2006 PROGRAM

8:15 a.m. Registration and Continental Breakfast, Atrium (Room 1-65), William T. Young Library

9:00 a.m. Welcome by Dr. Steven W. Yates, Chairman, Department of Chemistry, University of Kentucky - Auditorium (Room 1-62), William T. Young Library

9:05 a.m. Introductory Remarks - Dr. Bert C. Lynn, Department of Chemistry, University of Kentucky

9:10 a.m. Dr. Richard M. Caprioli, Vanderbilt University
"In situ Molecular Imaging and Profiling of Proteins in Tissues Using Mass Spectrometry in Biological and Clinical Research"

Profiling and Imaging MALDI MS can be used to assess the spatial distribution of peptides and proteins in biological samples, and is especially effective in its application to tissue sections. Applications range from low-resolution images of peptides and proteins in selected areas of tissue to high resolution images of tissue cross sections. Using a raster of the tissue surface by a laser beam, images of samples are produced in specific m/z values, or ranges of values. Each spot on the sample irradiated by the laser is approximately 30-50 microns in diameter and typically covers the m/z range 1000-100,000. Individual m/z values can then be assembled from the mass spectra to produce selected m/z images. Sections obtained from any tissue type can be imaged to locate tissue specific peptides and proteins in X, Y coordinates of the tissue. We have employed the technology in studies of a variety of diseases, including several types of cancers, neurodegenerative diseases and kidney diseases, comparing proteins differentially expressed in diseased tissue with those in the corresponding normal tissue. This will be illustrated with studies of breast tumor biopsies and also those for human glioblastomas. In the latter, MS patterns have also been correlated with patient outcomes. This has been applied to a protocol termed histology-directed molecular analysis of tissue and biopsy specimens. Imaging MS has also been applied to drug targeting and metabolic studies with analysis of specific tissues after systemic drug administration. Whole animal sagittal sections have been imaged to measure molecular changes in proteins in multiple organs and correlating this with drug concentrations in these same organs.

10:10 a.m. Break (Refreshments Available)

10:45 a.m. Poster Session, Room CP-137, Chemistry-Physics Building

11:45 a.m. Buffet Lunch, Alumni House [Please return registration card by March 17, 2006 for reservations]

2:00 p.m. Dr. John R. Yates, The Scripps Research Institute
"Mass Spectrometry Analysis of Large Cellular Structures"

A component to understanding biological processes involves identifying the proteins expressed in cells as well as their modifications and the dynamics of processes. Several major technologies have benefited from large scale genome sequencing of organisms. The sequence data produced by these efforts can be used to interpret mass spectrometry data of proteins and thus enables rapid and straightforward analysis of protein data from experiments. Proteins separated by gel electrophoresis and 2-dimensional gel electrophoresis can now be rapidly identified enabling more comprehensive analyses of biochemical and molecular biology experiments. New approaches have also emerged for protein analysis such as direct identification of proteins in mixtures without gel separation. By digesting protein mixtures and separating peptides with liquid chromatography directly into tandem mass spectrometers, sufficient information can be obtained to identify the peptides and subsequently the proteins present in the mixture. As peptide mixtures become more complex better separation techniques such as 2-dimensional liquid chromatography are required to resolve the peptide components for analysis. Technologies and methods of proteomics will be described and applications illustrated by discussing experiments to identify proteins, modifications membrane proteins and membrane protein topology. Application to large cellular structures such as the Midbody, Golgi and Centriole will also be described.

3:00 p.m. Break (Refreshments Available)

3:20 p.m. Dr. R. Graham Cooks, Purdue University
"Biological Mass Spectrometry: Metabolomics, Tissue Imaging and Protein Separation"

Samples can be analyzed in the ambient environment, without any preparation, in very short times using desorption electrospray ionization (DESI). This method is shown to allow high throughput analysis of pharmaceutical preparations. It also is useful in studies of natural products and in metabolomics studies to differentiate closely related populations of samples, such as urine samples from healthy and diseased animals. The DESI method can also be used for direct tissue analysis, either for proteins or for lipids. In an unrelated experiment, mass spectrometry is used as a separation tool to prepare and collect pure protein samples by ion soft landing.

4:20 p.m. Closing Remarks - Dr. Bert C. Lynn, Department of Chemistry, University of Kentucky

(http://www.chem.uky.edu/seminars/naff/welcome.html)

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Thirty-Second Annual
Naff Symposium on

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established in the memory of
Anna S. Naff

Mass Spectrometry of Biological Systems

SPEAKERS

Richard M. Caprioli
John R. Yates
R. Graham Cooks

Friday, March 31, 2006

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