News

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Thermo Fisher Scientific Launches World's First "Tribrid" LC-MS, Transforming Life Sciences Research with Revolutionary Depth of Analysis and Usability

MINNEAPOLIS - *ASMS 2013* – (June 10, 2013) – Thermo Fisher Scientific Inc., the world leader in serving science, introduced the Thermo Scientific Orbitrap Fusion Tribrid liquid chromatography-mass spectrometry (LC-MS) system, combining its three mass analyzers – quadrupole, Orbitrap and linear ion trap – in a novel "Tribrid" architecture that offers unprecedented depth of analysis of complex biological samples.

The new Orbitrap Fusion LC-MS made its debut at the ASMS Conference on Mass Spectrometry and Allied Topics, being held in Minneapolis from June 9-13 at the Minneapolis Convention Center in **booth 154**.

"Our mission has been to create the highest-performing commercial mass spectrometer ever built," said Dr. Ian Jardine, chief technology officer, chromatography and mass spectrometry, Thermo Fisher Scientific. "Additionally, we wanted to make this power widely accessible to the science community and make it incredibly easy to use. In creating the Orbitrap Fusion, we have combined and improved our quadrupole, linear ion trap and Orbitrap technologies in an ultimately flexible research MS system – to arrive at an entirely new class of instrument that will transform our customers' science."

"Our largest challenges have been sensitivity and throughput," explained Dr. Steven Gygi, professor of cell biology at Harvard Medical School. "The Orbitrap Fusion instrument is revolutionary in allowing us to achieve much greater proteome-wide coverage with much greater quantitative accuracy than ever before."

One way the Orbitrap Fusion system can address throughput challenges is through tandem mass tags (TMT). This technique enables mass spectrometers to determine relative quantification of proteins in multiple samples simultaneously. The Orbitrap Fusion instrument dramatically increases depth and quality of data compared to previous tools to make TMT results far better. The new platform takes advantage of MS^3 selectivity to improve quantitative accuracy, and can collect twice as many MS^3 scans per unit time, at significantly greater sensitivity than was previously possible. New TMT reagents are also available from Thermo Fisher, allowing comprehensive, simultaneous analysis of up to 10 samples.

At the heart of the Orbitrap Fusion LC-MS is a configuration of three different mass analyzers that work together to raise analytical performance to new levels and enable completely new experimental methods:

- A quadrupole for precursor selection at isolation widths down to 0.4 amu for excellent sensitivity and selectivity;
- An ultra-high-field Orbitrap offering resolution in excess of 450,000 and scan rates up to 15 Hz for unsurpassed selectivity and speed of analysis;

- An ion routing multipole followed by dual-pressure linear ion trap providing MS^n HCD, CID and ETD fragmentations and fast, sensitive mass analysis with scan rates of up to 20 Hz. Synchronous precursor selection enhances the instrument's signal-to-noise ratio.

This Tribrid configuration enables users to positively identify larger numbers of low-abundance proteins faster than previously possible with existing commercial instruments. Its unique architecture enables simultaneous precursor isolation, fragmentation, and data acquisition in both the Orbitrap and linear ion trap mass analyzers. More high-quality data can be collected compared to existing instruments, expanding the range of possible experiments.

The ability to choose between fragmentation modes at any stage of MS^n analysis with detection by the Orbitrap or linear ion trap analyzer makes possible a range of novel experiments to achieve a new level of structural information from metabolites, glycans, posttranslational modifications and sequence polymorphisms.

In typical metabolomics experiments, scientists frequently encounter unknowns along with target compounds. To identify the unknowns, the sample must be rerun on an LC-linear ion trap instrument to obtain MS^n data. But it is difficult to match chromatography retention time on the second run, introducing substantial uncertainty. With its unique three mass analyzer configuration, however, the new Orbitrap Fusion Tribrid LC-MS addresses this problem, offering users the ability to transform many small molecule experiments by conclusively identifying unknowns as they are encountered.

Performance with Accessiblity

New intelligent software on the Orbitrap Fusion LC-MS provides Dynamic Scan Management (DSM), a capability that automatically adjusts scan parameters as experiments are running to achieve optimal results.

The Orbitrap Fusion system features a novel, easy-to-use drag and drop method editor that removes most of the guesswork from setting up complex methods. This is part of a comprehensive suite of MS software that supports the platform's unprecedented usability. It includes:

- Thermo Scientific Freestyle software, a new data visualization tool that also facilitates rapid method development and data quality assessment.
- Thermo Scientific Proteome Discoverer, a comprehensive software application for protein identification.
- Thermo Scientific Compound Discoverer software, used to perform small molecule structural identification in a wide range of applications.
- Thermo Scientific SIEVE software for differential quantitative analysis of proteomic and small molecule samples.
- mzCloud software, a novel mass spectral database that supports identification and structural elucidation of unknowns.

To see the entire Thermo Fisher portfolio of new mass spectrometry instruments, software and consumables, visit Thermo Scientific booth 154 or online at www.thermoscientific.com/asms or www.thermofisher.com/news.

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