

#### **Orbitrap™ Technology HRAMS Potentiates Metabolomic Research**

Sensitive but Stable High Resolution Mass Spectrometry

by Tosapol Anukunwithaya, PhD MS Product Specialist



### •••• FUNDAMENTAL OF MASS SPECTROMETER





The basis in mass spectrometry (MS) is the <u>production</u> of **ions**, that are subsequently <u>separated or filtered</u> according to their **mass-to-charge (m/z) ratio**, and <u>detected</u>.





#### *m*/*z* = ( molecular weight + charge ) / charge





### **Information Rich Data**





### **Mass Spectrometry – Block Diagram**





### ION SOURCE

**IONIZATION TECHNIQUES** 





# Ionization



• **Ion sources :** Converts sample molecules (neutral) into charged molecules or molecular ions.

#### Type of ionization techniques

- Atmospheric Pressure Ionization (API)
  - Electrospray Ionization (ESI)
  - Atmospheric Pressure Chemical Ionization (APCI)
  - Atmospheric Pressure Photo Ionization (APPI)
- Matrix Assisted Laser Desorption Ionization (MALDI)



### **Atmospheric Pressure Ionization (API)**









# **Electrospray Ionization (ESI)**





### **Atmospheric Pressure Chemical Ionization (APCI)**





Polarity of analytes determines the ionization source.



ESI	Electrospray	ionization
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- APPI Atmospheric pressure photo ionization
- APCI Atmospheric pressure chemical ionization
- GC/MS Gas chromatography / Mass spectrometry



### MASS ANALYZERS





### **Mass Spectrometry – Block Diagram**





- Operate under high vacuum environment (prevent ions from bumping into gas molecules).
- Actually measure mass-to-charge ratio of ions (m/z).
- Key specifications are **resolution**, mass measurement **accuracy**, and **sensitivity**.
- Several kinds exist: for ion traps, quadrupole, time-of-flight and orbitrap are most used.



### Mass Analyzer : Ion Trap





- Consists of ring electrode and two end caps
- Principle very similar to quadrupole
- Ions stored by RF & DC fields
- Scanning field can eject ions of specific m/z



### Mass Analyzer : Quadrupole





Uses a combination of RF and DC voltages to operate as a mass filter.

- Has four parallel metal rods.
- Lets one mass pass through at a time.
- Can scan through all masses or sit at one fixed mass.



### Quadrupole → Triple Quadrupoles (QqQ)









Scan Mode	Q1	Q2	Q3	Purpose
Full Scan	Scanning	Pass All	Pass All	MW Info.
SIM (Selected Ion Monitoring)	Fixed m/z	Pass All	Pass All	Quantitation
SRM (Selected Reaction Monitoring)	Fixed m/z	Pass All (+CE)	Fixed m/z	Targeted Quantitation
Product	Fixed m/z	Pass All (+CE)	Scanning	Structural Info.
Neutral Loss	Scanning	Pass All (+CE)	Scanning	Analyte Screening
Precursor	Scanning	Pass All (+CE)	Fixed m/z	Analyte Screening



#### Full Scan Mode

Purpose: Survey scan of a chromatographic peak

Full Scan				
	Scannii	ng Pass All	Pass All	MW Info.
	Q1 Scannin	g RF	Only	Q3 RF Only
<sup>:</sup> ull scan Q1: 🛃	$\sim$	$\sim$ -	<u>.</u>	$\sim$







SIM is in essence a full scan acquisition on a relatively narrow mass

window (defined as center mass / scan width)











"Simultaneous" monitoring of

multiple transitions









RT: 2.28 - 5.89 SM: 15G







http://www.youtube.com/watch?v=LFB14D8pkoc



### HIGH RESOLUTION MASS ANALYZERS





# **Mass Analyzer : Time-of-flight (TOF)**



- A package of ions is accelerated by a potential V into a field free flight tube.
- The time t<sub>flight</sub> needed for ions to reach a detector placed at distance d is measure.
- Small ions have higher velocity than large mass ions therefore their time of flight in the tube are different and related to m/z ratio



# Mass Analyzer : Time-of-flight (TOF)

- Resolution limited by:
  - Length of TOF flight tube
  - Kinetic energy distribution
  - Propagation delay in detector
- Sensitivity limited by:
  - Ion stability
  - Ion transfer efficiency





### ••••• ORBITRAP MASS ANALYZER



Alexander Makarov



### **Mass Spectrometry – Block Diagram**





### **Mass Spectrometry – Block Diagram**





Anal. Chem. 2000, 72, 1156-1162

#### Electrostatic Axially Harmonic Orbital Trapping: A High-Performance Technique of Mass Analysis

#### Alexander Makarov\*

HD Technologies Ltd., Atlas House, Simonsway, Manchester, M22 5PP, U.K.

This work describes a new type of mass analyzer which employs trapping in an electrostatic field. The potential distribution of the field can be represented as a combination of quadrupole and logarithmic potentials. In the absence of any magnetic or rf fields, ion stability is achieved only due to ions orbiting around an axial electrode. Orbiting ions also perform harmonic oscillations along the electrode with frequency proportional to  $(m/z)^{-1/2}$ . These oscillations are detected using image current detection and are transformed into mass spectra using fast FT, similarly to FT ICR. Practical aspects of the trap design are presented. High-mass resolution up to 150 000 for ions produced by laser ablation has been demonstrated, along with high-energy acceptance and wide mass range.




- An ion packet of a selected m/z enters the field.
- Increasing voltage squeezes ions.
- Voltage stabilises and ion trajectories are also stabilized.
- Angular spreading forms a rotatating ring.





- lons trapped in an **electrostatic field.**
- Central electrode kept on high voltage.
- Outer electrode is split and able to pick up an **image current** induced by ion packets moving inside the trap.



#### **Characteristic frequencies:**

- Frequency of rotation  $\omega_{arphi}$
- Frequency of radial oscillations  $\omega_r$
- Frequency of axial oscillations  $\omega_z$

$$U(r,z) = \frac{k}{2} \cdot \left\{ z^2 - r^2 / 2 + R_m^2 \cdot \ln(r / R_m) \right\}$$

A. Makarov, Anal. Chem 2000, 1156-1162



## Mass Analyzer : Orbitrap<sup>™</sup> Technology





## Mass Analyzer : Orbitrap<sup>™</sup> Technology





## Mass Analyzer : Orbitrap<sup>™</sup> Technology



http://planetorbitrap.com/q-exactive-plus#.WmoCMeRG3IX



#### **Orbitrap™ Technology HRAMS Potentiates Metabolomic Research**

Sensitive but Stable High Resolution Mass Spectrometry

by Tosapol Anukunwithaya, PhD MS Product Specialist



- HRAMS = **High Resolution Accurate Mass S**pectrometry
- Mass Resolution = ability of a mass spectrometer to distinguish between ions of nearly equal m/z ratios (isobars).
- Mass Accuracy = the precision of which the mass is measured by the mass spectrometer.



## **Mass Resolution**







• Mass error reporting in **ppm** (relative mass error):

$$Mass\,error = \frac{Measured - Theoretical}{Theoretical} \times \ 10^6 = ppm$$

• Exact Mass is the mass of an ion with a given empirical formula calculated using the exact mass of the most abundant isotope of each element

Example $M = 249$ :	CH_+	249.0070	C = 12.0000
<u>Example</u> (W 213)	$C_{19}H_7N+$	249.0580	H = 1.0078 N = 14.0031
	C <sub>13</sub> H <sub>19</sub> N <sub>3</sub> O <sub>2</sub> +	249.1479	N - 14.0031
			O = 15.9949

S = 31.9721



• Main advantage: the possibility to determine the elemental composition of individual molecular or fragment ions, a powerful tool for the structural elucidation or confirmation.





## **Mass Resolution and Accuracy**

#### Isobaric compounds separation





• **Removing interferences:** High resolution is very important for samples with complex matrix (e.g. biological, food), since they will contain a significant number of background ions.



- High resolution is needed for:
  - Separating co-eluting molecules with close masses
  - Mass accuracy
  - Good quantitation results

Figure 1: Analysis of the MH<sup>+</sup> peak of Pirimicarb at 15,000 and 80,000 resolution.





Signal intensity does not change with resolution with the Orbitrap detector



## **Stability : Robust and Reproducible HRAMS**





 Peak intensity (area) variation during 900 injections (blue) with according mass accuracy (peak apex scan, red)



Robustness With Aflatoxin G2 In Wheat Matrix

• peak area 🔺 mass accuracy (ppm)



## **Orbitrap Applications Universe**





# Sci Spec MS Technology in Pharma Research

Drug Discovery	Drug Formulation	<b>Preclinical Evaluation</b>				
<ul> <li>Natural Product</li> <li>Unknown compound identification</li> <li>Plant metabolic pathway</li> <li>Synthetic Compounds</li> <li>Molecular mass confirmation</li> </ul>	<ul> <li>Determination of active compound concentration</li> <li>Solubility test</li> <li>Stability test</li> </ul>	<ul> <li>in vitro Testing         <ul> <li>Permeability test</li> </ul> </li> <li>in vivo Testing         <ul> <li>Toxicological study</li> <li>Pharmacokinetic study</li> </ul> </li> </ul>	<ul> <li>Metabolism Study         <ul> <li>Target/ Non-target metabolite identification</li> </ul> </li> <li>Metabolomics</li> </ul>			
High Resolution	High So	High Resolution				



Your Scientific Specialist

### •••• ORBITRAP<sup>™</sup> TECHNOLOGY HRAMS POTENTIATES METABOLOMIC RESEARCH





- Metabolomics is the scientific study of chemical processes involving metabolites, the small molecule intermediates and products of metabolism.
- Specifically, metabolomics is the "systematic study of the unique chemical fingerprints that specific cellular processes leave behind", the study of their small-molecule metabolite profiles.



## **Metabolomics**



FIGURE 3 | Integration of multi-omics and clinical data into TTM. (A) Herbal plants and herbal medicines. (B) Chemical characterization of herbal plants, herbal medicines, and biofluids using targeted and untargeted metabolomics. (C) Clinical trial of herbal plants and herbal medicines by cell lines, animal, or human models. (D) Biofluid for metabolome analysis. (E) Integrative analysis of different omics data and clinical data. (F) Systems biology network. (G) Individualized data.

Khoomrung et al. (2017)



## **Challenges of Metabolomics**



- Diversity in structures and physical chemical properties
  - Require multiple technologies to capture a metabolome
- Many isomeric and isobaric species

   Require high resolving power for correct ID
- Very low to very high concentrations
  - Require High sensitivity and wide dynamic range
- No single database to identify all unknown metabolites
  - Require extensive library or fragment ion prediction based on compound structure

## **Sci** Diverse Physical Properties among Metabolites

#### **Metabolites**

triglycerides cholesterol esters diacylglycerols sphingomyelines phosphatidylcholines phosphatidylethanolamines other phospholipids fatty acids eicosanoids & metabolites bile acids bilirubin amino acids, amines organic acids sugars Other polar:

e.g. purines & pyrimidines





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## **Sensitivity : 5 Orders of Dynamic Range**

Quantitation of Citric Acid using orbitrap analyzer achieved at low fmole sensitivity using full scan MS





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## **Untargeted Metabolomics Workflow**





## **Sci** Enhance your Research with Compound Discoverer



https://goo.gl/YvAS2j

## **Sci** Compound Discoverer : Retrospective for Unknowns





### **Compound Discoverer : Flexible Workflows**

Use common, predefined • workflows or create your Input Files own Select Spectra Integrate your own **nodes** ullet

- New in version 3.0: •
  - Metabolika™ pathways
  - Stable isotope labeling
  - mzLogic<sup>™</sup> annotation of unknown compounds
  - Interactive heat map with hierarchical clustering
  - mzVault 2.1 create spectral libraries from CD results



Align Retention

Times



# Compound Discoverer : Identifying Unknowns

Compound Discoverer 3.0.0.294				– o ×
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		<b>→</b> <sup>‡</sup> ×	Mass Sportnum	<b>•</b> ‡ :
Compounds Compou	HAKKAISAN KAN-CHIKU KIKUSUI	KUBOTA	Mass Spectrum F28 #310, RT=1.413 min, MS1, FTMS (+ F30 #1276, RT=1.394 min, MS1, FTMS (- T+ F30 #1277, RT=1.396 min, MS2, FTM 6 . Compound Identification 6 . Compound Identification 6 . Compound Annotations 7 . Predict Compositions 7 . Search ChemSpider 7 . Search Mass Lists 7 . Search mzCloud 7 . Search mzVault	259.09216 [244:06021 [21:08372] 247.12862 244.14464 [220] 240 260
P Checked Name	Predicted Composition Metabolitie Search	FISh Coverage	Molecular Weigi  7. Pathway Mapping  A Map to BioCyc Pathways  Map to KEGG Pathways	athways Metabolika Pathways
6083 🖙 📃 L-Pyroglutamic acid	C5 H7 N O3		129.0424 Map to KESG Fathways	
6084 🛱 🔲 Propionic acid	C3 H6 O2		74.0366 🦓 Map to Metabolika Pathways	
6085 垣 🔲 Ribonolactone	С5 Н8 О5		148.0368	3
6086 🛱 🔲 Tropinone	C8 H13 N O		139.0995 8. Compound Scoring	
6087 🖶 🔲 Propionic acid	C3 H6 O2		74.0366 📣 Apply mzLogic	
6088 🖶 🛄 L-Valine	C5 H11 N O2		117.0787	8
6089 + Propionic acid			239471 A Dottorn Cooring	5
			A Pattern Scoring	•
Show Related Tables				



#### **Compound Discoverer : Database Hub**

- lee							_			
Brite menu   Do	wnload htext   Download js	on] Deoxynivalenol								
Natural toxins		Q enlarge	Systematic / IUPAC Name: (3β,7α)-3,7,15-Tr	rihydroxy-12,13-	epoxytricho	thec-9-en-8-on	ie			
			ID: Reference6191							
<b>, , , , </b>	One-click mode	ОЧ	Other Names: 4-Deoxynivalenol; 4-Desoxynivalenol; Dehydronivalenol; Desoxynivalenol; Bd Toxin : more							
Fungal toxins Mushroom toxins		ОН								
		0								
Mycotoxins			Citass. Matural Ioxins							
Aflatoxir	13	Vomitorin also known as deorvnivaler	nol (DON) is a type B trichothecene, an epoxy-sesu	uitemenoid This	mycotoxin	occurs predom	ninantly in	grains such :	as wheat har	lev nats
C06800	Aflatoxin B1	rye, and corn, and less often in rice, sorg	hum, and triticale.	ancipenola. mia	myootoxin	occurs predon	in failuy in	grains suorr	as wheat, bai	icy, oats,
C16753	Aflatoxin B2									
C16754	Aflatoxin G2	ChemSpid	or							
c16754 c16755	Aflatoxin G2 Aflatoxin G1	ChemSpid	er				Sea	rch ChemSp	bider	Q
c16754 c16755 c16756	Aflatoxin G2 Aflatoxin G1 Aflatoxin M1	ChemSpid Search and share chem	<b>er</b> istry				Sea	rch ChemSp	bider	Q
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C16754 C16755 C16756 Trichothe C09662 C19952 C09738	Aflatoxin G2 Aflatoxin G1 Aflatoxin M1 ecenes Diacetoxyscirpenol HT-2 Toxin T-2 Toxin	ChemSpid Search and share chem Simple Structure Advanced His Found 1 result Search term: Deoxynivalenol (Found by	er istry tory				Sea	rch ChemSp	oidər Comme This Re	
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### **Compound Discoverer : Metabolic Pathway**





#### **Compound Discoverer : Statistics**

vorktiow i ree					
	14	Align Retention Times	10		
	E	Detect Unknown Compounds	9		
		Group Unknown Compounds	8		
Fill Gaps	14	Predict Compositions	16	Search mzCloud	22
Mark Background Compounds	20	Search Chem Spider	230	Map to KEGG Pathways	13
m	]	8			

Statistics

24

Analysis

- Differential Analysis : t-test, ANOVA /w post-hoc tests, ratios & fold changes
- p-value adjustment for FDR
- Principal Component Analysis (PCA)
- Normalization
- Descriptive Statistics



- Introduction of mass spectrometry
- Key Features of Orbitrap<sup>™</sup> Technology HRAMS
  - High Resolution and Accurate
  - Sensitive but Stable
- Compound Discoverer
  - Powerful workflow to identify non-target compounds for metabolomic research



# **Sci** Reference Sites for Orbitrap Analyzer (1)

No.	Company	Department	Model	Application
1	Faculty of Medicine, Siriraj Hospital	Medical Proteomics Unit	LTQ XL Orbitrap	Education
2	Chulabhorn Research Institute (CRI)	Biotechnology Laboratory	Orbitrap ELITE	Research
3	Charoen Pokphand Foods (CPF)	Quality Control Department	Q Exactive	R & D
4	Department of Livestock Development, Ministry of Agriculture and Cooperatives	Bureau of Quality Control of Livestock Product	Q Exactive	Food and Agriculture
5	Faculty of Medicine, Siriraj Hospital	Department of Pharmacology	Q Exactive	Education
6	Faculty of Medicine, Chulalongkorn University	Center of Excellence in Systems Biology	Q Exactive Plus	Research
7	National Center for Genetic Engineering and Biotechnology (BIOTEC), NSTDA	Biomolecular Analysis and Application Laboratory (SBMA)	Orbitrap Fusion	Research


## **Sci** Reference Sites for Orbitrap Analyzer (2)

No.	Company	Department	Model	Application
8	Synchrotron Light Research Institute (SLRI)	Applied Research for Industry Division	Q Exactive Plus	Research Service
9	Chulabhorn Graduate Institute (CGI)	Chemical Biology	Q Exactive Focus	Research
10	Kokoku Innovative Technology	Center of Rubber Innovation	Q Exactive Focus	Research
11	National Center for Genetic Engineering and Biotechnology (BIOTEC), NSTDA	Plant Physiology and Biochemistry Laboratory	Q Exactive Focus	Research
12	Institute of Forensic Medicine (IFM), Police Hospital	Department of Toxicology	Q Exactive Focus	Forensic Toxicology
13	National Center for Genetic Engineering and Biotechnology (BIOTEC), NSTDA	National Omics Center	Q Exactive HF-X	Research



## **Thank You for Your Attention**



Your Scientific Specialist