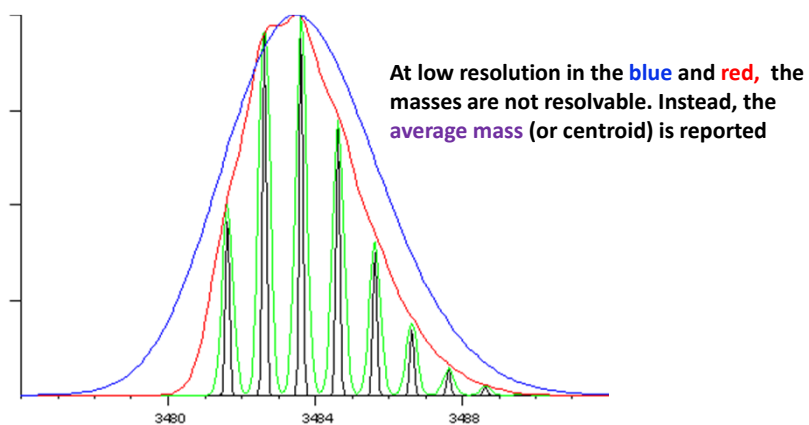
Liquid chromatography-Mass Spectrometry

- **PROS**
 - **Almost all compounds can be analyzed by LC-MS**
 - Exceptions - hydrocarbons do not ionize
 - **Several orders of magnitude increased sensitivity compared to NMR**
 - **Can collect MS, MSMS and ion mobility data**
- **CONS**
 - **Not uniformly quantitative**
 - **Mass spectral libraries are not well enough developed**
 - **Chromatographic separation not adequate**
 - **Retention time reproducibility not as good as GC-MS**

Mass spectrum of a compound



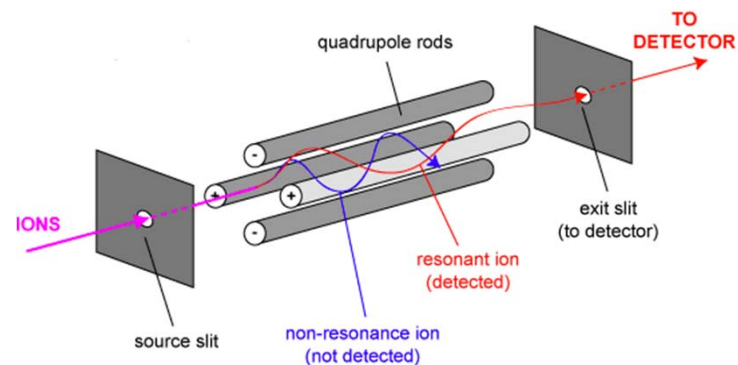
Mass resolution



Selecting the mass spectrometer

- It is necessary to use an instrument to measure:
 - The mass of the metabolites accurately
 - To provide sufficient mass resolution to distinguish the isotopes associated with each metabolite
- There are several types of MS detectors
 - Quadrupole
 - ion trap
 - time-of-flight (TOF)
 - Orbitrap
 - Fourier Transform-Ion Cyclotron Resonance (FT-ICR)

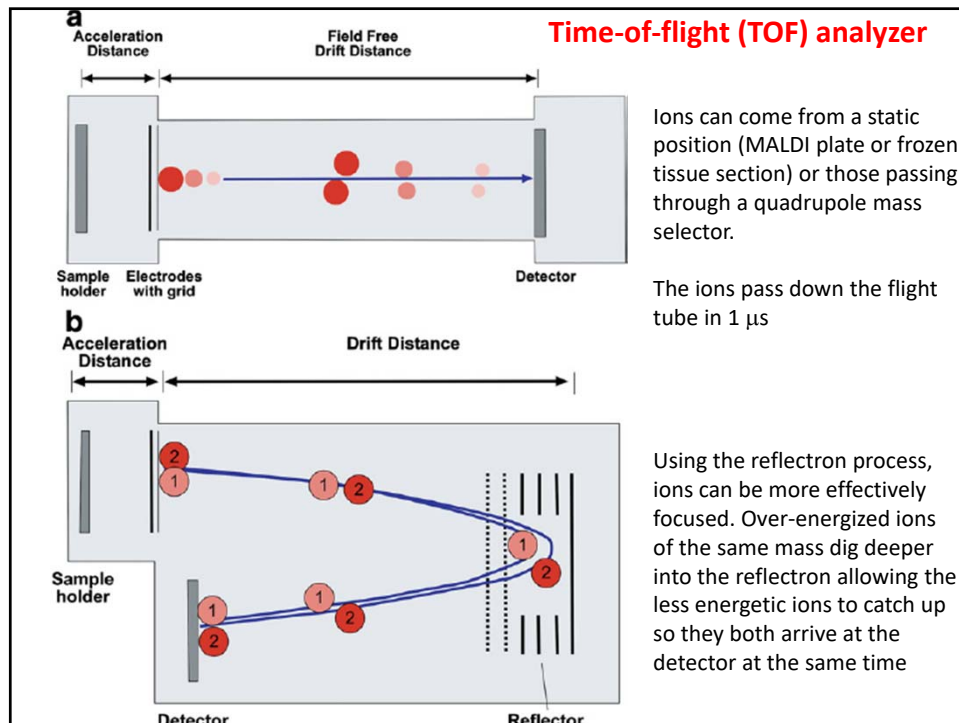
Quadrupole mass filter



Consists of four parallel rods. Each opposing rod pair is connected together electrically, and a radio frequency (RF) voltage with a DC offset voltage is applied between one pair of rods and the other. This causes the ions to rotate in spirals as they go through the quadrupole. For a given voltage, only ions of a specific m/z can pass through. The voltage can be scanned to generate a mass spectrum or held constant to allow one ion to pass through.

The mass spectrometer

- **For untargeted analysis it is important to have high mass resolution, accuracy and speed**
 - Initial data analysis is performed on the molecular ions
 - Each metabolite has a unique mass (m/z)
 - Nonetheless, a particular mass, however exact, is not necessarily a unique metabolite
- **Fourier transform-ion cyclotron resonance and Orbitrap instruments have the greatest mass accuracy**
 - However, their performance is time-dependent and is degraded significantly using short acquisition times (<100 ms)
 - They are best used for follow up experiments



TOF is the mass analyzer of choice for untargeted metabolomics

- Quadrupole-orthogonal time-of-flight (Q-tof)



Agilent 6500

Waters Synapt
G2/HMDS

Bruker



Sciex TripleTOF 6600

Current models have 30-80,000 mass resolution and 1 ppm or better mass accuracy

Masses of elements and their isotopes

- Mass is defined using the mass of carbon-12 being 12.0000 (exactly) – the others have **mass defects**
- On this scale,
 - ^1H is 1.007825 and ^2H is 2.014102 (extra neutron)
 - ^{14}N is 14.003074 and ^{15}N is 15.000108 (extra neutron)
 - ^{16}O is 15.994915, ^{17}O is 16.999132 and ^{18}O is 17.999161
 - ^{31}P is 30.973761
 - ^{32}S is 31.972071 and ^{34}S is 33.967867 (4%)
- You can find the mass of every element and its isotopes and their natural abundances at
<http://www.nist.gov/pml/data/comp.cfm>
- The mass of a proton is 1.0072766 and that of an electron is 0.000548597

Predicted mass defects for $C_xH_nO_m$

| H atoms | Oxygen atoms | | | | | | | | | | |
|---------|--------------|--------|---------|---------|---------|---------|---------|---------|---------|---------|---------|
| | O=0 | O=1 | O=2 | O=3 | O=4 | O=5 | O=6 | O=7 | O=8 | O=9 | O=10 |
| 1 | 0.0078 | 0.0027 | -0.0023 | -0.0074 | -0.0125 | -0.0176 | -0.0227 | -0.0278 | -0.0329 | -0.0379 | -0.0430 |
| 2 | 0.0157 | 0.0106 | 0.0055 | 0.0004 | -0.0047 | -0.0098 | -0.0149 | -0.0199 | -0.0250 | -0.0301 | -0.0352 |
| 3 | 0.0235 | 0.0184 | 0.0133 | 0.0082 | 0.0031 | -0.0020 | -0.0070 | -0.0121 | -0.0172 | -0.0223 | -0.0274 |
| 4 | 0.0313 | 0.0262 | 0.0211 | 0.0160 | 0.0110 | 0.0059 | 0.0008 | -0.0043 | -0.0094 | -0.0145 | -0.0196 |
| 5 | 0.0391 | 0.0340 | 0.0290 | 0.0239 | 0.0188 | 0.0137 | 0.0086 | 0.0035 | -0.0016 | -0.0066 | -0.0117 |
| 6 | 0.0470 | 0.0419 | 0.0368 | 0.0317 | 0.0266 | 0.0215 | 0.0164 | 0.0114 | 0.0063 | 0.0012 | -0.0039 |
| 7 | 0.0548 | 0.0497 | 0.0446 | 0.0395 | 0.0344 | 0.0294 | 0.0243 | 0.0192 | 0.0141 | 0.0090 | 0.0039 |
| 8 | 0.0626 | 0.0575 | 0.0524 | 0.0473 | 0.0423 | 0.0372 | 0.0321 | 0.0270 | 0.0219 | 0.0168 | 0.0117 |
| 9 | 0.0704 | 0.0653 | 0.0603 | 0.0552 | 0.0501 | 0.0450 | 0.0399 | 0.0348 | 0.0297 | 0.0247 | 0.0196 |
| 10 | 0.0783 | 0.0732 | 0.0681 | 0.0630 | 0.0579 | 0.0528 | 0.0477 | 0.0427 | 0.0376 | 0.0325 | 0.0274 |
| 11 | 0.0861 | 0.0810 | 0.0759 | 0.0708 | 0.0657 | 0.0607 | 0.0556 | 0.0505 | 0.0454 | 0.0403 | 0.0352 |
| 12 | 0.0939 | 0.0888 | 0.0837 | 0.0786 | 0.0736 | 0.0685 | 0.0634 | 0.0583 | 0.0532 | 0.0481 | 0.0430 |
| 13 | 0.1017 | 0.0966 | 0.0916 | 0.0865 | 0.0814 | 0.0763 | 0.0712 | 0.0661 | 0.0610 | 0.0560 | 0.0509 |
| 14 | 0.1096 | 0.1045 | 0.0994 | 0.0943 | 0.0892 | 0.0841 | 0.0790 | 0.0740 | 0.0689 | 0.0638 | 0.0587 |
| 15 | 0.1174 | 0.1123 | 0.1072 | 0.1021 | 0.0970 | 0.0920 | 0.0869 | 0.0818 | 0.0767 | 0.0716 | 0.0665 |
| 16 | 0.1252 | 0.1201 | 0.1150 | 0.1099 | 0.1049 | 0.0998 | 0.0947 | 0.0896 | 0.0845 | 0.0794 | 0.0743 |
| 17 | 0.1330 | 0.1279 | 0.1229 | 0.1178 | 0.1127 | 0.1076 | 0.1025 | 0.0974 | 0.0923 | 0.0873 | 0.0822 |
| 18 | 0.1409 | 0.1358 | 0.1307 | 0.1256 | 0.1205 | 0.1154 | 0.1103 | 0.1053 | 0.1002 | 0.0951 | 0.0900 |
| 19 | 0.1487 | 0.1436 | 0.1385 | 0.1334 | 0.1283 | 0.1233 | 0.1182 | 0.1131 | 0.1080 | 0.1029 | 0.0978 |
| 20 | 0.1565 | 0.1514 | 0.1463 | 0.1412 | 0.1362 | 0.1311 | 0.1260 | 0.1209 | 0.1158 | 0.1107 | 0.1057 |

For positively charged ions, add **0.007276**

For negatively charged ions, subtract **0.007276**

Empirical formula

If the mass of an ion is known accurately enough,
then it is possible to write down its **empirical formula**

What is the mass of a metabolite?

- Hexanol

$$\begin{aligned} \text{C}_6\text{H}_{14}\text{O} &= 6*12.0 + 14*1.007825 + 15.994915 \\ &= 102.1044651 \end{aligned}$$

- Glucose

$$\begin{aligned} \text{C}_6\text{H}_{12}\text{O}_6 &= 6*12.0 + 12*1.007825 + 6*15.994915 \\ &= 180.063388 \end{aligned}$$

Masses of genistein's ions

- Genistein, $\text{C}_{15}\text{H}_{10}\text{O}_5$

$$\text{Mass} = 15*12.0 + 10*1.007825 + 5*15.994915$$

$$[\text{M}+\text{H}]^+ = \text{M} + 1.00727638 = 271.060073$$

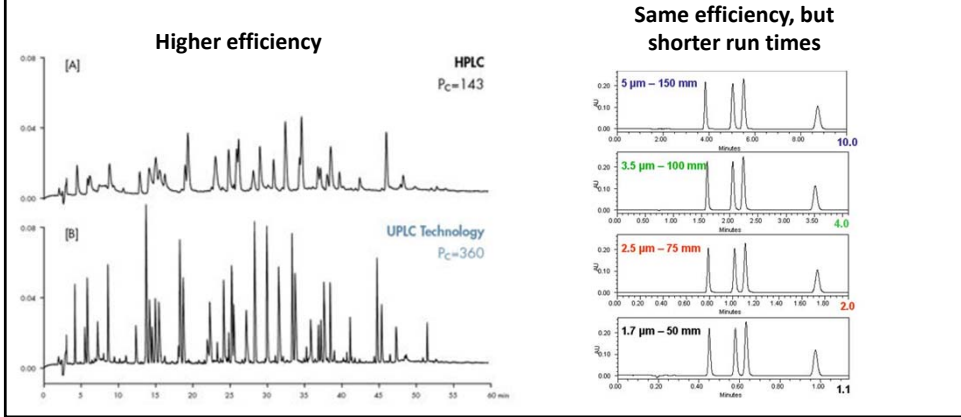
$$[\text{M}-\text{H}]^- = \text{M} - 1.00727638 = 269.045547$$

- If glucose is joined to genistein and water (H_2O) is eliminated, what are the values of the $[\text{M}+\text{H}]^+$ ion and the $[\text{M}-\text{H}]^-$ ion?

The LC

- **1D-approach**

- Use of reverse-phase, normal phase and HILIC phase
- particle size – smaller is more efficient, but back pressure is a problem



LC flow rate

- **Sensitivity is inversely related to flow rate**

- Slower flow gives more sensitivity



normal flow (0.2-0.4 ml/min)



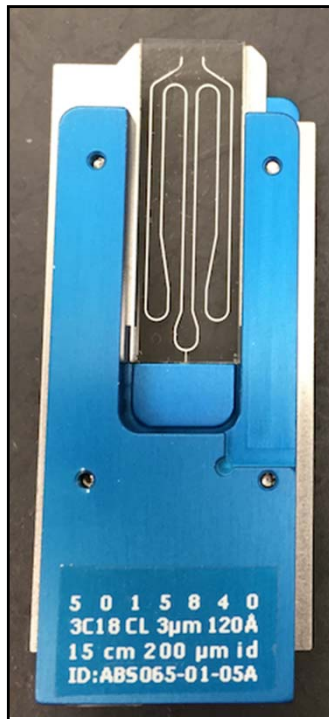
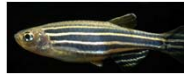
microflow/capillary (5-50 μl/min)



nanoflow (0.3-5 μl/min)

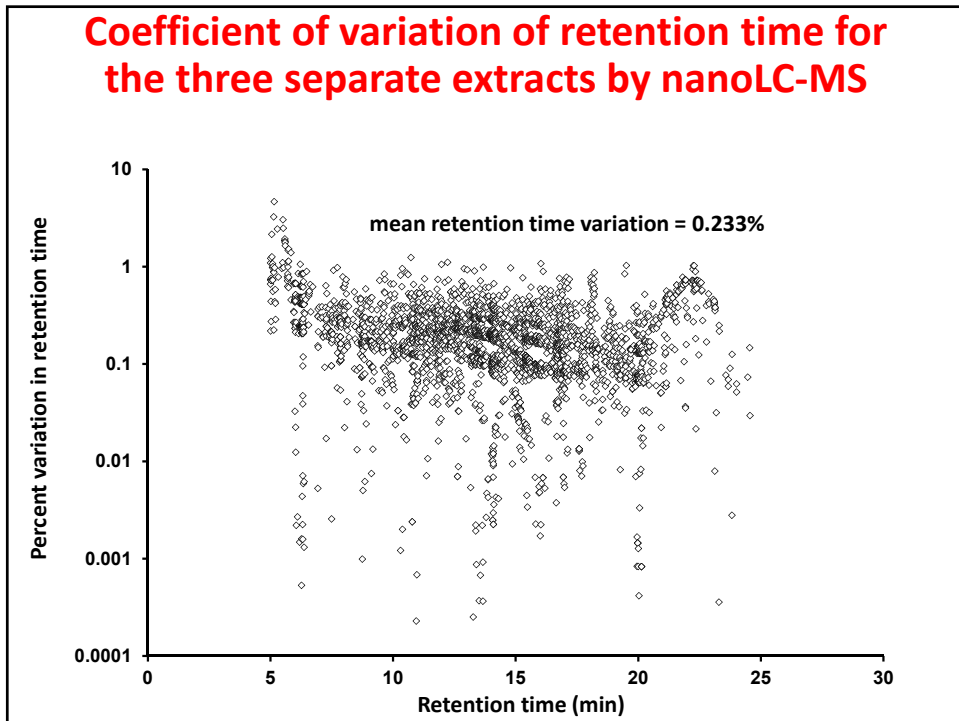
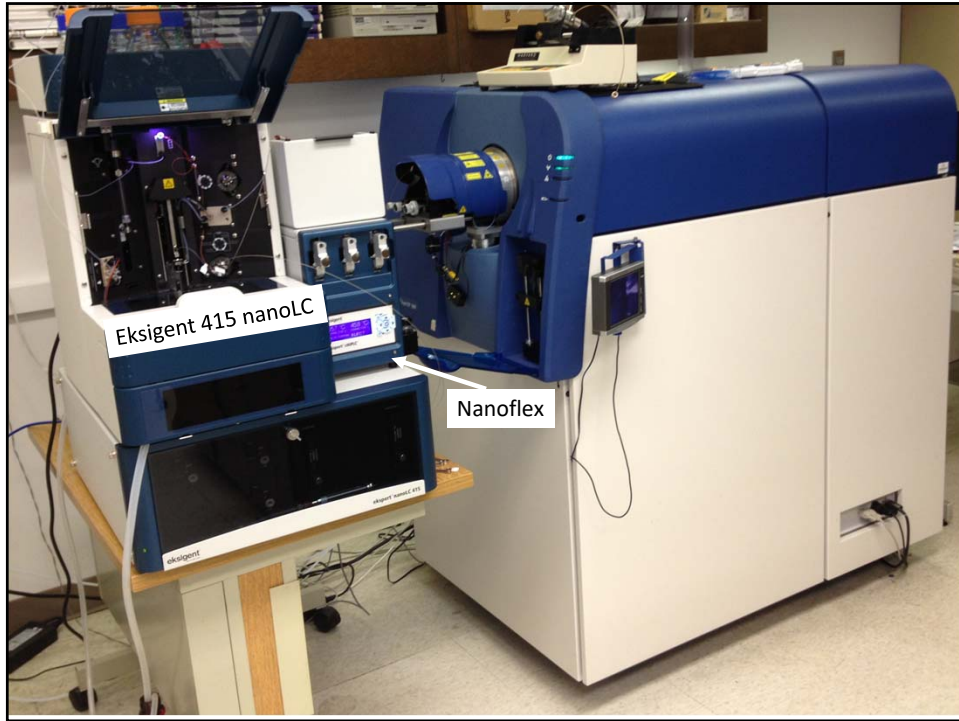
Optimizing nanoLC for metabolomics

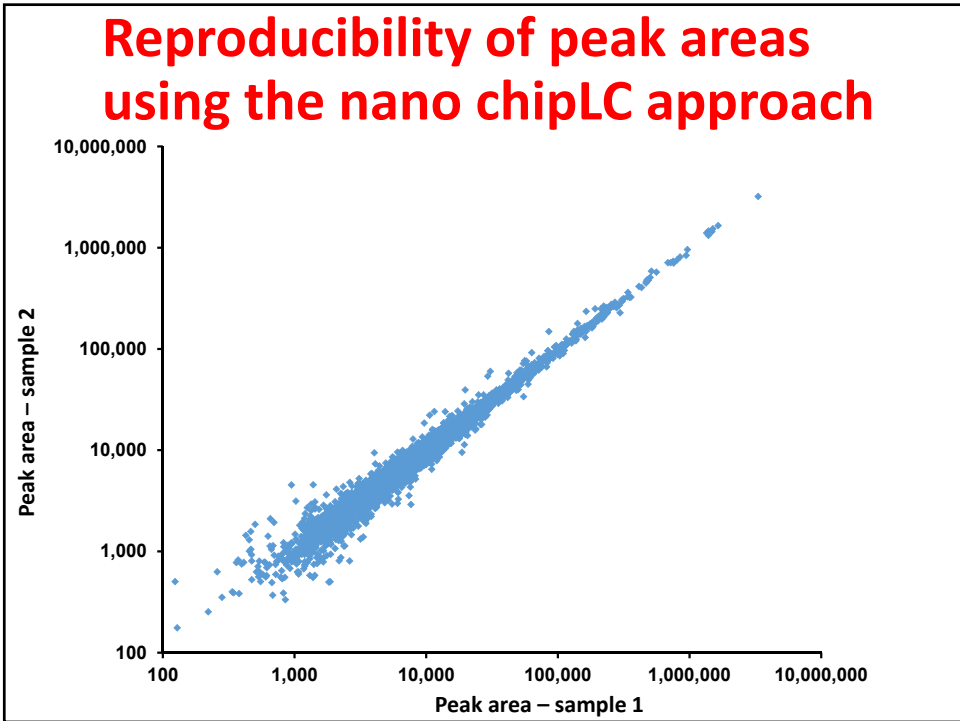
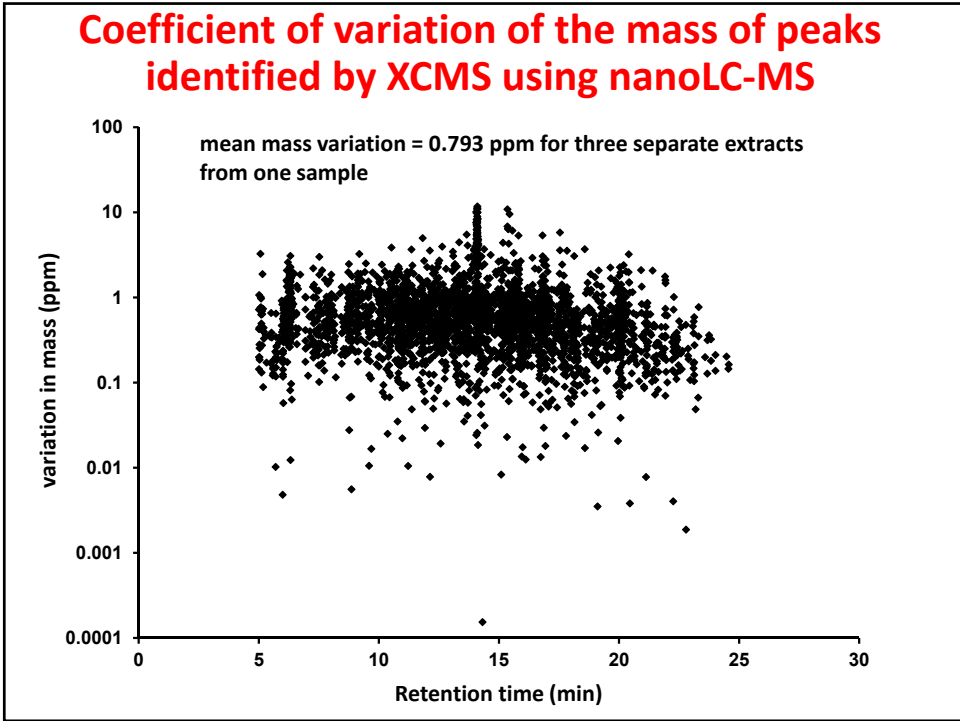
- Objective is to develop metabolomics for small animal model systems
 - *D. melanogaster*
 - *C. elegans*
 - *D. rerio*
- A single zebrafish yields about 1 μl of plasma
- Need to move down to the nanoscale
- Important to maintain consistency and quantitation
 - Reproducible columns and temperature



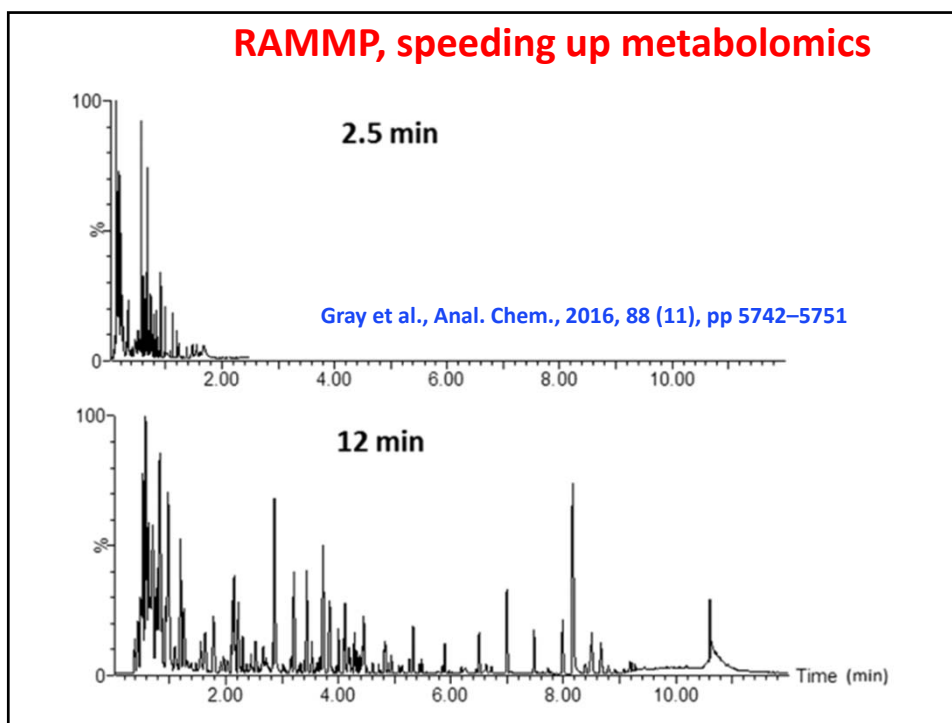
Close up of a nanochipLC cartridge (15 cm x 0.2 mm ID).

- Each long section of the column is ~ 2.5 cm (1 inch).
- Can be machined to a better tolerance.
- Simpler connections to the liquid stream.
- Can be placed in a temperature-controlled environment



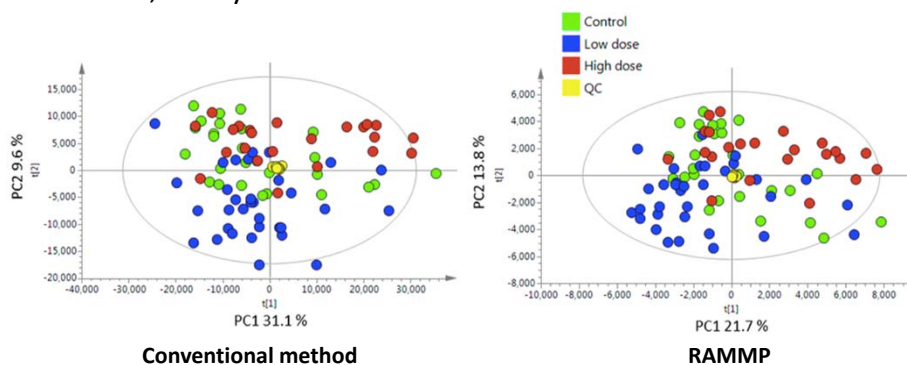


RAMMP, speeding up metabolomics



RAMMP

- There was a reduction in independent features
 - 19,000 by conventional method
 - 6,000 by RAMMP

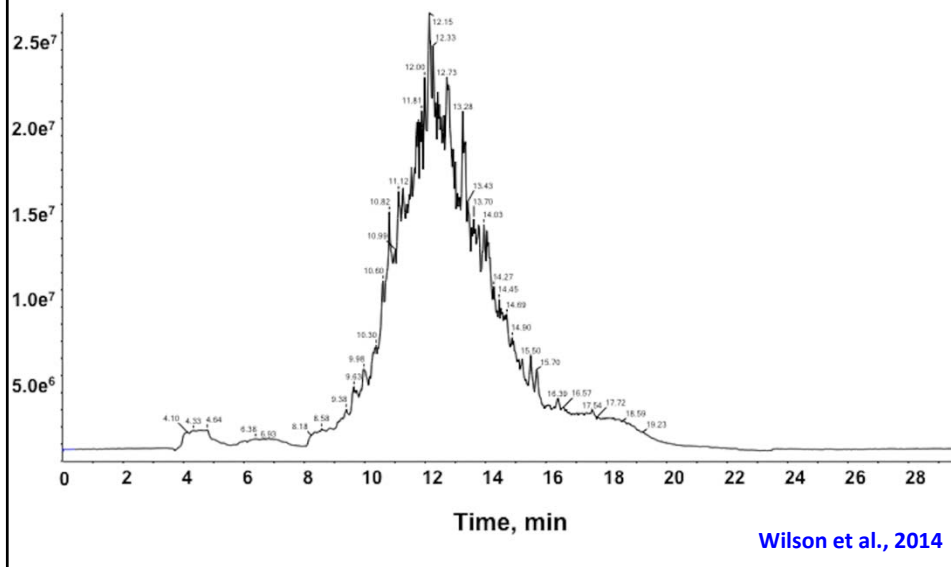


Gray et al., Anal. Chem., 2016, 88 (11), pp 5742–5751

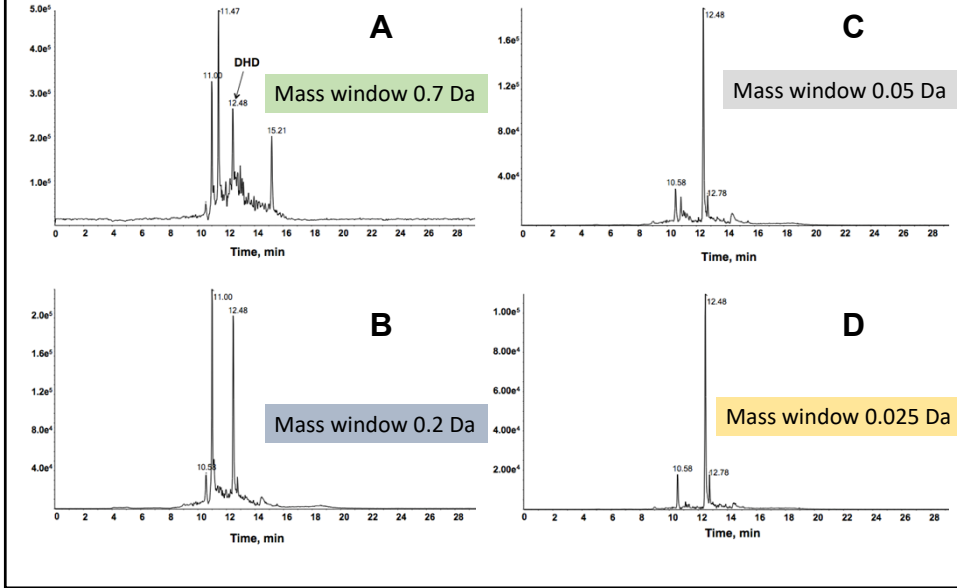
Selected ion monitoring

- The summation of all the ions collected in a GC or LC analysis is called the **total ion current (TIC)** and produces a **total ion chromatogram**
- By selecting a particular mass-to-charge ratio (m/z) value, one can see where a metabolite's molecular ion elutes from the column
 - This produces a **selected ion chromatogram (SIC or XIC)**
 - The quality of the SIC depends on the mass accuracy and resolution of the collected data

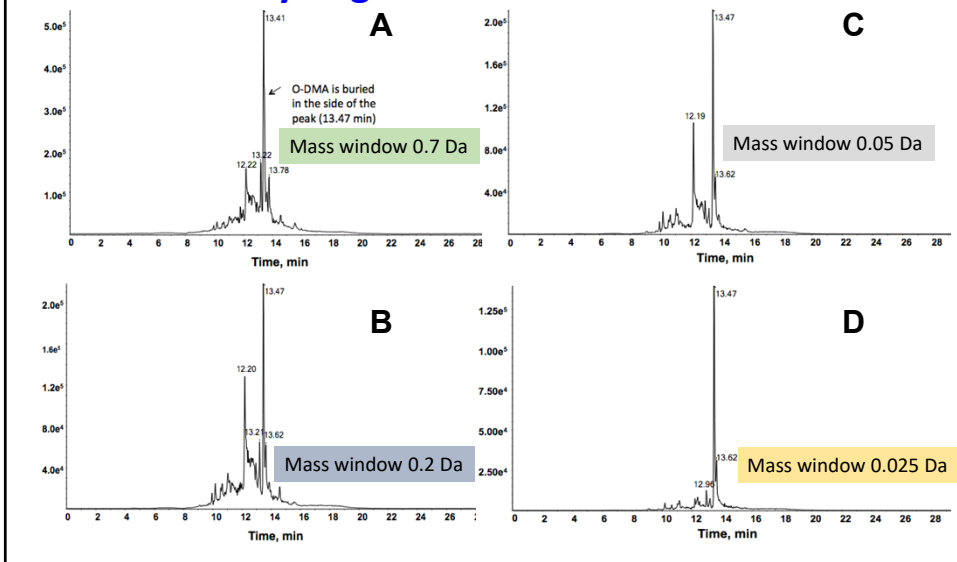
Example of a TIC of human urine



Selected ion chromatograms from TIC Dihydrodaidzein



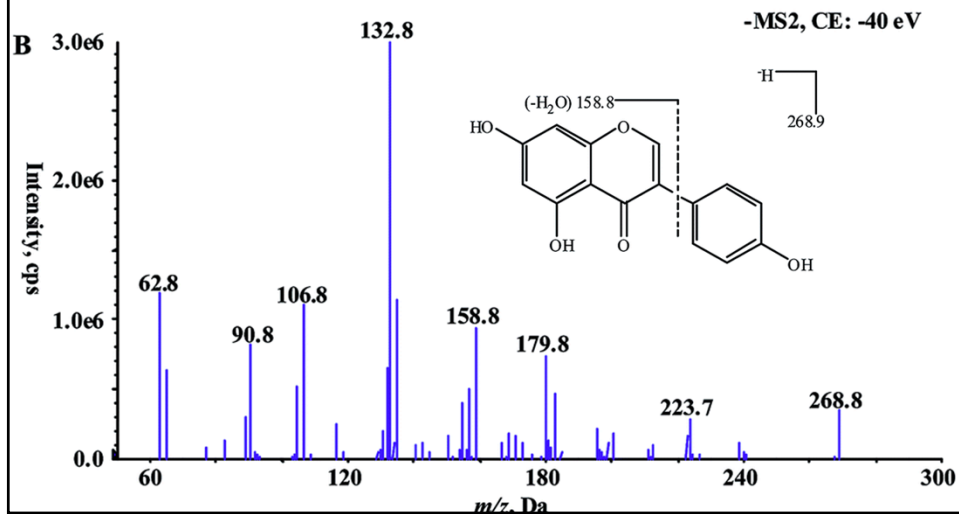
Selected ion chromatograms from TIC O-desmethyngolensin



MS/MS

- A second mass spectrum (MSMS) that is informative arises from isolating the molecular ion
- The molecular ion is heated, either by collision with neutral gas (quadrupole, ion traps) or by using IR radiation (FT-ICR)
 - The extra energy increases the stretching of critical bonds, leading to dissociation of the molecular precursor ion into charged product ions
 - These generate the MS/MS spectrum for a metabolite
 - Ion traps can also isolate a product ion and create MSⁿ spectra

MS/MS spectrum of genistein



Measuring a mass transition

- Instead of measuring the full MS/MS spectrum, ions from the MS/MS can be individually measured
- This is referred to as a **mass transition** from the molecular or precursor ion to a specific product ion
- It is also known as **reaction ion monitoring**

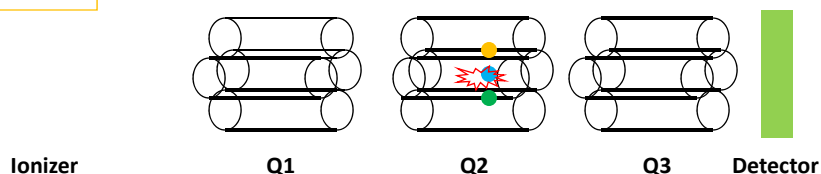
Targeted vs untargeted methods

- If we know what the metabolites to be measured are (from previous untargeted analyses, or prior knowledge), then a **multiple reaction monitoring (MRM)** approach is the best way to go since allows quantitative analysis of possibly 100s of metabolites
- If there is no hypothesis, but instead you want to generate hypotheses, then the untargeted approach is better.

Multiple reaction ion monitoring



Quantitative analysis of metabolites in a complex mixture carried out using a triple quadrupole instrument



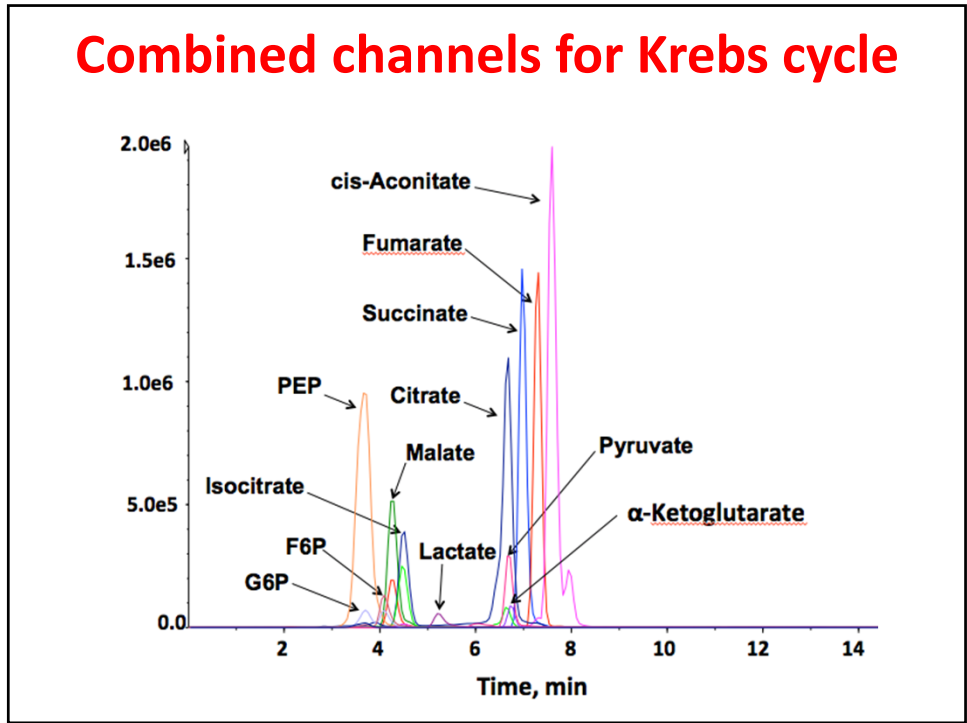
Based on precursor ion/product ion pair(s)

Courtesy, John Cutts

How many MRM transitions?

- Acquisition can be as little as 2 msec, but acquisition time determines sensitivity
- Fast switching electronics can measure as many as 500 different transitions per second
- Since measuring the area under a peak requires 10 data points, the number of transitions measured has to be matched against the shape and width of the chromatographic peaks – to be discussed in more detail later

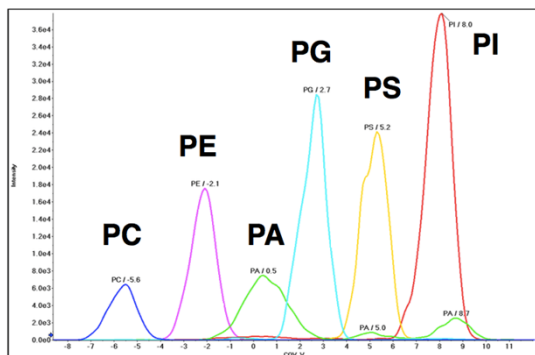
Combined channels for Krebs cycle



Ion mobility mass spectrometry

- Another method of separating classes of compounds as well as compounds with the same molecular mass

Experiment: MRM scan of 6 phospholipid standards with COV ramp



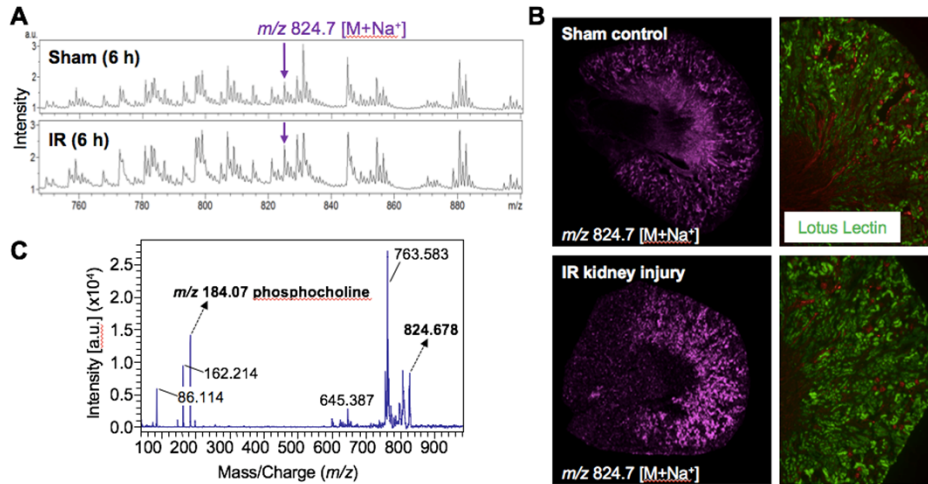
This is a gas-phase separation of these phospholipids, i.e., no chromatography

SCIEX use a differential mobility process outside of the mass spectrometer

Waters have a totally different approach to ion mobility

In their case, the ions are separated inside the mass spectrometer

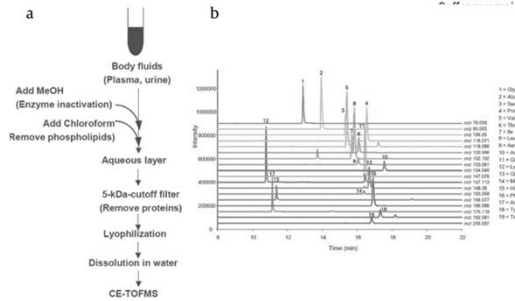
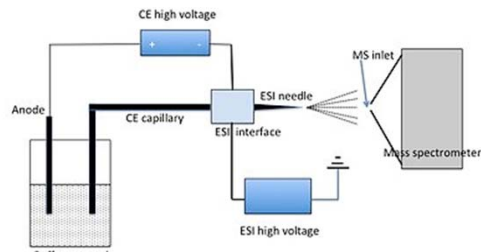
Imaging mass spectrometry



Generated by Janusz Kabarowski and Kelly Waters

Future methods in metabolomics

- Capillary electrophoresis (CE-MS)



Imaging metabolites in real time

- **In an ideal world, we want to measure metabolites without their degradation, spatially (preferably subcellularly) and with regard to time**
 - MS has high qualitative mass resolution and sensitivity, but it is destructive and not subcellular. Has poor time resolution
 - NMR is non-destructive and quantitative, but is not sensitive and not subcellular. Poor time resolution
- **Correlated anti-Stokes Raman Spectroscopy**
 - <https://bernstein.harvard.edu/research/cars-why.htm>
 - Is nondestructive, has high sensitivity and spatial and time resolution, but poor qualitative resolution (distinguishing metabolites)