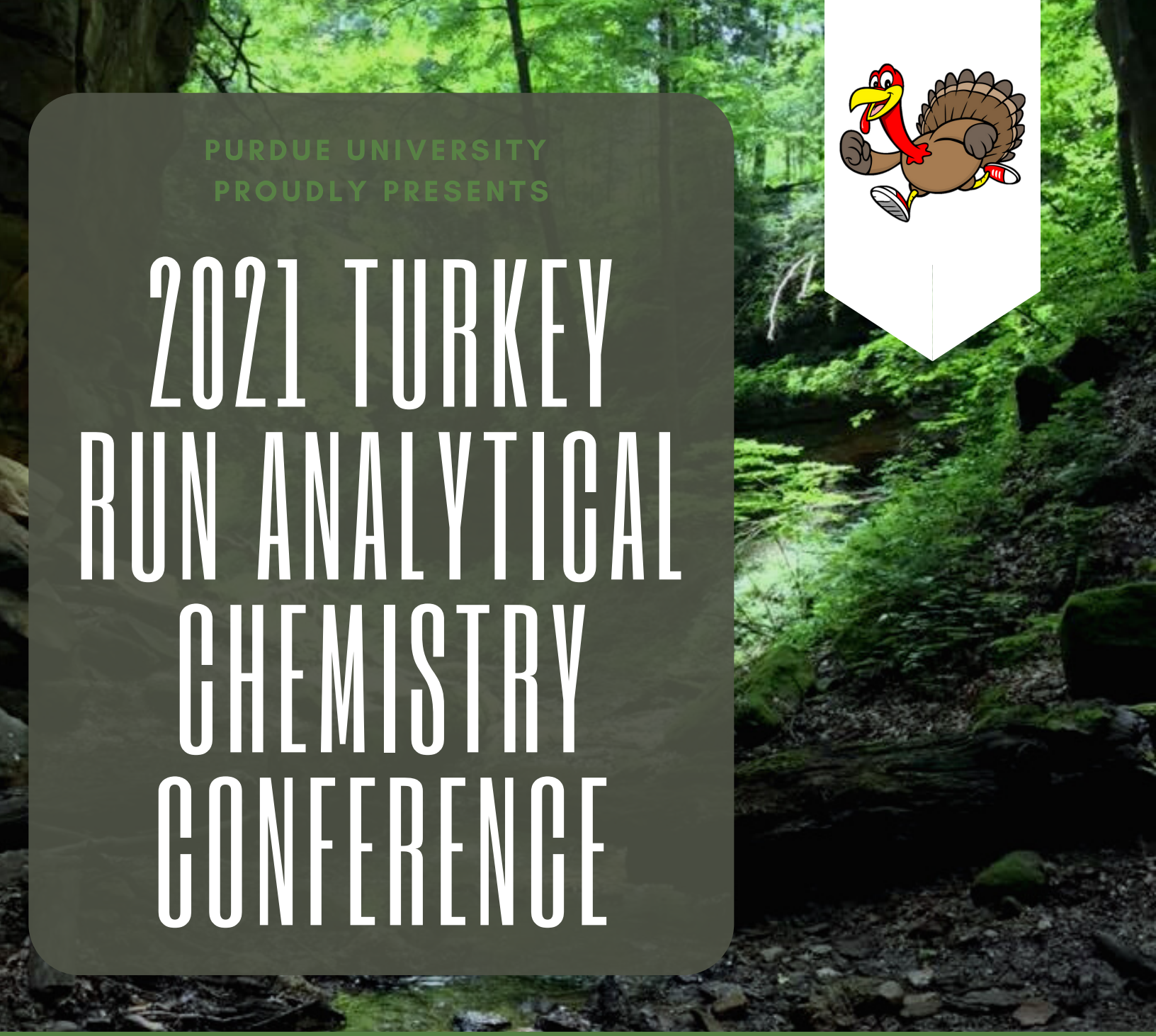

PURDUE UNIVERSITY
PROUDLY PRESENTS

2021 TURKEY RUN ANALYTICAL CHEMISTRY CONFERENCE

TURKEY RUN STATE PARK

MARSHALL, INDIANA

24-25 SEPTEMBER 2021

https://www.chem.purdue.edu/turkeyrun/

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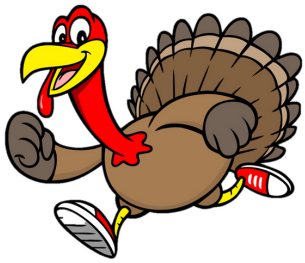
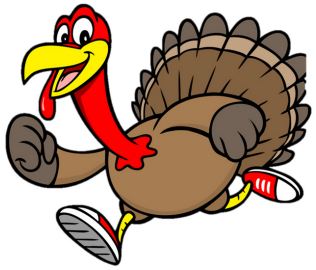


INTRODUCTION



Hello and Welcome to the 2021 Turkey Run Analytical Chemistry Conference! We are delighted to once again host this fantastic meeting in person. The Turkey Run Analytical Chemistry Conference has hosted more than 50 years worth of research presentations from some of the leading analytical chemistry departments nationwide with student representatives from the University of Illinois at Urbana-Champaign, Indiana University, Purdue University, and the University of Notre Dame organizing the conference on a rotating basis. We are also pleased to host attendees from The Ohio State University this year.

This year we have 129 registrants and have accepted 10 oral presentations and 68 poster presentations. The keynote speaker is Dr. R. Graham Cooks, the Henry Bohn Hass Distinguished Professor of Chemistry in the Aston Laboratory of Mass Spectrometry at Purdue University. He will be giving a talk entitled "What I Learned in Five Hoosier Decades."

We would like to extend a thank you to all the attendees, presenters, organizers, and sponsors for their support and enthusiasm for this year's conference, especially given the uncertainty posed by COVID-19. We would also like to thank the Turkey Run Inn for once again hosting this event and providing a beautiful venue for talking about great science.

FRIDAY
24 SEPTEMBER

3:00 - 6:30 PM

Check-In, *Lusk Room*

5:30 - 6:30 PM

Welcome & Keynote, *Lusk Room*

6:30 - 7:15 PM

Dinner Buffet Group A,
Narrows Restaurant

7:15 - 8:00 PM

Dinner Buffet Group B,
Narrows Restaurant

8:00 - 11:00 PM

Social Mixer, *Tennis Court Shelter*
Sponsored by Corteva, Inc.

SATURDAY
25 SEPTEMBER

7:30 - 8:50 AM

Breakfast Buffet, *Lusk Room*

9:00 - 10:15 AM

Oral Session I, *Lusk Room*

10:15 - 10:30 AM

Break

10:30 - 11:45 AM

Oral Session II, *Lusk Room*

11:45 AM - 1:30 PM

Lunch, Poster Set Up, & Free Time, *Outside Lusk Room*

1:30 - 2:45 PM

Poster Session A, *Lusk Room*

2:45 - 3:00 PM

Break

3:00 - 4:15 PM

Poster Session B, *Lusk Room*

4:30 PM

Closing Remarks & Conference Photo, *Front of the Inn*

2021 KEYNOTE SPEAKER

Dr. R. Graham Cooks

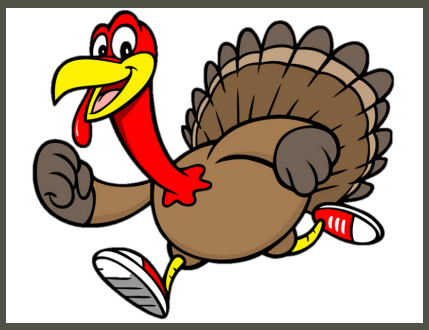
HENRY BOHN HASS DISTINGUISHED PROFESSOR OF CHEMISTRY, PURDUE UNIVERSITY

R. Graham Cooks has been honored as Elected Fellow for US National Academy of Sciences and National Academy of Inventors, Nobel Laureate Signature Award for Graduate Education in Chemistry, and Dreyfus Prize in the Chemical Sciences. In addition, he currently serves as codirector for the Center for Analytical Instrumentation Development at Purdue and is a strong advocate for the Jonathan Amy Instrumentation Facility in the Department of Chemistry. Prof. Cooks has served as major professor and advisor to more than 150 PhD students, and more than 300 graduate students, post-doctoral, and visiting scientists have worked and published with Prof. Graham Cooks. Briefly, research interests in his group include 1) ambient ionization and tandem mass spectrometry methods of analysis of complex mixtures, 2) mass spectrometry methods for cancer diagnostics, 3) high-throughput synthesis and analysis techniques, 4) instrumentation development, and 5) undergraduate laboratory training in mass spectrometry for chemical education. Prof. Cooks has published over 1500 research articles, ranks among the most cited chemists worldwide, been the recipient of numerous awards, accolades, and patents in his career, as well as authored numerous books on mass spectrometry, organic spectroscopy, and related reviews. Prof., Cooks` influential career in mass spectrometry research and technologies has resulted in several start-up companies (e.g. FLIR, Prosolia Inc., PurSpec, etc.). He received a Ph.D. from the University of Natal, South Africa with alkaloid chemist Prof. Frank L. Warren in 1965 and a Ph.D. from Cambridge University, Great Britain working with Dr. Peter Sykes in 1967. Graham has devoted his career to development of mass spectrometry methods and technologies to improve everyday life in the biological, environmental, forensic, materials, and analytical sciences. Prof. Cooks has been an ardent supporter of the Turkey Run Analytical Chemistry Conference from its onset. In addition to analytical chemistry he spends time gardening and following English literature.

In appreciation and recognition of his trailblazing career it is only fitting that Prof. Graham Cooks give the Keynote address at this year's Turkey Run Analytical Chemistry Conference!

ORAL PRESENTATIONS

LUSK ROOM



25 SEPTEMBER 2021 • LARK ROOM

ORAL SESSION

I

01

Machine Learning Framework for Accurate Prediction of Functional Groups from Tandem MS Experiments

Connor Beveridge (1), Prageeth R. Wijewardhane (1), Matthew Muhoberac (1), Nicolás M. Morato (1), Andreas Kaerner (2), Christopher J. Welch (3), Shane Tichy (4)
(1) *Purdue University*, (2) *Loxo Oncology @ Lily*, (3) *Indiana Consortium for Analytical Science and Engineering (ICASE)*, (4) *Agilent*

Structural elucidation of unknown compounds using tandem mass spectrometry (MS/MS) is an ongoing challenge. Expert chemists will often use common product ion peaks and neutral losses or peak matching software to predict structural aspects from MS/MS spectra, a process which is time consuming and limited by the molecular entries in the database.This work introduces a machine learning framework for the prediction of functional groups from MS/MS spectra without a need to search a database for prediction, as typically done. The models in this work are trained on data from the Mass Bank of North America (MoNA), a public database, and a custom MS/MS database acquired using a single high throughput desorption electrospray ionization (DESI) MS/MS platform from Professor Cooks Group. Additionally, a novel spectra representation is created for machine learning purposes by standardizing the spectra to the precursor ion m/z. Average molecular F1 of 87% (MoNA) and 76% (DESI) and average molecular accuracy of 94% (MoNA) and 87% (DESI) were obtained, indicating similar performance across databases towards validity of the machine learning framework

02

The MICRO Project: Hands-On, Inquiry-Based, Analytical Chemistry Labs on Paper

Rachel M. Roller (1), Jessica Zinna (1), Samantha Eyolfson (1), Kimberley A. Frederick (2), Renee S. Cole (3), Vincent T. Remcho (4), Marya Lieberman (1)
(1) *University of Notre Dame*, (2) *Skidmore College*, (3) *University of Iowa*, (4) *Oregon State*

The Making Introductory Courses Real while Online (MICRO) Project aims to create engaging, hands-on analytical chemistry experiments that are safe for both in-person and distance learning. By using paper microfluidic technology, MICRO labs cover traditional analytical lab techniques such as titrations, standard addition, calibration curves, and electrochemistry without relying on expensive instrumentation or hazardous chemicals. This presentation highlights a paper-microfluidics acid-base titration experiment, which has been used by over 2,000 general and analytical chemistry students at 20+ institutions in 2020-2021, and previews a lab that allows students to study enzyme kinetics and inhibitors with paper microfluidics. The titration experiment uses a paper microfluidic device with 13 wax-printed reaction zones containing varying concentrations of sodium hydroxide. This paper titrator can be used to measure the acidity of household acids such as vinegar, or to determine the solubility product constant of cream of tartar or baking soda. When adapted, it can be used to perform a variety of other experiments, including iodometric redox titrations and Job's method of continuous variation. Another experiment, which will demonstrate Michaelis-Menten enzyme kinetics and inhibition using a paper device and a cell phone camera, is currently in development. MICRO experiments cultivate scientific inquiry, and instructors who used MICRO labs report that their students were more engaged in the scientific process than in previous years. The MICRO Project offers an inexpensive way to teach inquiry-based analytical chemistry labs both inside and outside of the laboratory environment.

ORAL SESSION

I

03

Laser-induced Orbital Rotation of a Particle inside a Dual-Beam Optical Trap in Air

Amala Raj (1,) Bogdan Dragnea (1)
(1) *Indiana University*

Optical trapping offers a non-contact method for manipulation and characterization of microscopic particles and has found application as a powerful analytical technique in various scientific areas such as nanotechnology, biophysics, and many more [1]. To overcome the instabilities due to radiation pressure inherent to single beam traps in air, we constructed a counter-propagating dual beam trap with two focused, coaxial, near IR laser beams. Adding a transverse offset between the beams in this geometry of trapping, induced continuous orbital rotation of levitated micro-particles in air. Here, I will be presenting details of experimental and numerical analyses of particle dynamics in a dual-beam trap with transverse offset. By tuning the optical power, transverse offset between the beams, and the separation between the laser foci, different magnitudes of centrifugal forces were applied to a dielectric micro-particle levitated by optical forces. We found that silica microspheres can orbit up to a frequency of 2000 Hz at atmospheric pressure, which could be further increased by increasing the optical power, lowering the ambient pressure, or the particle diameter. We predict that the high Q factors achievable via orbital motion of a trapped particle will allow to apply the orbital trapping technique to probe surface reaction kinetics such as deposition, condensation, or sublimation on free single particles and microdroplets at atmospheric pressure by monitoring the change in orbital frequency and trajectory upon particle mass change.

1. D. Gao, et al., Optical Manipulation from the Microscale to the Nanoscale: Fundamentals, Advances and Prospects. Light: Science & Applications 2017, 6 (9).

04

High-throughput measurement of fatty acids on microbial colonies by optically-guided MALDI-TOF-MS workflow for screening enzyme mutant libraries

Kisurb Choe (1), Michael Jindra (2), Mason Pu (1), Huimin Zhao (1), Brian Pfleger (2), Jonathan Sweedler (1)
(1) *University of Illinois at Urbana Champaign*, (2) *University of Wisconsin at Madison*

Engineering an enzyme often involves creation of large numbers of mutants followed by screening the mutants to identify the variants that meet the engineering goal(s). The bottleneck for the process can be a high throughput assay to measure the chemical product of enzyme activity. For example, directed evolution of an enzyme is limited by the number of samples and the type of compounds that can be tested by the characterization approach.

A high throughput MALDI-ToF-MS workflow is developed for testing up to 5,000 enzyme mutants per day. The workflow measures the products of enzyme activity formed on microbial colonies in Petri dishes instead of liquid culture, greatly simplifying and accelerating the sample preparation and the chemical screen. A new web application has been created to enable image guided MALDI-ToF-MS analysis of randomly scattered microbial colonies, perform data analysis, and guide colony picking from Petri dishes. The computational tool is combined with an optimized sample preparation protocol that can prepare more than 3,000 colonies in 1 hr and achieve a reliable sensitivity for the MALDI-MS screen. By screening microbial colonies holding an enzyme mutant library, product profiles of three enzymes could be rapidly modified towards our desired goal. Built on commonly available experimental tools, the workflow is both easily implemented and readily adaptable by other labs.

ORAL SESSION

I

05

Suspension Stabilized Proteome Preparation (SSPP) for Long-Term Sample Storage and Transport of Proteomics Samples

C. Bruce Mousseau (1), Matthew M. Champion (1)
(1) *University of Notre Dame*

Efficient digestion of proteins into peptides is the standard for their identification and quantification using MS based proteomics approaches. Although robust and sensitive, these bottom-up methods are generally performed on fresh samples, in vitro cultured materials or preserved samples generated in laboratory or clinical environments. Conversely, genetic material can be extracted in situ in remote locations and preserved indefinitely without access to refrigeration, or sensitive reagents. As a consequence of this, there is virtually no capacity to perform proteomics experiments on remotely obtained samples or geographically distant clinical materials. This represents a significant barrier to progress in these potential research areas. In order to address this we have developed Suspension Stabilized Proteome Preparation (SSPP) a method for trapping and storing proteins on silica-based depth filters which can be completed in a single step using shelf-stable components. This process facilitates transport to equipped facilities for digestion and analysis. Proteins prepared by this approach are stable for extended periods of time at elevated temperatures based on rapid ageing studies. We were able to determine that proteins do not significantly refold or gain measurable activity over a two-week time period and peptides extracted from room-temperature and 37C stored samples for over a month are largely indistinguishable from new samples processed in parallel as measured by MALDI-TOF and LC-MS/MS. From this, we conclude that this is an effective method to prepare proteomics samples for future processing which does not require serial sample preparation with unstable reagents.

ORAL SESSION

II

06

Investigating interfacial phenomena with combined surface-sensitive spectroelectrochemistry

Kendrich Hatfield (1), Joaquín Rodríguez-López (1)
(1) *University of Illinois at Urbana-Champaign*

Electrochemical interfaces dictate the performance of a vast array of technologies, and elucidating their complex interfacial processes is paramount to understanding and improving operation. Scanning electrochemical microscopy (SECM), which uses a nano- to microscale electrode to probe surfaces, has arisen as a powerful tool to investigate parameters such as charge transfer kinetics and flux of electroactive species to/from the interface. However, SECM generally offers little information on chemical structure and speciation. We complement SECM with Raman spectroscopy, which gives rich vibrational information that helps identify chemical changes. Normal Raman spectroscopy is a low sensitivity technique, however, and therefore can be difficult to use to probe species restricted to the interfacial region. We leverage surface-enhanced Raman scattering (SERS), which is a many-fold signal enhancement phenomenon that occurs at certain nanostructured surfaces, to sensitively detect surface events while simultaneously using SECM to interrogate or induce surface electrochemistry.
Recently, we have shown the feasibility of SERS-SECM with a self-assembled monolayer of 4-mercaptopyridine on silver nanoparticles. We used 4-mercaptopyridines pH-dependent Raman signal to detect surface pH changes with SERS as we modulated the nearby pH with proton-coupled electrochemical reactions at an SECM probe. Currently, we are developing a system to investigate carbon electrodes with SERS-SECM. In particular, we are coating substrates with poly(3,4-ethylenedioxythiophene) (PEDOT), a prominent conductive polymer with potential applications in a variety of electronic devices, and applying SERS-SECM to better understand the link between its chemical structure and electrochemical reactivity. We hope this technique becomes applicable for a multitude of relevant interfaces in the future.

07

Molecular Characterization of Volatility-Fractionated Bio-Oil Surrogate of Fuel

Emily Halpern (1), Christopher P. West (1), Anusha P.S. Hettiyadura (1), Alexander Laskin (1)
(1) *Purdue University*

The chemical characterization of various volatility-separated fractions of bio-oils is very challenging due to the complexity of the mixture and the range of physicochemical properties of the components. It is essential to classify bio-oil components with respect to their major chemical types and functional groups to inform the deoxygenation processing of crude bio-oil surrogates and their viability as an energy source. Due to the range of volatilities of the molecular components, fractionation of the bulk bio-oil can be used to modify the composition so that it contains only components of interest. Here, we investigate chemical composition of volatility-segregated fractions of bio-oil separated using aerosol generation and sampling techniques. The molecular characterization of the bio-oil fractions was achieved using ultrahigh performance liquid chromatography interfaced with a photodiode array detector and high-resolution mass spectrometry (UHPLC-PDA-HRMS) with both electrospray ionization (ESI) and dopant-assisted atmospheric pressure photoionization (APPI). Molecular characterization allows description of the individual species present in the bio-oil sample based on estimated values of double bond equivalence, volatility, and elemental ratios. By comparing the mass absorption coefficients of bio-oil fractions with different volatility, we were able to show that the less volatile fractions absorb more than the bulk sample due to the evaporation of volatile compounds. Through calculations of DBE and volatility, we see that the volatile, fuel-like fractions appear in higher pressure fractions, allowing us to separate them from those that can be upgraded. This work provides insight on the molecular components of representative bio-oils and provides an opportunity to improve design and engineering of novel bio-oil fuels.

ORAL SESSION

II

O8

Automated Protein Sample Preparation at the Meso-Scale

Sadie R. Schultz (1), Matthew M. Champion (1)
(1) *University of Notre Dame*

Mass spectrometry-based proteomics is the dominant method for measuring protein and proteomes from complex mixtures. Bottom-up approaches are methods in which proteins are digested or proteolyzed prior to LC-MS/MS analysis. Peptides are fragmented, and proteins are inferred via peptide spectral matching. Throughput of these samples is surprisingly low; a core facility proteomics lab might analyze <20 samples/day per instrument using nanoLC-MS/MS. As a consequence of this, automation of proteomics is rare, and virtually all preparation is performed by hand. We have developed fully automated sample preparation procedures using a lower-cost Andrew Alliance pipetting robot. The robot uses traditional pipettes; simplifying the interface and making protocols transparent in that they closely mirror the steps a scientist takes. The robot utilizes a low-precision deck with an HD camera to correct for play and slap in the peripherals. This also enables agnostic sample inputs with respect to tube type; something common in labs. It is fully compatible with heaters, shakers, and vacuum manifolds necessary for these tasks. We have developed fully modular protocols for the major stages in proteomics preparation; denaturation/reduction/alkylation, protease digestion and reverse-phase solid phase extraction desalting. We have also developed stand-alone procedure for common secondary tasks in proteomics like Zip-Tip, and are developing procedures to perform automated MALDI-target spotting and mini-style filter based (S-Trap) digestions. The data generated is comparable or superior to manual preparation, less subject to random error and failures associated with manual repetitive tasks.

O9

Controllable Particle Trapping in Microfluidic Devices through Plasmonic Nanoaperture Array Generated Optical Traps

Brigham Pope (1), Mi Zhang (1), Ryan Jacobson (1), Suhun Jo (1), Joseph B. Holmes (1), Bogdan Dragnea (1), Stephen Jacobson (1)
(1) *Indiana University*

Optical traps, first invented by Arthur Ashkin,5 make possible a wide range of particle analytics that would be immensely beneficial in a microfluidic device. Plasmonic nanoapertures have often been used to integrate optical traps into a microfluidic channel, thereby eliminating intense alignment and beam-shaping requirements, though they typically only operate in the near-field where surface polarized polaritons dominate. In this work, we put forward nanoaperture arrays that operate in the Fresnel region, creating diffraction patterns that allow for trapping through the entire depth of a microchannel. Nanoaperture optical traps were modeled by multiple computational (discrete dipole approximation and COMSOL) and experimental (photolithographic mapping and fluorescence microscopy) models. We have successfully trapped fluorescently labeled polystyrene nanoparticles with diameters ranging from 2 μm to 20 nm. Further trapping and modelling experiments were conducted to delineate the advantages of plasmonic nanolens trapping over conventional optical traps. These advantages are: confinement, extension, and shaping of the trapping intensity pattern; plasmonic resonance for increased and controllable trapping power; and optical trap control that comes from optimized relative nanoaperture spacing. A quantitative analytic for characterizing nanoaperture traps is put forth. Future experiments will investigate the separative abilities of these nanoaperture arrays as well as apply said separations and other nanoaperture-aided analytics to the study of extracellular vesicles and their contents.

ORAL SESSION

II

O10

Charge switching chemistries for the structural elucidation of methyl branched lipids

Caitlin E. Randolph (1), Stephen J. Blanksby (2), Gaurav Chopra (1), Scott A. McLuckey (1)
(1) *Purdue University*, (2) *Queensland University of Technology*

While mass spectrometric platforms have become established techniques for lipid analysis, the extensive structural diversity of lipids remains a significant challenge. Branched fatty acids (FAs) are often saturated FAs containing one or more sites of methyl chain branching along the hydrocarbon backbone. Branched lipids, including branched chain FAs, are prevalent in nature, serving vital biochemical and biophysical roles. However, conventional MS-based techniques are particularly limited for the structural elucidation of saturated and branched lipids. Thus, mass spectrometric techniques capable of (1) discerning straight-chain lipid variants from their methyl branched counterparts and (2) assigning the site(s) of methyl chain branching in branched lipids are desirable. Here, we utilize charge switching strategies to reveal hidden features of lipid molecular structure.

In a first approach, a gas-phase ion/ion platform utilizing charge inversion reactions was employed for the structural elucidation of branched lipids. Here, FA anions, derived from either direct negative nESI of fatty acid structures or CID of complex lipid anions, are derivatized in the gas-phase with magnesium bis-terpyridine reagent dications to generate charge inverted [FA H + MgTerpy]+ complex cations. Predictable fragmentation patterns of charge-inverted FA complex cations permit unambiguous isomeric distinction of branched and non-branched FA molecular structures and confident identification of methyl branching point.

In an alternate approach, an online LC-MS/MS strategy with post-column charge switch derivatization is under development. Here, chromatographic separation of branched and non-branched FA isomers is first achieved. Following the separation of lipid isomers, post-column derivatization by an additional constant flow of magnesium bis-terpyridine reagent solution will yield a [FA H + MgTerpy]+ complex cation analogous to that generated in the gas-phase via ion/ion reactions. Subsequent collisional activation of charge-switched FA cations provides unique product ion spectra influenced by lipid structure. While a great deal of lipidomics workflows employing LC-MS/MS rely on retention times and comparison with authentic reference standards, this approach will eliminate the need for standards compounds, which are often not commercially available.

POSTER SESSION

A

LUSK ROOM

25 SEPTEMBER 2021 • 1:30- 2:45 PM • LARK ROOM

POSTER SESSION

GROUP A

A1

Design of a Capillary Isoelectric Focusing Electrospray Ionization-Mass Spectrometry Interface (cIEF-ESI-MS) With Robust Characteristics.

Caitlin Kerr (1), Bonnie Huge (1), Matthew Champion (1)
(1) *University of Notre Dame*

Proteomes are a complex mixture with high dynamic range and numerous proteoforms (protein isoforms). Due to this complexity, there is an unmet need to obtain higher-resolution separations of these isoforms, in particular for analysis using "Top-down" proteomics methods. Capillary electrophoresis is a powerful separation tool for biological samples. Two of the most popular modes of capillary electrophoresis are capillary zone electrophoresis (CZE) and capillary isoelectric focusing (cIEF). CZE has been used to conduct proteolytical analysis, but is limited by low loading capacity. In contrast, cIEF, which separates amphoteric molecules based on isoelectric points (pI), utilizes the entire separation volume, and is orthogonal to the separations achieved with CZE and reverse phase liquid chromatography. Coupling cIEF to Electrospray Ionization-Mass Spectrometry (ESI-MS) has been a challenge the past couple of decades. The concentration of ampholytes for high-resolution pH gradients is mutually exclusive with robust ESI. Currently, dilution of the ampholytes or off-line dialysis prior to MS have been used with success. However, dilution reduces the focusing power and capacity of cIEF. We have developed two on-line instrumental cIEF-ESI-MS techniques: (1) An in-line desalting device to diminish the ampholyte concentration prior to entering the mass spectrometer and (2) Paramagnetic ampholytes. We have coupled paramagnetic beads to ampholytes to mobilize and remove them at the ESI-interface using permanent magnets. Progress towards these interfaces will be presented.

A2

Self-supervised Clustering of Mass Spectrometry Imaging Data

Hang Hu (1), Jyothsna Padmakumar Bindu (1), Julia Laskin (1)
(1) *Purdue University*

Mass spectrometry imaging (MSI) is widely used for the label-free molecular mapping of biological samples. The identification of colocalized molecules in MSI data for understanding biochemical pathways is challenging since complex MSI data are too large for manual annotation. Conventional computational ion image colocalization methods underuse the spatial information. Meanwhile, the adaptation of deep learning methods is impeded by the small size of MSI data for training convolutional neural networks (CNN). Herein, we introduce a robust self-supervised clustering approach, which enables efficient colocalization of molecules in individual MSI data by retraining a CNN and learning representations of high-level molecular features without annotations.
MSI data of one mouse uterine tissue section obtained using nanospray desorption electrospray ionization (nano-DESI) was used as a benchmark. From these data, we manually selected 367 ion images and clustered them into 13 classes. In order to adapt a pre trained CNN, every ion image was converted into the RGB format. In the self-supervised clustering framework, we firstly re-trained a CNN encoder to learn ion image representations through contrastive learning. Next, ion images were clustered using a spectral clustering algorithm. Finally, we utilized self-labeling approach to fine-tune both the encoder and classifier with confidently classified ion images. The benchmark data was utilized for model evaluation. This method achieved 92.7% classification accuracy on the benchmark data without any manual annotation. Isotopic recall was also calculated to evaluate clustering results for unannotated MSI data.

POSTER SET-UP

11:45 AM - 1:30 PM, LARK ROOM

POSTER SESSION

GROUP A

A3

Fluorescence-Detected Mid-Infrared Photothermal Microscopy

Minghe Li (1), Aleksandr Razumtcev (1), Ruochen Yang (1), Youlin Liu (1), Lynne S. Taylor (1), Garth J. Simpson (1)
(1) *Purdue University*

Fluorescence-detected mid-infrared photothermal (F-PTIR) microscopy is demonstrated for sub-diffraction limited mid-infrared microspectroscopy of model systems and applied to probe phase transformations in amorphous solid dispersions. To overcome the diffraction limit in infrared imaging, highly localized temperature-dependent photothermal effect is an attractive alternative indicator to infrared absorption. Photothermal atomic force microscopy infrared spectroscopy (AFM-IR) achieves nanometer resolution by monitoring heat caused expansion but only restricted on the surface. For 3D imaging, optically detected photothermal infrared (O-PTIR) combines an infrared laser with a visible probe source with to transduce photothermal refractive index changes. The sensitivity of O-PTIR is ultimately limited by the relatively weak dependence of refractive index with temperature, exhibiting changes of ~0.01% per oC. Fluorescence-detected photothermal mid-infrared (F-PTIR) spectroscopy is demonstrated herein to support 3D imaging with improved photothermal sensitivity. In F-PTIR, temperature dependence of fluorescence quantum efficiency (~1-2% per oC) was shown to be a sensitive reporter on highly-localized absorption of infrared radiation. Utilizing the intrinsic high sensitivity of fluorescence-based detection, F-PTIR offers an order of magnitude improvement in signal to noise over the previously dominant O-PTIR. Furthermore, unlike O-PTIR, spatial resolution in F-PTIR is not theoretically limited by the diffraction limit of light as predicted by simulations. Initial F-PTIR proof of concept studies are described for microparticle assemblies of silica gel and polyethylene glycol, followed by applications of F-PTIR for analysis of localized composition within phase-separated domains induced by water vapor exposure of an amorphous solid dispersion (ritonavir in copovidone). Further work on label-free ultraviolet F-PTIR (UVF-PTIR) measurements based on two-photon excited intrinsic autofluorescence is demonstrated using tryptophan microcrystal.

A4

Automated DESI High Throughput Screening for Directed Evolution

MyPhuong T. Le (1), Rui Huang (2), Jared C. Lewis (2), Daniel Hu (3), Matthew M. Champion (3), Christopher J. Welch (4), Nicolás M. Morato (1), Dylan T. Holden (1), and R. Graham Cooks (1)
(1) *Purdue University*, 2 *Indiana University*, 3 *University of Notre Dame*, (4) *Center for Bioanalytical Metrology*

Directed evolution is a revolutionary technique where enzymes are iteratively mutated to become versatile synthetic catalysts. The ability to engineer and tailor enzymes holds promise for providing the capability to perform traditionally complicated chemical transformations with high specificity and efficiency. Thus, analytical methods and technologies that allow for the simplification and acceleration of directed evolution workflows are highly desirable. High throughput screening of successfully evolved colonies has previously been developed and proven to be of great utility. Here we demonstrate a workflow for the automated screening and analysis of live bacterial colonies directly from culture plates using the Purdue Make It high throughput platform. By using image recognition algorithms coupled with DESI-MS/MS analysis, we were able to directly and rapidly identify colonies with mutated RebH enzyme capable of facilitating the arene halogenation of a non-native substrate, tryptoline. Image-processing software was developed to identify bacteria colonies from photos of the culture plate using a Difference of Gaussians algorithm provided by the Scikit-image package . The coordinates of the colonies in relation to the DESI plateholder are automatically extracted. The optimal screening path (3 times faster than traditional spot-to-spot rastering) is determined prior to automated DESI screening of the culture plate.
Full MS screening revealed distinct spectra between the culture medium and bacteria colonies, in both of which the ionized substrate tryptoline (m/z 172) was visible. Signal for the chlorinated product (m/z 207), however, was of low intensity and isobaric with a background species. Tandem MS experiments on m/z 207 were successfully employed to confirm the presence of the desired product. Colonies were characterized most successfully by the presence of m/z 178 (fragment of chlorinated tryptoline) with high intensity relative to m/z 129 (fragment of the background signal at m/z 207). The ratio of m/z 178 to m/z 129 in the MS/MS spectra of m/z 207 could then be used distinguish successful and unsuccessful colonies. The process is non-destructive and requires minimal sample workup, thus it is expected to significantly accelerate directed evolution experimentation. Other modified microorganisms and substrates will be explored using this method.

POSTER SET-UP

11:45 AM - 1:30 PM, LARK ROOM

POSTER SESSION

GROUP A

A5

Diffusion Imaging by Fourier Transform-FRAP with Multiphoton-excited Patterned Illumination

Dustin Harmon (1), Andreas Geiger (1), Jiayue Rong (1), Ziyi Cao (1), Nita Takanti (1), Mazin Hakim (1), Luis Solorio (1), Garth Simpson (1)
(1) *Purdue University*

Multiphoton-excited Fourier transform fluorescence recovery after photobleaching (FT-FRAP) is implemented for quantitatively evaluating normal and anomalous diffusion and fractional recovery of proteins in complex matrices and heterogeneous samples. Diffusion characterization is routinely performed to quantify the mobility of proteins in cells, pharmacology, and food science. Conventional fluorescence recovery after photobleaching (FRAP) allows for the diffusion characterization while being noninvasive and rapid, however conventional point bleach FRAP suffers from low signal-to-noise due to shallow bleach depths, the need for precise knowledge of the photobleaching beam profile for accurate analysis, potential bias from sample heterogeneity, and poor compatibility with multiphoton excitation due to local heating. In pattern illuminated FT-FRAP, a custom nonlinear optical beam-scanning microscope enables a comb bleach profile spread over the field of view. The time-dependent fluorescence recovery is concentrated to points in the spatial Fourier domain leading to a large signal-to-noise enhancement. Analysis in the Fourier domain greatly simplifies the mathematical treatment as the dependence on the bleach profile is removed. Diffusion at multiple length scales can be quantified using the multiple spatial harmonics of the fluorescence recovery. Spatial-frequency peak shape analysis allows for the simultaneous determination of diffusion at every location in the field of view. Peaks in the spatial Fourier domain are shifted to the origin followed by an inverse Fourier transform to generate fluorescence recover maps. Binary masks are applied to segmented regions or each pixel is fit to a diffusion model to generate diffusion images.

A6

Measurement of the Gas Phase Stability of Immunoglobulin G by Cyclic Ion Mobility Spectrometry

Rachel Buckley (1), Lucas W. Henderson (1), Edie M. Sharon (1), David E. Clemmer (1)
(1) *Indiana University*

Immunoglobulin proteins possess a unique tertiary structure, consisting of light and heavy chain sequences of amino acids. This macromolecular structure plays a critical role in regulating the function of these proteins. Variable temperature nano-electrospray ionization (nESI) has previously been used to study the solution phase equilibrium conformational landscape of different proteins. Collisional activation has proved useful for probing and measuring the gas phase conformational landscape. Here, we use collisional activation (CID) to probe various solution phase landscapes for the protein Immunoglobulin G subclass two kappa (IgG2). Cyclic ion mobility (IMS) is used to enhance gas phase mobility separation. Varying degrees of activation were employed to characterize and understand the gas phase landscape.

POSTER SET-UP

11:45 AM - 1:30 PM, LARK ROOM

POSTER SESSION

GROUP A

A7

Single-Entity Electrocatalysis on Particle Ensembles Prepared by Template Synthesis

Natasha Siepser (1), Myunghoon Choi (1), Sasha E. Alden (1), Lane A. Baker (1)
(1) *Indiana University*

Within the electrochemistry field, there is growing interest in the synthesis of nanomaterials and the ability to investigate their properties at the single-entity level. Herein, we present a platform that combines template synthesis of Au tubule ensembles, particle electrodeposition, and a scanning droplet probe technique to individually measure the electrocatalytic activity of each particle or tubule. First, Au tubule ensembles were prepared by an electroless deposition protocol to fill the pores within a track-etched polycarbonate membrane with Au. Then, metal particles were electrodeposited on top of the Au tubules. The electrocatalytic activity at the particles and Au tubules were assessed at the single-entity level with correlative scanning electrochemical cell microscopy (SECCM) and electron microscopy. The presented particle preparation strategy offers advantages, over more traditional strategies, for single-entity studies, such as, zero background current signal due to the insulating nature of the polymer membrane support and controlled particle dispersity by selecting a porous membrane of desired pore density.

A8

Development of imaging-based spatial omics technology to study cellular and subcellular spatial architecture of biological systems

Marisa Asadian (1)
(1) *University of Illinois at Urbana-Champaign*

Imaging-based high-resolution spatial transcriptomics (I-HiRST) is a combinatorial and sequential fluorescence in situ hybridization (FISH) method that allows for mapping of the RNA at single-molecule level. I-HiRST technology captures heterogeneous RNA expressions with spatial context between cells in tissues, which provides a deeper understanding of differential RNA expression and intercellular interactions. Using our I-HiRST technology we have identified genes of human bone osteosarcoma (U2OS) cells and localized gene expression in the honey-bee brain. The combinatorial FISH-based RNA profiling, however, is not possible with either small cells or highly abundant genes. Additionally, studying ST of bacteria, which plays an important role in human health, is a largely unknown area that has been limited by our ability to see at 30-20 nm scale. To overcome these challenges, expansion microscopy (ExM) has been integrated into our I-HiRST technology, which increases the resolution in imaging by embedding the biological specimen in a swellable polymer, which expands linearly and isotropically when placed in an aqueous solution. In the conventional method of ST-ExM, an expansion factor of 2 has been demonstrated, however, an expansion factor of 8-10 is required for studying highly abundant genes and ST of bacteria. To further increase the expansion factor, I have utilized a new monomer, N,N-dimethylacrylamide (DMAA) in ST-ExM, where I was able to obtain an expansion factor of 10 in water and an expansion factor of 5 using saline sodium citrate (SSC). Iâ€™m currently working on improving DMAA expansion for ST, and studying its binding specificity to fluorescent dyes, DNA probes, and RNA. DMAA monomer will further be utilized in I-HiRST-ExM of the honey-bee brain, which will be the first study of its kind, with anticipation of an optimized ST-ExM to map the spatial organization of hundreds of RNA species in various small bacteria.

POSTER SET-UP

11:45 AM - 1:30 PM, LARK ROOM

POSTER SESSION

GROUP A

A9

Chemical Imaging of Atmospheric Biomass Burning Particles from Forest Fires Collected over Western USA

Felipe A. Rivera-Adorno (1), Jay M. Tomlin (1), Kevin A. Jankowski (1), Ryan C. Moffet (2), Matthew Marcus (3), Swarup China (4), Rebecca Washenfelder (5), Ann M. Middlebrook (5), Daniel Knopf (6), Lisa Azzarello (7), Alessandro Franchin (8), Jian Wang (9), Alexander Laskin (1)
(1) *Purdue University*, (2) *Sonoma Technology,* (3) *Lawrence Berkeley National Laboratory*, (4) *Pacific Northwest National Laboratory*, (5) *National Oceanic and Atmospheric Administration, (*6) *Stony Brook University*, (7) *York University*, (8) *National Center for Atmospheric Research*, (9) *Canadian Light Source Inc.*

Biomass burning aerosols (BBA) impact the atmospheric chemistry and physics by altering the radiative forcing and cloud formation propensity, which have further consequences on visibility, human health and climate. Variability in the chemical composition, viscosity, morphology and internal structure of individual BBA within smoke plumes play a vital role in atmospheric processes, such as gas-particle partitioning, ice nucleation and heterogeneous chemistry. To improve our understanding of the chemical and physical properties of BBA and how these change during atmospheric aging, samples were collected during the 2019 FIREX-AQ field study. An aerosol collector was used to sample ambient BBA particles for later chemical imaging. Scanning transmission X-ray microscopy (STXM) was used to study the internal mixing and chemical speciation of carbon, allowing us to distinguish between organic carbon, elemental carbon (soot), and inorganic components. Additionally, a scanning electron microscope (SEM) was applied to provide information on the size and morphology of particles, and elemental composition on a particle-by-particle basis. Our results suggested that daytime-collected samples were dominated by organic carbon, while nighttime samples had traces of inorganic material. SEM and STXM results showed differences between the morphology and viscosity of daytime and nighttime particles. Daytime samples were rich in liquid-like particles but after ageing, viscous particles where the dominant components. In contrast, nighttime particles appeared to be liquid-like, regardless of their distance from the emission source. Organic volume fraction measurements suggested that freshly emitted particles had higher contribution from organic components, compared with aged samples, which could imply the condensation of volatile organic compounds on the existing particles during atmospheric ageing. Ongoing work involves the correlation of our data with real-time records from co-deployed instruments that measured concentrations of trace gases, aerosol mass concentrations and optical properties.

A10

The effect of struvite and Fe-doped struvite on photochemical reactions of guaiacyl acetone in the presence of 3,4-dimethoxybenzaldehyde

Maria Misovich (1), Manoj Silva (2), Jonas Baltrusaitis (2), Alexander Laskin (1)
(1) *Purdue University*, (2) *Lehigh University*

Struvite (NH4MgPO4â€¢6H2O) is a low solubility mineral frequently found in fertilizers. Struvite fertilizers are advantageous because they release phosphorus slowly, reducing the probability of phosphorus runoff and eutrophication. Struvite synthesis is achieved by introducing MgO nanoparticles to an aqueous solution containing ammonium and phosphate ions. When doped with transition metals such as iron (Fe), MgO forms Fe-doped struvite. Guaiacyl acetone (GA), a prominent product found in biomass burning emissions, partitions rapidly into the aqueous phase, suggesting that it is a relevant proxy compound to represent organic species in terrestrial aquatic systems. When irradiated in the presence of triplet excited carbon (3C*), GA has been found to undergo rapid oxidation reactions to form monomeric and dimeric products along with pyrolytic-like products resulting from Norrish photochemistry. This study aims to determine the effect of struvite and Fe-doped struvite on the photoreactions of aqueous GA in the presence of 3,4-dimethoxybenzaldehyde (DMB), a source of 3C* frequently found in biomass burning emissions. Struvite serves as a heterogenous catalyst, while Fe-doped struvite introduces additional photochemical reactions into the aqueous system. A solar simulator was used to mimic sunlight. Three solutions were irradiated: a control solution containing only GA and DMB, a solution containing GA, DMB, and undoped struvite, and a solution containing GA, DMB, and Fe-doped struvite. Samples of the resulting reaction mixtures were collected at 0, 20, 60, and 120 minutes and filtered to remove struvite and colloidal material. Additionally, the nonpolar components were extracted into organic solvent before filtering. Chemical components of the mixtures were analyzed using reversed phase liquid chromatography interfaced with a photodiode array detector and an ESI-HRMS Orbitrap mass analyzer. Our results indicate that introducing struvite or Fe-doped struvite into the system results in the formation of several unique chromophores not found in the control system. Top down mass absorption coefficient (MAC) plots indicate that total absorbance decreases with irradiation in all three systems, but that the rate is impacted by the presence of struvite and Fe-doped struvite. Elemental formulas and structures were assigned for several chromophores.

POSTER SET-UP

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POSTER SESSION

GROUP A

A11

Abiotic Synthesis and Structural Elucidation of Unique Microdroplet-Generated Peptide Species

Dylan T. Holden (1), Nicolás M. Morato (1), R. Graham Cooks (1)
(1) *Purdue University*

Protein synthesis is a necessary process for both the creation and sustenance of life. This is typically achieved through the condensation of amino acids, a process that is thermodynamically and kinetically unfavorable in aqueous environments due to the elimination of a water molecule for each peptide bond formed. Largely facilitated in vivo by enzymatic reactions, a set of conditions permitting abiotic production of simple peptides from free amino acids in water is an essential prerequisite for the origin of life. The air-water interface of confined volume systems such as primordial atmospheric aerosols, protocells, or sea spray, has been shown to exhibit unique chemical reactivity compared to bulk solution and may provide a plausible locale to overcome entropic and energetic barriers in abiotic peptide synthesis. In this work we report the spontaneous formation of various dipeptides and dipeptide-like molecules from free amino acids in aqueous microdroplets formed by electrospray ionization and analyzed using tandem mass spectrometry (ESI-MS/MS) without the need for catalysts, salts, or modifications to pH. Product ion spectra for nearly all of the suspected dipeptide products match those of the corresponding reference compounds apart from the unusual and reproducible inclusion of one-to-two peaks of significant intensity. To our knowledge these fragment ions have not been previously reported. These findings, as well as spectra collected from further stages of MS, suggest the microdroplet-mediated synthesis of peptide structural isomers, highly complex rearrangement processes during fragmentation, and/or unusual site(s) of protonation on the presumed dipeptide. Structural elucidation of these species is inferred through a systematic study of the fragmentation profiles following variation of ionization and fragmentation conditions, as well as substrate functionalization and choice of solvent. We also report the use of pre-activation broadband waveforms to perturb the various ionic structures of isolated ions prior to fragmentation. This study exemplifies the unique reactivity of aqueous microdroplets and may provide greater insight into the role of interfacial reactions in prebiotic chemistry.

A12

Metabolic Profiling of Human Brain Tissue for Glioma Diagnosis by Targeted Desorption Electrospray Ionization Mass Spectrometry

Rong Chen (1), Hannah Marie Brown (1), R. Graham Cooks (1)
(1) *Purdue University*

Glioma is a highly invasive brain cancer, and its most effective treatment involves tumor resection during surgeries. The intraoperative distinction of glioma from surrounding normal tissue increasingly relies on molecular diagnostics, since it offers high sensitivity, near-immediate analysis, and clinically relevant information including prognostic genetic mutations. N-acetylaspartic acid (NAA) is recognized as a diagnostic metabolite of glioma and has been investigated by desorption electrospray ionization mass spectrometry (DESI-MS) to predict tumor cell percentage in glioma biopsies. The inclusion of additional diagnostic metabolites will likely improve the accuracy and robustness of the current DESI method.
To that end, we have conducted a systematic screening of glioma biomarkers using extracts from 32 unmodified human brain samples with known pathology. Specifically, full scan mass spectra in both polarities and the intensities of abundant transitions were recorded for each extract by nanoelectrospray (nESI). Statistical analysis was applied on MS data to unveil the most diagnostic molecular features; then molecular identities were assigned based on exact masses and fragmentation patterns. The most diagnostic biomarkers include gamma-aminobutyric acid (GABA), creatine, carnitine, hexane-1,2,3,4,5,6-hexol, as well as the established biomarker NAA. Subsequently, new DESI methods incorporating these five biomarkers were developed and their ion abundance ratios, instead of their absolute MS signals, were adopted for tissue characterization. The four best performing ratios were carnitine vs. creatine, creatine vs. arginine, GABA vs. choline, and hexol vs. NAA. When used to diagnose 29 freshly prepared brain smears, all showed sensitivities >90%, specificities >80%, and accuracies >85%. The enhanced diagnostic power offered by the inclusion of additional biomarkers and the fast sample analysis offered by DESI-MS (ca. 5min) allow rapid and accurate glioma diagnosis, which could prospectively guide glioma resection surgeries and improve patient outcomes.

POSTER SET-UP

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POSTER SESSION

GROUP A

A13

Accurate Characterization of Singly and Double Substituted Lindqvist Polyoxovanadates

Solita Wilson (1), Ellen Matson (2), Julia Laskin (1)
(1) *Purdue University*, (2) *University of Rochester*

Polyoxovanadates (POV) with a V6O7 core are capable of multielectron redox activity, so they are excellent candidates for applications in electrochemical technology. To enhance their chemical and redox properties, atom by atom metal doping is used to precisely construct these Lindquist metal cores. However, metal doped POVs are difficult to separate using traditional separation methods. This obstructs their accurate characterization of structural and redox properties. Mass spectrometry provides a unique opportunity to examine the structures of heterometallic POVs. In particular, ion soft-landing experiments combined with the in situ electrochemical techniques recently developed by our group enables the structural and electrochemical characterization of well-defined anions and cations purified in the gas phase. Therefore, ion soft-landing experiments is used to purify POV complexes and obtain measurements of their redox properties and infrared vibrations in the absence of interferences for the first time. Furthermore, the platform can be kept under vacuum and characterized in an absolute atmosphere providing precise characterization. We present the characterization of synergistic substitutions of 1 to 2 WO moiety into the homovanadate Lindqvist core [V6O7(OMe)12]. We observe a tunable anodic shift in potentials due to substitution of W metal. This is consistent with other single metal atom substitutions reported in the literature. Respectable quantitative electrochemical values can be extrapolated for the cyclic voltammograms and are then reported.

A14

Separation of submicron particles with in-plane nanofludic devices

Elizabeth A. Ruscitti (1), Tanner W. Young (1), Stephen C. Jacobson (1)
(1) *Indiana University*

We are interested in the continuous separation of submicron particles based on their hydrodynamic size without causing excessive strain or deformation of the particles of interest. The idea of performing liquid biopsies by analyzing extracellular vesicles (EVs) is just one example where a gentle, yet continuous separation method is desired. The most common methods of EV separation are ultracentrifugation, size-exclusion chromatography, flow cytometry, and immunoaffinity-based strategies. However, these methods are generally low throughput, may structurally damage the particles, and often require dilute samples. Here, we present microfluidic devices with in-plane nanoscale features that are milled with a focused ion beam (FIB) instrument to separate submicron particles. The separations combine flow, physical barriers, and inertial effects to fractionate these particles based on their hydrodynamic properties.

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POSTER SESSION

GROUP A

A15

Ion Current Rectification in Reconfigurable Membrane Filter Stacks

Michael P. Kappler (1), Stephen C. Jacobson (1)
(1) *Indiana University*

Ionic current rectification has garnered considerable attention over the past decade due to its role in many applications. For instance, the phenomenon is integral in nanofluidic circuitry to form diodes and transistors, pre-concentration of analytes of interest, and desalination processes. Ionic current rectifiers are capable of permselective transport of ions. Permselectivity is most often achieved through partial or complete overlap of the electric double layer across a nanoscale conduit which leads to preferential transport of counter-ions relative to co-ions. When asymmetry is applied to the system, this transport imbalance can yield high and low conductance states at applied potentials with equal magnitude and opposite polarity. There are a number of examples of device designs capable of producing non-ohmic current behavior; however, many ion current rectifying devices require expensive materials or fabrication techniques and are time-consuming to produce. In this work, we present an ionic current rectifier composed of stacked membrane filters, in which the filters have cylindrical pores and the stack induces the asymmetry. These devices are inexpensive and simple to fabricate and can be easily reconfigured to produce different rectification behavior. With rectifiers composed of polycarbonate track-etched (PCTE) membrane filters and double-sided tape, we have achieved rectification ratios up to 20 with excellent reproducibility.

A16

Broad-bandwidth Photothermal Microscopy for Real-time Studies of Nanoparticle-assisted Melting and Resolidification

Suhun Jo (1), William L. Schaich (1), Bogdan Dragnea (1)
(1) *Indiana University*

Interfacial effects and dependence of physical properties on size and shape can make phase change process strikingly different at nanoscale from those in bulk matter. A light-absorbing nanoparticle embedded in a material can thermally trigger phase transition which is tightly localized in space and time. Here, we present the concept of a broad-bandwidth photothermal microscopy, which enables monitoring such phase change processes with high spatial and temporal resolution. When a heating beam is absorbed by the nanoparticle, intensity of scattered probe light changes depending on physical state of the matrix. By measuring the transient intensity change vs time, we identified different dynamics of heat diffusion in solid/liquid state of fatty acids: faster in solid due to higher thermal conductivity. In addition, phase change in the vicinity of the nanoparticle and growing thickness of the melted layer under stronger heating light was experimentally observed for the sample. In order to have a deeper understanding of the results, a simulation model was developed and it showed good semi-quantitative agreement with the experimental results.

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POSTER SESSION

GROUP A

A17

Multipore Resistive-Pulse Sensing Characterization of Extracellular Vesicles

Tanner W. Young (1), Stephen C. Jacobson (1)
(1) *Indiana University*

Recently, research related to characterizing extracellular vesicles (EVs) has increased at a rapid rate, largely due to their influence in biological systems and potential impact in drug discovery. EVs are naturally produced, membrane-bound, nanoscale particles that are linked to cell-cell communication and propagation of diseases. The cargo carried by EVs mimics that of the parent cells from which they were derived and can be diagnostic of the parent cells that they originate from. Conventional characterization techniques for EVs include dynamic light scattering (DLS), nanoparticle tracking analysis (NTA), transmission electron microscopy (TEM), and more recently, charge detection mass spectrometry (CDMS). To make similar measurements in solution, we are developing resistive-pulse sensing devices with multiple pores in series, which are fabricated in-plane on glass substrates by focused ion beam (FIB) milling. Because resistive-pulse sensing characterizes individual particles, we can easily correlate their size and pore-to-pore times, unlike DLS and NTA, which provide distributions for entire populations. Precision of the resistive-pulse sensing is further improved by passing the particles through multiple pores in series. In this presentation, we will discuss fabrication and characterization of the nanofluidic devices and their application to the measurement of EVs from various sources, including bovine milk, human urine, and plants.

A18

Metabolomic and Lipidomic Profiling of Vegetative and Sporulated Bacillus subtilis by Rapid Microwave Induced Extraction

L. Edwin Gonzalez (1), Lucas J. Szawlinski (1), Brett Marsh (1), Anna Leech (2), Scott Donahue (2), Mitch Wells (2), R. Graham Cooks (1)
(1) *Purdue University*, (2) *FLIR Systems Inc.*

The detection of biological warfare agents has been of great interest since the anthrax attacks following the events of September 11, 2001. Anthrax is a lethal respiratory disease caused by Bacillus anthracis, a gram-positive bacterium that, when starved, produces an ultra-resistant spore coat. The Bacillus spore coat consists of multiple layers of laccases, superoxide dismutases and catalases, and dinuclear metalloproteins that effectively protect these organisms from extreme environmental conditions. This coat makes detection of the organism very difficult, and consequently hinders the timely responses to potential threats. Harsh conditions or prolonged exposure to toxic chemicals are able to break the spore coat, but they also damage the DNA and other biomolecules, such as dipicolinic acid (DPA), which are typically used for identification of this microorganism. Alternative strategies to remove the spore coat include inducing sporulated bacteria to revert to their vegetative state, so allowing for easier membrane rupture and DNA extraction. However, these methods pose a serious hazard to scientific and clinical staff. Detection of DPA and other biomarkers using mass spectrometry (MS) coupled to curie-point pyrolysis or MALDI has also proven of some interest, but they require inactivation of the spores prior to analysis or laborious sample preparation, which limit their point-of-care applicability. In this work we describe a new and simple methodology for the rapid (1 min) lysis of Bacillus spores using a conventional microwave oven. The obtained lysate is directly analyzed using nano-ESI MS, allowing the detection of DPA and characteristic lipids by tandem MS. Using Bacillus subtilis as a model organism, we compare differences in the lipid profiles between vegetative and sporulated bacteria, which allow for rapid discrimination between vegetative and sporulated states and maybe even species of Bacillus.
We would like to thank and acknowledge the Department of Homeland Security for their support of this work.

POSTER SET-UP

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POSTER SESSION

GROUP A

A19

SMART: Single Molecule Fluorescent Activation in Real Time for Molecular Computations and Sensing

Harshit Arora (1), Prof. Gaurav Chopra (1)
(1) *Purdue University*

Can molecules perform computations and respond to stimuli as logical and mathematical operations? Molecular logic gates have been used to perform diverse Boolean logic operations (e.g. AND, OR, XOR, NOR, NAND, INH, EnOR among many) either in combination or in sequence â€“ a field that have been greatly advanced in the last decade.1 Of several chemical systems, fluorescent molecules have gained tremendous momentum in building such logical circuits with multiple analytes (protons, metal ions, biomolecules etc.) as inputs and change(s) in the molecular fluorescence as one of the predominant outputs (or readouts). Recently, simple molecular logic gates have been developed with differential outputs (emission readout) in the presence of chemically and structurally similar bio-thiols such as cysteine (Cys), homocysteine (Hcy) and glutathione (GSH).2 In general, these three low-molecular weight bio-thiols are potent antioxidants that are often involved in the interception of reactive oxygen species (ROS) and other toxins thereby, regulating the complex cellular redox environment. However, the current logic gates have limitations: (i) the logic gates are too simplistic and do not have dependent responses that limit their use for complex logical circuits, (ii) there is limited ability to differentiate between responses of chemically and structurally similar molecules, such as Cys and Hcy bio-thiols. Specifically, current molecular logic gates use Cys and Hcy as one input that limit their ability to perform differentiable Boolean operations, and (iii) current logic gates are not resettable which is important while constructing a memory-based molecular logical circuit with possibilities of storing information in write-read-erasable format. We have addressed all these problems and have rationally constructed a resettable molecular logical circuit using an oxazinoindoline-based system as our SMART (Single Molecule Fluorescent Activation in Real Time) scaffold to yield contrasting outputs for differentiating structurally similar bio-thiols including a relay strategy with protic and aprotic solvents in combination with copper (II) ions. We expect our work to open new directions towards developing a molecular computer to sense complex chemical microenvironments.

1 Sundus, et al. Chem. Soc. Rev. 47.7 (2018): 2228-2248.
2. Longwei, et al. Chem. Comm. 53.98 (2017): 13168-13171.

A20

Pt/Polypyrrole Quasi-References Revisited: Robustness and Application in Electrochemical Energy Storage Research

Dipobrato Sarbapalli (1), Abhiroop Mishra (1), Joaquín Rodríguez-López (1)
(1) *University of Illinois at Urbana-Champaign*

The choice of reference electrodes for non-aqueous electrochemical measurements in the field of energy storage is often a challenge due to factors like: i) lengthy experiments (>1 day), ii) the lack of alternatives to the commonly used Ag/Ag+ reference electrode (RE), iii) introduction of junction potentials, and iv) the possibility of sample contamination from foreign ions. Therefore, quasi-reference electrodes (QREs) such as Ag wire and Li metal strip are preferred and utilized in such measurements. However, small changes in electrolyte composition can cause large potential drifts in quasi-reference electrode potentials, and their surfaces may be reactive to the solution. As a solution, we propose an alternative QRE based on polypyrrole electrodeposited on Pt wire (PPyQRE) encased in a glass tube with the open end sealed with commercial frits. While freestanding PPyQRE wires have been reported in the literature, simple encasing of the PPyQRE overcomes the above-mentioned drawbacks of QREs while providing a reliable reference potential that is closer to the performance of an RE. Testing with a redox mediator dissolved in solution via cyclic voltammetry and bulk electrolysis revealed a stable reference potential over multiple charge/discharge cycles with minimal drift (~5 mV) after ~2.25 days of operation, when using the encased PPyQREs. These references were also used in the testing of multi-layer graphene Li-ion anodes, which often involve cycling samples at highly reducing potentials (< 3 V vs. Fc/Fc+) over long durations (>1 day). While in the same testing conditions the Ag/Ag+ electrode led to observable Ag deposits on the graphene and large potential drifts (~50 mV), the PPyQRE exhibited no measurable drift, revealing changes in voltammetric features that were obscured by reference drift when using Ag/Ag+. These results highlight the advantages of using an encased PPyQRE as a simple and practical reference electrode for electrochemical measurements in the field of non-aqueous energy storage research.

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POSTER SESSION

GROUP A

A21

Amperometric Oxygen Sensors for Application in Energy Storage Systems

Abhiroop Mishra (1), Zachary T. Gossage (1), Dipobrato Sarbapalli (1), Md Sazzad Hossain (1), Joaquín Rodríguez-López (1)
(1) *University of Illinois at Urbana-Champaign*

In late 1990s, a lot of research efforts were focused on the development of ultramicroelectrodes (UME) based blood gas sensors. The mass-transfer limited current in these electrodes was shown to be proportional to the concentrations of the dissolved oxygen. Thereby, these sensors provide a convenient way to measure the amount of gases in the system of interest. Since the UME sensors work by facilitating the inner-sphere oxygen reduction reaction (ORR), their performance varies depending on electrode material and the nature of solution. The efficiency of these sensors in common aqueous and non-aqueous media is well documented, however, their performance in widely used non-aqueous battery electrolytes remains undemonstrated. Therefore, it is critical to fill this knowledge gap and to evaluate the performance of UME based oxygen sensors to extend their applicability for development of mitigation strategies for oxygen related degradation in the next-generation energy storage systems.
Here, we present a systematic study to evaluate the performance of different UME based oxygen sensors in the model electrolyte system of LiPF6 and TBAPF6 in ethylene carbonate:diethyl carbonate (1:1) respectively. Several sensors ranging from the traditional gold and platinum UMEs to the more recent polymer modified UMEs (Poly(3,4-ethylenedioxythiophene) or PEDOT) are investigated for the ORR. Additionally, the effect of Li-ions on ORR response at these probes is studied. The results suggest that ORR in the presence of Li-ions leads to the formation of an insoluble product which fouls the UME active surface. Li-ion concentration, as low as 5mM, prevents the attainment of mass-transfer limited steady-state current. The PEDOT UME turns out to be a promising candidate as it provides excellent selectivity towards ORR and is non-responsive towards other redox processes in the potential window of interest. Additionally, we also demonstrate the methodology for extracting useful parameters such as diffusion coefficient of oxygen in the given media using these probes. This work creates a foundation for combining the UME based probes with other advanced analytical techniques such as Scanning Electrochemical Microscopy for the real time investigation of processes such as gas evolution from electrodes and for elucidating oxygen related degradation mechanisms in different energy storage systems.

A22

Droplet Imbibition Mass Spectrometry

Taghi Sahraeian (1), Abraham Badu-Tawiah (1)
(1) *The Ohio State University*

Droplet imbibition technique has recently been introduced to the field of Mass Spectrometry (MS) with a multifaceted applicability. We hope to push the boundaries of detection strategies for fleeting intermediates to study different reactions mechanisms as well as ultrasensitive high throughput analysis for the diverse fields of application. In this work, we present a droplet imbibition (pickup) mass spectrometry experiment that allows short-lived intermediates to be captured in an “on-droplet” chemistry and hence, take advantage of surface activity and accelerated reaction rate of different species in real time. This methodology also enables the analysis of small volumes of complex mixtures directly and rapidly in an array fashion without sample preparations. This process offers ≤ 7 pg/mL sensitivity in picoliter analyte volumes and is applicable for direct analysis of proteins, lipids, and small organic compounds. Five individual samples can be analyzed in under 30 s without any carry over effects. The droplet imbibition MS platform uses an optimized glass capillary tip (tip size ~5 µm, with protruding edge of 7 mm in length) to contain the sample to be analyzed. The tip of the capillary is sampled by rapidly moving (~100 m/s) charged microdroplets derived from an electrospray emitter, which transfer the desorbed analyte directly to the MS inlet for subsequent characterization. This “on-droplet” experiment enabled us to elucidate the mechanism of Katritzky chemistry and Claisen rearrangement. The homemade array droplet imbibition setup was used for the first time to showcase the high-throughput capabilities of this technique. Demonstrated capabilities include 1) complex biofluid analysis without pre-treatment, 2) ultra-small volume analysis resulting in ultrasensitive detection, 3) surface effects leading to reduced matrix effects and high quantitative abilities, and 4) high throughput analysis of raw biological samples. Ultimately, droplet imbibition mass spectrometry showed extraordinary mechanistic and analytical capabilities including high throughput analysis and fast and reliable ultra-small volume biofluids detection.

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GROUP A

A23

pH-Responsive Chemical Tools for Glial Cells

Krupal P. Jethava (1), Palak Manchanda 1, Priya Prakash (1), Harshit Arora (1), Gaurav Chopra (1)
(1) *Purdue University*

Amyloid² (A²) accumulation is one of the major pathological hallmarks of Alzheimer's disease (AD). It is known that, in adult healthy brain, resident macrophages of the central nervous system called microglia are essential for clearing misfolded proteins like Aî² by engulfing the prey particles during phagocytosis by forming extended cellular processes. Microglial phagocytosis is essential to regulate brain function during health and disease. Impaired phagocytic function is related to the onset of AD and likely contributes to worsened disease outcome, but the underlying mechanisms of how this occurs remain poorly understood due to the lack of available tools. We have developed a well-characterized, human A²42 analogue (A² pH) that exhibits green fluorescence upon internalization into the acidic organelles of cells but is non-fluorescent at physiological pH. This allowed us to image, for the first time, glial uptake of A²pH in real-time in live animals. We find that microglia phagocytose more A²pH than astrocytes in culture, in brain slices, and in vivo. A²pH can be used to investigate the phagocytic mechanisms responsible for removing A² from the extracellular space, and thus could become a useful tool to study A² clearance at different stages of AD. In a similar manner, the development of pH-activable cell organelle targeting fluorescent probes will help control specific biochemical processes in live cells. To this end, we have developed a modular one-step synthetic strategy using a common reaction intermediate to obtain new lysosomal, mitochondrial and nucleus targeting pH-activable fluorescent probes based on a single boron dipyrromethane analogs. The divergent cell organelle targeting was achieved by synthesizing pH-activable fluorescent probes with specific functional group changes to the main scaffold resulting in differential fluorescence and pKa and show how functional transformation affects the cellular localization. We introduce a structure-organelle-relationship (SOR) framework targeting the nucleus, lysosomes, and mitochondria in primary mouse microglial cells. This work will result in future applications of SOR beyond imaging to target and control organelle-specific biochemical processes in disease-specific models.

A24

Development of Novel Small Molecule Dyes for Photodynamic Therapy and Photoacoustic Imaging

Catharine Brandy (1), Sarah Gardner (1), Jefferson Chan (1)
(1) *University of Illinois at Urbana-Champaign*

Reactive oxygen species (ROS) are transient and chemically reactive molecules often generated in the mitochondria. At endogenous concentrations, ROS have been shown to play a role in cellular signaling and redox homeostasis, but increased levels are associated with oxidative stress, can cause downstream damage to biomolecules, and can result in cellular apoptosis and necrosis. Photodynamic therapy takes advantage of this reactivity to kill diseased cells through the use of photosensitizers that generate ROS upon light activation. While this therapeutic technique is advantageous with spatial and temporal selectivity, current photosensitizers have limitations including shallow tissue penetration, white-light sensitivity, collateral damage of nearby healthy tissue, and high patient variability. To overcome some of these challenges, a novel near infrared (NIR) small molecule photosensitizer was developed, optimized, and evaluated. Various analogs of the hemicyanine dye (HD) scaffold were synthesized and assessed for their photosensitizing and general photophysical properties in vitro, in cellulo, and in vivo. It was demonstrated that modified HD dyes showed increased photosensitization capability, and red shifted absorbance and emission maxima. Current work is focused on utilizing the dyes for photodynamic therapy, as well as exploring the photoacoustic imaging capabilities of the molecule to allow for the development of a companion-based diagnostic imaging method at centimeter depths.

POSTER SET-UP

11:45 AM - 1:30 PM, LARK ROOM

POSTER SESSION

GROUP A

A25

Structural elucidation and isomeric differentiation/quantification of monophosphorylated phosphoinositides using gas-phase ion/ion reactions and dipolar DC activation

Kimberly Fabijanczuk (1), Hsi-Chun Chao (1), Scott McLuckey (1)
(1) *Purdue University*

Phosphoinositides, phosphorylated derivatives of phosphatidylinositols, are essential signaling phospholipids in all mammalian's cellular membranes. With 3 known phosphorylated derivatives of phosphatidylinositols at the 3-, 4-, and 5- positions along the myo-inositol ring, various fatty acyl chain lengths, and varying degrees of unsaturation, numerous isomers can be present.
Mass spectrometry (MS) has emerged as a powerful tool to analyze biomolecules, such as lipids which includes phosphoinositides. Currently, most approaches require solution-phase chemical derivations and extensive chromatographic separations prior to entrance to the mass spectrometer. These methods can be time consuming and result in loss of analyte during sample preparation. Shotgun-lipidomics has gained increasing popularity for lipid analysis due its fast and sensitive nature and requiring minimal sample volume without the need of prior chromatographic separation.
Shotgun-MS proves difficult to accurately identify and characterize phosphoinositides and their isomers. This work employs novel gas-phase ion chemistry to fully characterize phosphoinositides. The amount of phosphorylation and fatty acyl sum composition are readily obtained by ion-trap CID. Utilizing sequential ion/ion reactions and subsequent activation, differentiation and quantitative information can be gained of the isomeric pairs.

A26

High-Throughput Screening of Catalysts for Anode Reaction in Electro-catalytic CO2 Co-conversion Flow Cells

Raghuram Gaddam (1), Emiliana Cofell (1), Yuanya Zhao (1)
(1) *University of Illinois at Urbana-Champaign*

It is of critical importance to curb CO2 emissions, and one of the lucrative methods to achieve this is through electrochemical reduction of CO2 (CO2RR) to fuels and value-added products. Furthermore, coupling a CO2 flow-electrolysis system with renewable energy can help us achieve net-zero carbon emissions. Current co-electrolysis infrastructure employs Oxygen Evolution Reaction (OER) as the anode reaction. However, this is a relatively slow, and energy-intensive endothermic reaction. In this poster, we propose the oxidation of feedstock molecules as a more desirable alternative to OER in these CO2-reduction flow cells. One such feedstock molecule is Glycerol, which is a widely available and cheap by-product of soap and biodiesel production. Recently, our collaborators reported that a CO2 Reduction-Glycerol Oxidation co-electrolysis flow system reduces costs by over 50% as compared to a CO2RR-ORR flow system.
Just like OER, the Glycerol Oxidation Reaction (GOR) is also a catalytic process, and it is essential to explore catalysts for these reactions. In this poster, we showcase how Scanning Electrochemical Cell Microscopy (SECCM) can be employed to screen bi-metallic catalysts in a high-throughput fashion. SECCM is based on the Scanning Electrochemical Microscopy (SECM) technique, where instead of a standard Ultramicroelectrode (UME), we use a micro-pipette containing the species of interest to probe substrate surfaces.
Herein, we demonstrate the working of the SECCM technique using a standard redox mediator (Ferrocene). We then show the repeatability of the technique for the Glycerol Oxidation Reaction as well. Apart from probing standard solid substrates, it is also important for us to probe Gas Diffusion Electrodes (GDEs). GDEs are porous electrodes that enable the diffusion of gaseous species from one side to the other side where they interact with a catalyst layer and the electrolyte. Finally, we also show that even the GDEs can be probed reliably by this technique.

POSTER SET-UP

11:45 AM - 1:30 PM, LARK ROOM

POSTER SESSION

GROUP A

A27

Comprehensive Chemical Characterization of Nanoplastic Particles from Urban Emission Source

Ana C. Morales (1), Jay M. Tomlin (1), Christopher P. West (1), Felipe Rivera-Adorno (1), Yoorae Noh (1), Ryan C. Moffet (2), Swarup China (2), Brian T. O'Callahan (2), Patrick Z. El-Khoury (2), Andrew J. Whelton (1), Alexander Laskin (1)
(1) *Purdue University*, (2) *Pacific Northwest National Laboratory*

Nanoplastic particles are important and inadequately characterized environmental pollutants with significant adverse effects on aquatic and atmospheric systems, causing drastic impacts on human health through inhalation, ingestion, and skin penetration. The EnvNP investigated in this study were discovered in samples of multi-phase waste materials (i.e., water vapor, partially cured resin, particulates) emitted at urban sewer repair sites, where the operation process called plastic cured-in-place-pipes (CIPP) was employed. The CIPP installation procedure involves the chemical manufacture of a new plastic pipe inside an existing damaged pipe by injecting steam into the pipe, resulting in the generation and release of EnvNP and other chemicals into the air. Chemical imaging of the dry aerosol particles generated from the discharged waste showed abundant presence of small EnvNP particles in the size range of 100-500 nm, where smaller particles showed a higher degree of oxygenation. We use a combination of mass spectrometry techniques to enable molecular characterization of the EnvNP constituents and spectro-microscopy techniques to elucidate size distributions, morphology, and internal structures of EnvNP at the nanometer scale. This work provides a detailed description on the chemical composition of individual EnvNP particles related to CIPP manufacture, which is important in evaluating their contributions to urban environment.

A28

Unexpected Oxidations of Aromatic Sulfones to Sulfonic Acids in Microdroplets

Linggi Qiu (1), Michael Daniel Psimos (1), R. Graham Cooks (1)
(1) *Purdue University*

Droplet chemistry has attracted much attention due to its unique properties. Chemical reactions can be dramatically accelerated in droplets, enabling rapid synthesis and high throughput screening. Apart from enhanced reaction rates, reactions in microdroplets can exhibit completely different reactivities that are not observed in bulk reaction. Here we reported an unusual oxidation of aromatic sulfone to sulfonic acid in microdroplets under ambient condition without addition of acid, base or catalyst. The analogous reaction under conventional conditions (in bulk solution) requires either harsh conditions, such as strong base with an external promoter, or well-designed metal catalysts. Highly oxidative species - more powerful than hydrogen peroxide/hydroxyl radical - are produced in microdroplets and believed to be the oxidants.

The transformation from 4,4-sulfonylbis(2-methylphenol) (SBMP) to 4-hydroxy-3-methylbenzenesulfonic acid was observed in the methanol droplets generated by nano-electrospray ionization (n-ESI). Optimization of reaction conditions was followed by evaluation of efficiency by mass spectrometry analysis as the ratio of the ion intensity of the product to the total ion intensities of both the reactant and product. Higher conversion was observed with increased concentration of SBMP: it ranged from 0.55% to 49% with the concentrations from 0.1 mM to 20 mM. Changing the solvent from methanol to acetonitrile increased the conversion from 16% to 78%, suggesting that the reaction might be quenched by protic solvents. This assumption was supported by the result that the addition of small amount of water (5%) in acetonitrile caused conversion to drop from 78% to 25%.

The mechanism of this unexpected oxidation was studied. The addition of aqueous H2O2 or gaseous hydroxyl radical showed no increase in the conversion, demonstrating that hydrogen peroxide/hydroxyl radical, which is reported as the major reason for spontaneous oxidation in aqueous microdroplet, is not the oxidant in SBMP oxidation. Lower conversions were observed when this reaction was performed in the presence of a radical scavenger (TEMPO), proton acceptor (NH3) or electron donor (formic acid), suggesting that water radical cation generated at gas/solution interface might be the oxidant.

POSTER SET-UP

11:45 AM - 1:30 PM, LARK ROOM

POSTER SESSION

GROUP A

A29

Permeability and Breakdown of Tight Junctions in MDCKII Cell Monolayers

Cody Leasor (1), Kaixiang Huang (1), Lane A. Baker (1)
(1) *Indiana University*

The blood brain barrier (BBB) establishes the privileged domain of the central nervous system, regulating transport of molecules, ions and biochemicals with incredible selectivity. Dysfunction of the BBB has been implicated in neurological diseases such as Alzheimer's disease and amyotrophic lateral sclerosis. We aim to better understand the breakdown of the BBB and other tissue barriers by exploring the stability of tight junctions in a model epithelial cell line, Madin-Darby Canine Kidney II (MDCKII). Here, potentiometric-scanning ion conductance microscopy is used to non-invasively and simultaneously probe topographical and conductance maps of the MDCKII cell monolayers that are grown onto porous polyethylene membranes within a perfusion cell. To facilitate the breakdown of this model cellular system, a well-studied calcium chelator, EGTA, is applied to the basolateral side of the cell monolayers to weaken the cell-cell tight junctions by chelation of Ca2+ ions that bind junctional adhesion molecules. Additional preliminary work on advanced models of the BBB will also be described that provide a more relevant model of true in vivo systems.

A30

Reaction Acceleration in Bubbles: Katritzky Reaction in presence of surfactant to produce bubbles

Yanyang Hu (1), Lingqi Qiu (1), Brett Marsh (1), R. Graham Cooks (1)
(1) *Purdue University*

The rates at which chemical reactions proceed are fundamentally important. It has become clear over the past decade, that reactions in confined volumes such as thin films or microdroplets have enhanced reaction rate constants. The key explanation for the rate enhancement is the gas-liquid interface area due to (i) partial solvation of reagents at the gas-liquid interface which reduces the critical energy of reaction and (ii) strong electric fields at the interface that assists in bond making. Here we present a simple novel approach to accelerate reactions with a larger scale in bubbles generated by a continuous gas-feed to a solution. The 2 mL reaction solution with surfactant and bubbles gives 35-fold increase in surface-to-volume ratio compared to bulk and provides up to 190-fold acceleration for the commonly studied Katritzky transamination reaction. The results suggest that the reaction is a surface/near-surface phenomenon and there is no acceleration except that associated with the surface. Furthermore, the surfactant increases the apparent acceleration factor by a factor of 5, and this could be due to the weakening of surface tension or other physical or chemical effects of the surfactant.

POSTER SET-UP

11:45 AM - 1:30 PM, LARK ROOM

POSTER SESSION

GROUP A

A31

Fast-Speed Kinetics Information Extraction from Scanning Electrochemical Microscopy Facilitated by Machine Learning and Finite-Element Analysis

Yuanya Zhao (1), Joaquín Rodríguez-López (1)
(1) *University of Illinois at Urbana-Champaign*

In a lot of cases, researchers find themselves in situations where analytical expressions for processes of interest are not readily available. Generally, computational simulations are turned to for help under such circumstances to fit experimental data to simulated ones, extrapolating desired characteristic parameters of the tested system. Manual fitting is usually low-efficient and time-consuming especially for complicated settings due to both potential interactions between impacts of different properties and large ranges of possible values for each variable. In this study, the power of machine learning, a computational technology that has attracted a numerous amount of research attention across STEM fields and beyond, is utilized to speed up this process, enabling fast data analysis. The idea is applied to an scanning electrochemical microscopy (SECM) study where oxygen reaction reaction (ORR) catalysts are examined for their performance of conducting 2e- ORR. No analytical solution for the desired kinetic parameters (k0, ±, and selectivity) has been established due to the complexity of the system - both 2e- and 4e- ORR are happening simultaneously on the catalyst and furthermore, the current passing through each catalyst spot isn't accessible. The three parameters of interest affect acquired SECM data that embeds catalytic activities of each catalyst (a tip ORR LSV profile) concurrently. Despite the challenges intrinsic to this experimental setup, a good fitting between simulated and experimental data was achieved by machine learning in an efficient manner. An convolutional neural network was built and trained to accomplish this task. It took ORR LSV data as input and output a corresponding set of k0, ±, and selectivity. Simulated data acquired with COMSOL including a semi-exhaustive combination of the three target parameters were used as training data. When fed with experimental LSV files, the neural network predicted three target parameters that gave a simulated LSV curve well-fitted to the real-world data.

A32

Solid-Phase Extraction-Contained-Electrospray Ionization Mass Spectrometry for Rapid Analysis of Complex Lipid Mixtures

Benjamin Burris (1), Nava Ramazanli (1), Abraham Badu-Tawiah (1)
(1) *The Ohio State University*

Microreactors such as charged microdroplets and thin films, promote accelerated rates for chemical reactions. Given the novelty of this field, the application of microreactors to large biomolecular systems is limited and the practical applications of such techniques have not yet manifested in clinical settings. In the present study, the contained-electrospray ionization (contained-ESI) mass spectrometry (MS) platform is coupled to solid-phase extraction (SPE) to perform on-line analysis of complex lipid solutions. The application of contained-ESI platform to perform accelerated hydrolysis of lipids by lipase enzymes has already been shown to be capable of accelerating the rates of hydrolysis by two to three orders of magnitude of neat lipid solutions but studying complex mixtures remains challenging without pre-treatment or separations techniques. Home-packed solid-phase extraction cartridges are produced using silica-based sorbent and are connected to a home-built contained-electrospray platform. The contained-ES platform contains four variable inputs: sheath gas, two reagents (lipase and lipid), and headspace vapor. These four variables can be modulated to finely tune reaction conditions within a cavity to promote mixing and accelerated reactions between lipase and lipids. Lipid samples can be introduced from the SPE column directly into the contained-ES platform. Neat samples of lipids were prepared using a variety of acyl chain lengths and headgroup identities and rates of hydrolysis for the bulk conditions and the droplet conditions were compared using an established protocol to reliably extract lipid classes. The culmination of the work is the application of such a platform to the analysis of a biological sample. At present the work contains preliminary data to demonstrate the efficacy of the platform to retain a wide array of lipids from a lipid sample derived from human plasma.

POSTER SET-UP

11:45 AM - 1:30 PM, LARK ROOM

POSTER SESSION

GROUP A

A33

Use of Variable Temperature ESI-MS to Probe the Thermodynamics of Proteins, Protein Complexes, and Other Biological Molecules

Kristie Baker (1), Philip Lacey (1), Benjamin Jones (1), Vicki Wysocki (1)
(1) *The Ohio State University*

A variable temperature electrospray ionization source, provided by the Russell lab of Texas A&M University and coupled with mass spectrometry (vT-ESI-MS), allows for specific control over solution temperature before analytes enter the instrument. A thermoelectric chip is utilized to allow for cooling and heating of the solution to temperatures within a range of roughly 5-100C. Nano-electrospray mass spectrometry allows for a protein complexs native conformation to be retained in the gas-phase; thus, solution-phase changes such as thermal denaturation or dissociation of bound ligands will be reflected in the subsequent mass spectrum as a function of solution temperature as long as there is no gas-phase restructuring on the timescale of the MS measurement. These solution-phase changes can be observed through differences in charge state distribution and the deconvolved mass. Fragmentation methods, such as surface-induced dissociation (SID), can further characterize the large biological molecules through fragmentation patterns and retention, or lack, of bound ligand following fragmentation. Results will be presented for both protein complexes (streptavidin: biotin, C-Reactive protein: phosphocholine Ca2+), and tRNA.

A34

Implementation of a Digitally Driven Dual Quadrupole (qQ) System on an Extended Mass Range (EMR) Orbitrap via the HCD Cell

Benjamin Jones (1), Jacob W. McCabe (2), Thomas E. Walker (2), Sophie R Harvey (1), Kristie L. Baker (1), Adam P Huntley (3), Dalton T. Snyder (1), Gordon A. Anderson (4), Peter T. A. Reilly (3), David H Russell (2), Vicki H. Wysocki (1)
(1) *The Ohio State University*, (2) *Texas A&M University*, (3) *Washington State University*, (4) *GAA Custom Electronics*

Native mass spectrometry (nMS) is a powerful analytical tool to study the structure of proteins and protein complexes in the gas phase. nMS retains non-covalent interactions into the gas phase using gentle or cool ion transfer conditions that minimize ion activation. A Reverse-Entry Ion Source (REIS), developed in the Russell lab at Texas A&M University is optimized for efficient desolvation while minimizing ion activation; this enables the introduction of high mass protein complex ions to an Orbitrap via the HCD cell. The REIS has been modified to include a differentially pumped dual quadrupole system between the ionization source and the transfer region to the HCD cell. The first quadrupole, denoted q1 is a collisional activation region allowing for removal of adducts or residual solvent via collision-induced activation. The second quadrupole, denoted Q2 is a digitally driven selection quadrupole, implemented using technology developed in the Reilly lab at Washington State University, allowing high mass selection that has been demonstrated up to ~12,000 m/z using GroEL, an 801 kDa 14mer protein complex. This configuration enables the study of mass selected ions that have been collisionally activated in q1 for adduct removal and further interrogation by HCD after mass selection. This instrument can be operated in a complex-down or top-down mode by adjusting the activation potentials in q1 and in the HCD cell. The modular design of this instrument platform enables the addition of additional technologies to the system. Drift tube ion mobility has been installed on the system at Texas A&M university (Russell lab) following the dual quadrupole system and surface-induced dissociation is being installed on the system at The Ohio State University (Wysocki lab). The technologies will then be coupled in a qQ-SID-IM-Orbitrap configuration enabling high resolution ion mobility, and mass studies of complex protein complex systems.

POSTER SET-UP

11:45 AM - 1:30 PM, LARK ROOM

POSTER SESSION

GROUP A

A35

Molecular Investigation of the Multi-Phase Photochemistry of Fe(III)-Citrate in Environmental Water Mimics

Christopher P. West (1), Jackson Ryan (1), Ana C. Morales (1), Maria M. Misovich (1), Anusha P. S. Hettiyadura (1), Felipe Rivera-Adorno (1), Jay M. Tomlin (1), Andrew Darmody (1), Peng Lin (1), Brittany N. Linn (1), Alexander Laskin (1)
(1) *Purdue University*

Upon dissolution of FeIII into various natural aquatic systems, organic carboxylic acids efficiently chelate FeIII to form photo-catalytically active [FeIII-carboxylate]2+ complexes that undergo a wide range of photochemistry-induced radical reactions. The chemical composition and environmental transformations of these mixtures are ambiguous, making it challenging to estimate their environmental impact. To investigate photochemical processing of FeIII-carboxylates at molecular-level, we conduct comprehensive experimental study employing UV-visible spectroscopy, liquid chromatography coupled to photodiode array and high-resolution mass spectrometry, FlowCam, and spectro-microscopy imaging. In this study, aqueous solutions of FeIII-citrate were photolyzed under 365 nm light and apparent quantum yield of Ð¤ ~ 0.02, followed by in-depth chemical analysis of reacted mixtures withdrawn at different times of the experiment. The apparent photochemical reaction kinetics was expressed as two generalized consecutive reactions of Reactants (R),Intermediates (I), Products (P) with the reported rate constants of j1 ~ 0.12 min-1 and j2 ~ 0.05 min-1, respectively. In this generalization, R depicts a range of dissolved FeIII-citrate initial components, I corresponds to FeII-aqua/organic intermediates, and P represents final reaction products. Molecular characterization of the photolyzed solutions indicates that R and I compounds are water-soluble organic and Fe-organic species, while P compounds are a mixture of water-soluble and colloidal materials. The latter were identified as Fe-carbonaceous colloids of ~ 0.3 and 5.5 µm sizes formed at long photolysis times. The carbonaceous content of these colloids was identified as unsaturated organic species with low oxygen, indicative of their plausible pyrolytic-like formation mechanism at oxygen-deprived conditions typical for the extensively photolyzed mixtures. Based on the molecular characterization results, we discuss the comprehensive reaction mechanism of the FeIII-citrate photochemistry and report on the formation of previously unexplored colloidal reaction products, which may contribute to atmospheric and terrestrial light-absorbing material in aquatic environment.

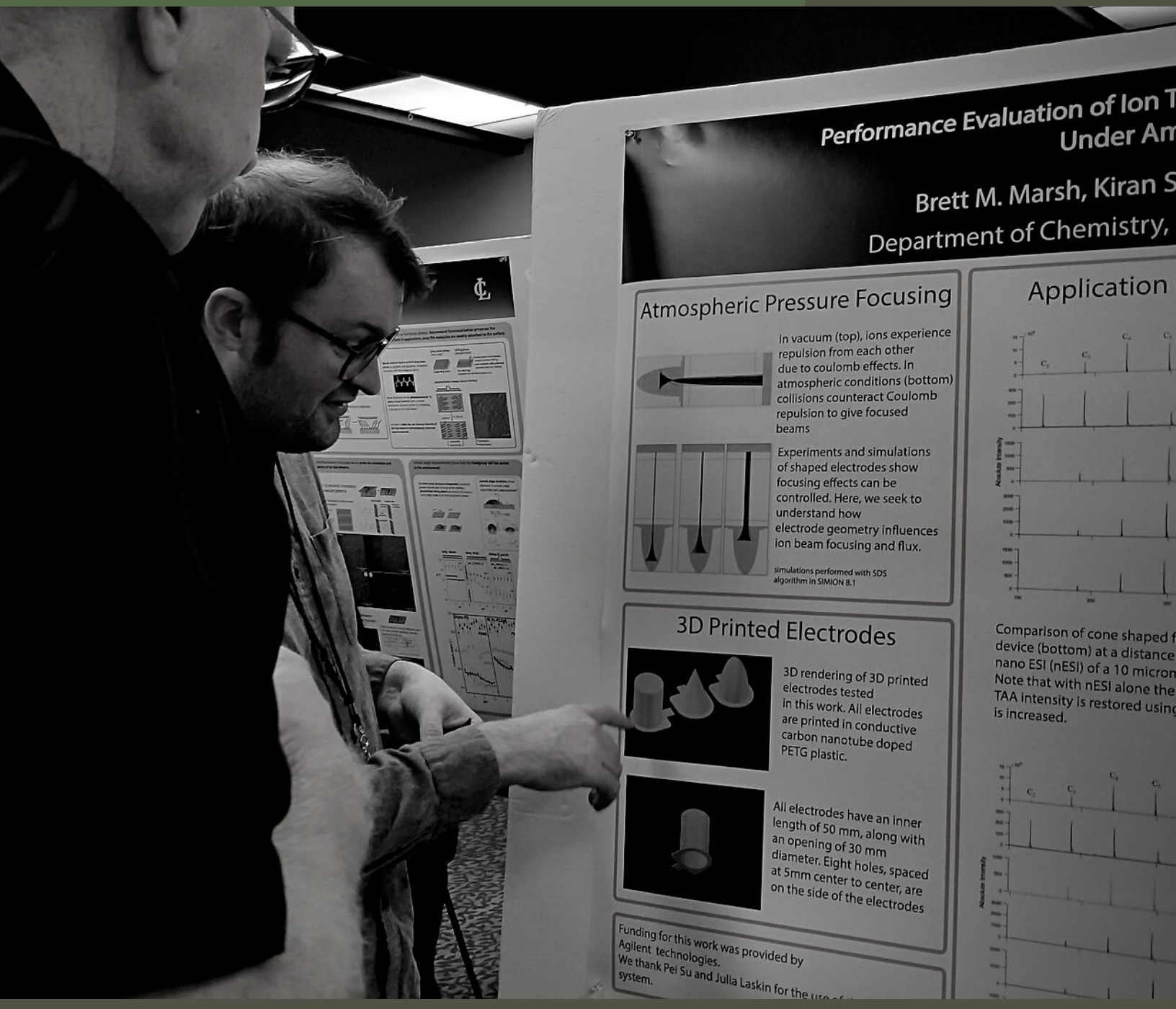
POSTER SET-UP

11:45 AM - 1:30 PM, LARK ROOM

POSTER SESSION

B

LUSK ROOM



25 SEPTEMBER 2021 • 3:00- 4:15 PM • LARK ROOM

POSTER SESSION

GROUP B

B1

High-spatial Resolution Imaging and Identification of isomeric and isobaric lipids using Nano-DESI Coupled to Ion Mobility Spectrometry

Daisy Unsihuay (1), Ruichuan Yin (1), Daniela Mesa Sanchez (1), Manxi Yang (1), Yingju Li (1), Xiaofei Sun (1), Sudhansu K. Dey (1), Julia Laskin (1)
(1) *Purdue University*

Herein, we describe the design and implementation of a portable nano-DESI platform onto an Agilent 6560 IM-QTOF system for improved lipid imaging of biological tissues. Proof-of concept experiments using mouse uterine sections demonstrate that simultaneous spatial localization and on-the-fly characterization of lipids can be performed with high-spatial resolution of better than 25 Âµm. IM separation allows us to distinguish between different species observed in nano-DESI MSI experiments based on the systematic trends in drift times observed for different types of adducts and levels of unsaturation. Moreover, calculation of the CCS values substantially improves the chemical specificity thereby providing unambiguous identification of endogenous lipid species.

We demonstrate the power of IM separation for distinguishing different localization of isomeric species, whichcannot be achieved based on the accurate m/z measurement. Specifically, we use peak deconvolution to extract ion images of isomeric species that are not well separated in our instrument. For example, we found the presence of two isomers after deconvoluting a broad peak centered at m/z 343.2272. We identified this molecule as hydroxydocosahexaenoic acid (HDoHE), which is the oxidized form of FA 22:6. We hypothesized that the two isomeric components result from the addition of the OH group to different double bonds in the fatty acyl chain. Upon matching our experimental values to CCS databases, we identified the two isomers as 14-HDoHE and 17-HDoHE. Fractional distribution images used to visualize the relative abundance of each isomeric component, reveals lower abundance of14-HDoHE in the luminal epithelium region of the mouse uterine tissue in comparison with 17-HDoHE.

Furthermore, IM separation efficiently eliminates isobaric and isomeric interferences originating from solvent peaks, overlapping isotopic peaks of endogenous molecules extracted from the tissue, and in-source fragmentation, which is critical to obtaining accurate concentration gradients in the sample using MSI.

B2

Enhancement of Lipid Signals with Ammonium Fluoride in negative mode nano-DESI Mass Spectrometry Imaging

Miranda Weigand (1), Manxi Yang (1), Hang Hu (1), and Julia Laskin (1)
(1) *Purdue University*

Lipids play an important role in many biological processes and their structural diversity presents challenges for untargeted mass spectrometry analysis. Nanospray desorption electrospray ionization mass spectrometry imaging (nano-DESI MSI) enables ambient imaging of biological tissue sample utilizes a tailored solvent for extraction of analytes. Herein, we use nanospray desorption electrospray ionization mass spectrometry imaging (nano-DESI MSI) to explore the use of a solvent additive for enhanced detection of lipids in mouse tissues. Although lipid classes including, fatty acids and phospholipids are readily observed in nano-DESI MSI, other lipid classes such as eicosanoids and glycosphingolipids are difficult to detect due to their low abundance and low ionization efficiency in negative ion mode. We evaluated the ability of ammonium fluoride (NH4F) to improve detection of lipids in negative ion mode and observed that lipids detected as [M-H]- ions were improved 10-460-fold with the use of NH4F added to the solvent. Nano-DESI MSI experiments performed using NH4F enabled enhanced imaging of low abundant lipids without any adverse effect on the noise level. Overall, our results demonstrate improved sensitivity for MSI of fatty acids and phospholipids observed on biological tissues.

POSTER SET-UP

11:45 AM - 1:30 PM, LARK ROOM

POSTER SESSION

GROUP B

B3

Automating Optimization of Experimental Parameters for Pulsed Introduction of Neutral Reagents in Tandem Mass Spectrometry Experiments Based on Diagnostic Gas-phase Ion-molecule Reactions

Armen Beck (1), Ruth Anyaeche (1) ,Prageeth Wijewardhane (1), Judy Kuan-Yu Liu (1), Kawthar Alzarieni (1), Jifa Zhang (1), Sanjay Iyer (1), Hilkka Kenttämaa (1), Gaurav Chopra (1)
(1) *Purdue University*

A method is being developed to automate the complete analytical cycle to carry-out diagnostic gas-phase ion-molecule reactions with unknown analytes. The process has been divided into four sub-tasks: 1) optimization of experimental parameters for pulsed introduction of neutral reagents used for diagnostic gas-phase ion-molecule reactions in linear quadrupole ion trap mass spectrometers, 2) selecting best neutral reagents to be used for a given analyte, 3) autonomous ion-molecule reaction analysis, and 4) interfacing developed modules with the instrument to make it fully autonomous. Two critically important parameters are the time that the neutral reagent is pulsed into the mass spectrometer (pulsing time) and the time that is used to pump out the reagent (pumping time) before pulsed introduction of the next reagent. Currently, one must examine each reagent and inlet channel individually while varying the pulsing time and the pumping time in order to manually optimize these times. The parameter optimization has been prototyped with employment of the Paddy software package around the Paddy Field Algorithm, a genetic optimization algorithm that propagates via a Gaussian process without direct inference of the underlying objective function. Moreover, the selection of neutral reagents as well as the analysis of diagnostic product formation is currently done manually. The neutral reagent selection module which is being developed incorporates a hybrid methodology which use an expert-based model as well as a machine learning based decision tree model. Finally, the analysis will be done in an automated expert-based manner. Our goal is to develop a full autonomous system which uses a genetic algorithm to optimize two parameters for any neutral reagent introduced into a LTQ XL linear quadrupole ion trap mass spectrometer via a 9-pulse-valve reagent introduction system and use individual modules to identify plausible neutral reagents for a given unknown analyte as well as analyze results to give plausible functionalities of the unknown analyte. This autonomous system which is being developed can be extended to any mass spectrometry devices across industry and academia, with a human-in-the-loop prototype currently under development.

B4

Fully Autonomous Platform for Tandem Mass Spectrometry Experiments Based on Diagnostic Gas-phase Ion-molecule Reactions

Prageeth Wijewardhane (1), Armen Beck (1), Ruth Anyaeche (1), Judy Kuan-Yu Liu (1), Kawthar Alzarien (1), Jifa Zhang (1), Sanjay Iyer (1), Hilkka Kenttämaa (1), and Gaurav Chopra (1)
(1) *Purdue University*

We are developing a methodological framework automate the complete analytical cycle to carry-out diagnostic gas-phase ion-molecule reactions with unknown analytes. The process has been divided into four sub-tasks: 1) optimization of experimental parameters for pulsed introduction of neutral reagents used for diagnostic gas-phase ion-molecule reactions in linear quadrupole ion trap mass spectrometers, 2) selecting best neutral reagents to be used for a given analyte, 3) autonomous ion-molecule reaction analysis, and 4) interfacing developed modules with the instrument to make it fully autonomous. Two critically important parameters are the time that the neutral reagent is pulsed into the mass spectrometer (pulsing time) and the time that is used to pump out the reagent (pumping time) before pulsed introduction of the next reagent. Currently, one must examine each reagent and inlet channel individually while varying the pulsing time and the pumping time in order to manually optimize these times. The parameter optimization has been prototyped with employment of the Paddy software package around the Paddy Field Algorithm, a genetic optimization algorithm that propagates via a Gaussian process without direct inference of the underlying objective function. Moreover, the selection of neutral reagents as well as the analysis of diagnostic product formation is currently done manually. The neutral reagent selection module which is being developed incorporates a hybrid methodology which use an expert-based model as well as a machine learning based decision tree model. Finally, the analysis will be done in an automated expert-based manner. Our goal is to develop a full autonomous system which uses a genetic algorithm to optimize two parameters for any neutral reagent introduced into a LTQ XL linear quadrupole ion trap mass spectrometer via a 9-pulse-valve reagent introduction system and use individual modules to identify plausible neutral reagents for a given unknown analyte as well as analyze results to give plausible functionalities of the unknown analyte. This autonomous system will be extended to any mass spectrometry instruments across industry and academia, with a human-in-the-loop prototype being developed.

POSTER SET-UP

11:45 AM - 1:30 PM, LARK ROOM

POSTER SESSION

GROUP B

B5

Proteoform-selective imaging of tissues using mass spectrometry

Manxi Yang (1), Hang Hu (1), Pei Su (2), Paul M. Thomas (2), Jeannie M. Camarillo (2), Joseph B. Greer (2), Bryan P. Early (2), Ryan T. Fellers (2), Neil L. Kelleher (2), Julia Laskin (1)
(1) *Purdue University*, (2) *Northwestern University*

Post-translational modifications dramatically increase the complexity of the proteome and affect protein structure and activity, which determine their function in biological systems. Ambient ionization plays an important role in studying proteoforms. Its high sensitivity and ability to generate multiply charged protein ions make it a powerful tool for top-down proteomic analysis of intact proteins. However, traditional proteomics workflows do not preserve the spatial information. Nanospray desorption electrospray ionization (nano-DESI), an ambient ionization technique, which relies on a localized liquid extraction and electrospray-like ionization, is an excellent tool for mass spectrometry imaging (MSI) of proteoforms. Herein, we report first results of proteoform-selective imaging of tissue sections using nano-DESI MSI. Our experiments reveal region-specific differences in proteoform concentrations in tissues. Rat brain tissue sections were used as a model system. Tissue sections were delipidated by washes in ethanol solutions and chloroform before nano-DESI MSI. MSI experiments were performed on a Q-Exactive HF-X Orbitrap mass spectrometer equipped with a custom-designed nano-DESI source. Proteoforms were extracted into the liquid bridge formed between two fused capillaries using of ACN/H2O/CH3COOH (65/34/1, v/v/v) as a working solvent and ionized by ESI at the mass spectrometer inlet. On-tissue top-down proteomics experiments were performed using targeted MS/MS on an adjacent section with higher-energy collisional dissociation. Proteoforms were identified by matching their intact masses and MS/MS data against the database. We characterized the spatial distributions of more than thirty proteoforms of sixteen proteins in rat brain tissue sections. In general, modified proteoforms show a similar localization to the corresponding unmodified proteins, which is consistent with the expression of their coding genes in specific regions. Differences in proteoform localization are revealed by examining ratio images generated by plotting the ratio of the individual proteoform signal to the sum of signals of all proteoforms of a particular protein in each pixel of the image. The differential expression of individual proteoforms across the tissue section reflects differences in the biochemical pathways associated with different PTMs.

B6

Molecular-Specific Photolysis of Atmospheric Brown Carbon

Diego Calderon Arrieta (1), Ana Morales (1), Anusha Hettiyadura (1), Chunlin Li (2), Yinon Ruddich (2), Alexander Laskin (1)
(1) *Purdue University*, (2) *Weizmann Institute of Science*

Light-absorbing organic aerosol (aka Brown Carbon) produced by biomass burning (BB) has a significant impact on global and regional air quality, public health, and climate. in this work we investigate molecular composition of BrC and its atmospheric transformations in laboratory experiments simulating their photolitically induced transformations. We probe composition and optical properties of individual BrC species using high performance liquid chromatography (HPLC) equipped with a photodiode array (PDA) detector for UV-visible analysis of separated chromophores along with high resolution mass spectrometry (HRMS) for compositional analysis. Results of the HPLC-PDA-HRMS analysis reveal composition-specific atmospheric lifetimes of BrC species, indicating highly complex physicochemical properties of atmospheric BrC. This study provides insight to the atmospheric ageing of BrC in BB emission plumes.

POSTER SET-UP

11:45 AM - 1:30 PM, LARK ROOM

POSTER SESSION

GROUP B

B7

Photoacoustic probe for biopsy-free assessment of copper status in murine models of Wilson's disease and liver metastasis

Melissa Lucero (1), Shengzhang Su (1), Joe Forzano (1), Jefferson Chan (1)
(1) *University of Illinois at Urbana-Champaign*

The development of photoacoustic (PA) probes that can monitor disease biomarkers in deep-tissue has the potential to replace invasive medical procedures such as biopsies. PA imaging is a powerful technique that uses light to generate sound waves within tissue which can be detected as ultrasound to obtain high resolution images in vivo. However, such probes must be highly optimized for in vivo performance and exhibit an exceptional safety profile. In this study, we have developed PACu-1, the first PA probe designed for biopsy-free assessment (BFA) of hepatic Cu via PA imaging. PACu-1 features a Cu(I)-responsive trigger appended to an aza-BODIPY dye platform that has been optimized for ratiometric sensing. Owing to its excellent performance, we were able to detect basal levels of Cu in healthy wildtype mice. To evaluate the performance of PACu-1 for the detection of elevated Cu, we employed a Wilson's disease model and a liver metastasis model. Briefly, Wilson's disease is a genetic disorder characterized by accumulation of Cu in the liver due to a defect in the ATP7B Cu exporter. Additionally, hepatic Cu has been
shown to be elevated in cancer metastasis. To further showcase the potential impact of PACu-1 for BFA, we designed and conducted two blind studies where in the first study we were able to successfully identify a WD animal from a group of healthy control mice and, in the second study, we were able to stratify a group of 12 animals (6 WD and 6 wildtype) with greater than 99.7% confidence.

B8

Modification of a hemicyanine platform for optimized deep tissue photoacoustic imaging

Sarah H Gardner (1), Catharine J Brady (1), Cameron C Keeton (1), Dr. Anuj K Yadav (1), Melissa Y Lucero (1) Shengzhang Su (1), and Jefferson K Chan (1)
(*1) University of Illinois at Urbana-Champaign*

Photoacoustic (PA) imaging is emerging as a powerful imaging modality due to its increased depth penetration, resolution, and low background compared to similar modalities (i.e. fluorescence). However, since most PA imaging agents are repurposed fluorescent molecules, many lack the photophysical properties ideal for PA imaging, such as a low fluorescent quantum yield, low pKa, and high extinction coefficient. We, therefore, aimed to optimize the popular hemicyanine dye platform to meet these needs and allow for deep tissue PA imaging. To this end, we generated PA-HD, a hemicyanine dye with an endocyclic sulfur and chloride group ortho to the alcohol handle. These modifications additionally led to a red shifted absorption, which we predicted would allow for ratiometric imaging by shifting the caped imaging agent into the NIR window. By appending triggers for common analytes (H_2O_2, ^{2}-galactosidase, and nitroreductase) in cancer and Alzheimer's disease, we showed the generalizability of this platform to generate activatable probes. Finally, we used these three probes to perform ratiometric tumor and brain imaging, which was impossible with the previous hemicyanine platform.

POSTER SET-UP

11:45 AM - 1:30 PM, LARK ROOM

POSTER SESSION

GROUP B

B9

Ambient Merging of Ion Beams Using Conductive Meshes of Defined Geometric Curvatures

Saquib Rahman (1), Brett M. Marsh (1), R. Graham Cooks (1)
(1) *Purdue University*

A roadblock to increasing sensitivity in ionization mass spectrometry is the low rate of ion transfer from an ambient ion source to the detector. Since nESI ionization efficiencies are often < 10%, the most straightforward way to increase ion current is to multiplex emitters. Experiments with two nESI emitters containing two different tetraalkylammonium bromide solutions sprayed through a curved mesh into the mass spectrometer show both species appearing at reasonable relative ion intensities in the corresponding mass spectrum, while only one of the species appears at a reasonable ion intensity in the absence of the mesh. IonCCD images collected with two emitters and a curved mesh reveal that the beam profile from the two emitters is indeed merged to some degree. Varying the degree of curvature of the mesh as expected, changed the extent of beam merging, with meshes with lower degrees of parabolic curvature showing a greater separation between the beam profiles from the two emitters. In addition to varying the mesh curvature, experiments with the mass spectrometer also revealed that a DC voltage applied to the mesh can change the spatial distribution of ions entering the inlet. To further understand these phenomena, the effect of changing the angle between the emitters, the tip diameter of the emitter, as well as the addition of more emitters were also investigated in similar experiments.

B10

Manipulation of Ion Types via Gas-Phase Ion/Ion Chemistry for the Structural Characterization of the Glycan Moiety on Gangliosides

Hsi-Chun Chao (1), Scott A. McLuckey (1)
(1) *Purdue University*

Gangliosides consist of a glycan head moiety containing one or more sialic acids and a ceramide chain. The analysis of glycan moiety among different subclass gangliosides, including GM, GD, and GT gangliosides, categorized based on the numbers of sialic acid, remains a challenge for shotgun lipidomics. We present a novel approach coupling shotgun MS and gas-phase ion chemistry to modify the ganglioside anions for differentiation of the glycan moiety among different groups of gangliosides. The followed ion-trap collisional induced dissociation allows us to better characterize the glycan moiety from the targeted gangliosides. For GM3 and GM1 gangliosides, elimination of possible contamination is achieved via a simple charge inversion reaction in the gas phase. Besides, we can identify the possibly fucosylated sites on the fucose conjugated GM1 gangliosides. Isomeric differentiation among GD1a and GD1b pair, and GT1a, GT1b, and GT1c group is also accomplished while performing different gas-phase ion/ion reactions, which are simple and rapid for the reaction. We also proposed a workflow for profiling gangliosides from biological samples. The proposed workflow was applied to analyze the porcine brain, and a total of 34 gangliosides were profiled among only 20 m/z values. We also proposed a strategy using pure component product ion spectra couple with total least square method to relatively quantify two isomeric pairs, GD1a/b-C36:1 and GD1a/b-C38:1. The results demonstrated the applicability and strength of using the shotgun mass spectrometry coupled with gas-phase ion/ion chemistry to characterize the glycan moiety structures on different subclasses from gangliosides.

POSTER SET-UP

11:45 AM - 1:30 PM, LARK ROOM

POSTER SESSION

GROUP B

B11

Multiagent consensus equilibrium in molecular and electronic structure determination

Jiayue Rong (1)
(1) *University of Illinois at Urbana-Champaign*

MACE is demonstrated for the integration of experimental observables as constraints in molecular structure determination and for the systematic merging of multiple computational architectures. MACE is founded on simultaneously determining the equilibrium point between multiple experimental and/or computational agents; the returned state description (e.g., atomic coordinates for molecular structure) represents the intersection of each manifold and is not equivalent to the average optimum state for each agent. The moment of inertia, determined directly from microwave spectroscopy measurements, serves to illustrate the mechanism through which MACE evaluations merge experimental and quantum chemical modeling. MACE results reported combine gradient descent optimization of each ab initio agent with an agent that predicts chemical structure based on root-mean-square deviation of the predicted inertia tensor with experimentally measured moments of inertia. Successful model fusion for several small molecules was achieved as well as the larger molecule solketal. Fusing a model of moment of inertia, an underdetermined predictor of structure, with low cost computational methods yielded structure determination performance comparable to standard computational methods such as MP2/cc-pVTZ, and greater agreement with experimental observables.

B12

Global Discovery of Sequence Bias in Substitution Translational Errors

Taylor Lundgren (1), Matthew Champion (1), Patricia Clark (1)
(1) *University of Notre Dame*

Ribosomal fidelity is integral to cellular health. Aminoglycoside antibiotics compromise ribosomal fidelity to kill bacteria. Understanding the biochemical basis of ribosomal fidelity is a key to improving antibiotic therapies. Previous measurement of substitutions in aminoglycoside treated E. coli via mass-spectrometry found substitutions were sequence dependent and not random. Substitutions identified in steady-state protein populations carry an undetermined survivorship bias for stable proteins and may not reflect real substitution frequencies. We performed global quantification of peptides and substitutions from whole-cell and a puromycin enriched nascent-chain proteome of E. coli in the presence and absence of sub-lethal amounts of kanamycin. We found nascent peptides isolated using this approach were enriched for substitutions changing charge or hydropathy. Three substitutions (D to M, M to F, N to W) were significantly increased following kanamycin treatment in nascent but not in mature peptide fractions. Our results suggest a subset of the proteome is degraded or rendered undetectable after synthesis, representing a population of missing biochemical data. Ultimately, understanding actual translation error frequencies may allow for better antibiotic treatment.

POSTER SET-UP

11:45 AM - 1:30 PM, LARK ROOM

POSTER SESSION

GROUP B

B13

Acetylation Dynamics in Mycobacterium tuberculosis Revealed Using Trapped Ion-Mobility Spectrometry and PASEF Proteomics

Daniel D. Hu (1), Kathleen R. Nicholson (1), Patricia A. Champion (1), Matthew M. Champion (1)
(1) *University of Notre Dame*

Mycobacterium tuberculosis (M. tb), the cause of tuberculosis, is an infectious disease that kills more than 2 million people/yr. M. tb survives intercellular uptake by macrophages in part by shifting metabolism to utilize long-chain fatty acids (FA) and cholesterols (CHO) as carbon sources. This induces a large change in gene expression, resulting in phenotypes required for the pathogen to multiply. We previously observed that pathogenic Mycobacteria also modulate the number of post-translationally modified (PTM) proteins with N-terminal protein acetylation (NTA). NTA is the modification of an acyl group to the ±-amino protein N terminus. It is implicated in protein stability, pathogenesis, sub-cellular targeting and other functions. NTA is catalyzed using an acetyl-CoA acyl-donor. Acetyl-CoA is essential for the metabolism of FA and CHO, which are essential for pathogenesis. Thus, we hypothesize that bacterial growth on FA and CHO modulate the NT-acetylome to effect disease. Utilizing the high depth and coverage provided by TIMS-PASEF-MS/MS, we measured and quantified the N-termini from 441 proteins in Mycobacteria grown on Cholesterol, Octanoate, or Glycerol. This includes at least 6 proteins associated with pathogenesis. Here, we demonstrate that protein acetylation is divergent on bacteria grown in CHO or FA as compared to glycerol. We performed these measurements at different growth times and prove that acetylation is temporally regulated. We developed a visualization and scoring factor to measure the contribution changes in the acetylation of specific proteins due to increases in occupancy of the acyl-site in contrast to changes in protein expression.

B14

Pulse-picking coherent anti-Stokes Raman scattering microscopy for highly sensitive chemical imaging

Matthew Clark (1), Gil Gonzalez (1), Chi Zhang (1)
(1) *Purdue University*

Coherent Raman scattering (CRS) microscopy is advantageous in chemical and biological imaging due to its increased sensitivity (106) over conventional spontaneous Raman imaging. However, the generated signal in CRS is still orders of magnitude weaker than in fluorescence imaging. Recent developments have demonstrated high sensitivity improvement, even down to single-molecule detection. Though, these developments require the use of exogenous Raman tags or metal surfaces. We introduce a pulse-picking technology based on an acousto-optic modulator (AOM) to significantly increase sensitivity for coherent anti-Stokes Raman (CARS). The AOM is driven by a function generator with modulation frequency and duty cycle control. This pulse-picking enhances the pulse peak power at low duty cycles while maintaining the same average power. We demonstrate an over 1000-times improvement in the sensitivity for CARS imaging. This method also improved the sensitivity of second harmonic generation (SHG) and two-photon excitation fluorescence (TPEF) imaging about 20-times. Our method generates strong TPEF and SHG signals using picosecond lasers with very low laser power (~10 mW on the sample) while maintaining high CARS spectral resolution for high chemical selectivity. The low excitation laser power minimizes phototoxicity for imaging live biological samples. Using cell and tissue samples, we highlight the potential of our pulse-picking technology for highly sensitive label-free multimodal chemical imaging.

POSTER SET-UP

11:45 AM - 1:30 PM, LARK ROOM

POSTER SESSION

GROUP B

B15

Generative Adversarial Linear Discriminant Analysis

Ziyi Cao (1), Youlin Liu (1), Casey J Smith (1), Alex M Sherman (1), Garth Simpson (1)
(1) *Purdue University*

Generative adversarial linear discriminant analysis (GALDA) is demonstrated to enable full-dimension linear discriminant analysis (LDA) of Raman spectral data sets in which the number of parameters p greatly exceeds the number of measurements n (i.e., p>n). LDA is arguably the simplest supervised method for dimension reduction, retaining validity of common statistical tests lost in nonlinear analyses such as those employing artificial neural networks. Herein, we demonstrate linear generative adversarial strategies to address "overfitting" complications that commonly restrict the direct use of LDA at full dimension. Although inspired by the successes of generative adversarial neural networks (GANs) for minimizing overfitting artifacts in artificial neural networks, GALDA was built around an independent linear algebra framework distinct from those in GANs. Performance metrics were evaluated for GALDA together with other commonly available supervised and unsupervised methods for dimension reduction in simulated spectra generated an open-source Raman database (Romanian Database of Raman Spectroscopy). Following these proof-of-concept evaluations, resolution and overfitting were evaluated for GALDA and other common dimension reduction methods for Raman spectra derived from microscopy measurements of microsphereroids of the blood thinner clopidogrel bisulfate. From these collective results, the potential scope of use for GALDA is critically evaluated relative to alternative established spectral dimension reduction methods.

B16

PhyloTox: A phylogenomic approach to predicting species sensitivity across the Tree of Life

Ziyu Wang (1), Jonathan A. Karty (1), Jason A. Coral (1), Stephen P. Gaholt (1), Maria Bondesson (1), Jason M. Tennesson (1), Stephen C. Jacobson (1), Joseph R. Shaw (1)
(1) *Indiana University*

PhyloTox is a phylogenetic toxicological approach that uses a diverse suite of animal models to identify the functions of evolutionarily conserved groups of genes, metabolites, and biomolecular interactions. We are developing a proof-of-concept for chemical safety assessment that will help to solve the enormous public health crisis caused by human exposure to chemical pollutants. PhyloTox draws insights on gene functions by disrupting entire networks through chemical exposure with distantly related organisms. Through the highly interdisciplinary mix of genomics, metabolomics, evolutionary theory, bioinformatics and toxicology, we can better classify the potential effects across the Tree of Life based on the evolutionarily conserved molecular pathways of response.
In our current work, toxicological assays of chemicals, e.g., arsenic, on model organisms were conducted to establish concentration thresholds, where toxic benchmarks were determined. Metabolomic responses that were chemically induced were quantitatively measured for several organisms, e.g., zebrafish, fruit flies, and water fleas, with nano-electrospray-direct infusion-mass spectrometry (nESI-DI-MS). Significantly changing metabolites were revealed through machine-learning computational approaches and further characterized by targeted tandem MS analysis. With the cluster and structural information, chemically affected pathways were statistically assessed. To conclude, we have established a workflow for metabolomics related to the PhyloTox approach, and future work will correlate the observed metabolic changes with transcriptomic responses.

POSTER SET-UP

11:45 AM - 1:30 PM, LARK ROOM

POSTER SESSION

GROUP B

B17

Recent advances in deployability of paper-based field test for illicit drugs

Kathleen Hayes (1), Heather Whitehead (1), Christopher Sweet (1), Marya Lieberman (1)
(1) *University of Notre Dame*

Interest in presumptive field tests for illicit drug detection has increased in recent years as deaths from opioid overdoses have risen. Previously, a microfluidic paper analytical device for detecting (idPAD) was described that sensitively and specifically detects cocaine, crack cocaine, heroine, and methamphetamine by using a library of 12 colorimetric lane tests which detect functional groups found in illicit drugs and their cutting agents. Each drug elicits a unique color barcode which users match to standard barcodes for sample identification. Since its original publication, we have redesigned the idPAD to increase field-friendliness and deployability. One important modification is the introduction of a sample collection area. This collection area is outside of the colorimetric lane tests and protected from water exposure, so the sample can be stored and saved for downstream applications such as LC-MS/MS analysis. This collection area allows for drug samples to be transported more conveniently and safely than before. Average recovery from the collection area is 34% of the applied drug, and is stable for storage for up to 6 weeks. Analysis of idPADs has historically relied on users to match the color barcode with its corresponding drug. To eliminate the need for human judgement and increase efficiency, we are training a neural network to read barcodes and report drug identity. Another potential application of the idPAD for detecting hormones used for birth control, abortions, and hormone replacement therapy is being explored as a screening tool for social justice groups interested in ensuring quality of dosage forms in settings where access to such drugs is limited.

B18

Mass spectrometric analysis of atomically precise nanoclusters

Habib Gholipour-Ranjbar (1), Lidya Sertse (1), Hong Fang (1), Puru Jena (1), Julia Laskin (1)
(1) *Purdue University*

The idea of atom-by-atom design of small clusters and nanoparticles is becoming a reality with ever advancing experimental and theoretical approaches. Herein, the incorporation of the first-row transitional metal atoms into the core of a well-defined superatomic cluster, [Co6S8(PEt3)6]+, is examined and the effect of each heteroatom on the structure and properties of the cluster is investigated using high resolution electrospray ionization mass spectrometry (ESI-MS), ion mobility mass spectrometry (IM-MS), and collision induced dissociation (CID). ESI-MS analyses indicate that among the first-row transitional metals only Mn, Fe, and Ni atoms can be incorporated into the cluster core. IM-MS revealed that collision cross sections (CCS) of all the doped clusters, ([Co5MS8L6]+ , M=Mn, Fe, Niare similar to the CCS of the undoped cluster, [Co6S8(PEt3)6]+. This finding indicates that heteroatom incorporation into the cluster core does not alter its geometry. CID experiments of mass-selected clusters combined with theoretical calculations indicate the reduced stability of [Co5MnS8(PEt3)6]+ and [Co5FeS8(PEt3)6]+ clusters towards ligands loss in comparison with [Co6S8(PEt3)6]+ and [Co5Ni8(PEt3)6]+counterparts. This study shows that in the absence of single crystal data, structural characterization of isolated cluster ions in the gas phase combined with computational studies may be used to obtain unique insights into the structures and electronic properties of atomically precise clusters.

POSTER SET-UP

11:45 AM - 1:30 PM, LARK ROOM

POSTER SESSION

GROUP B

B19

Systematic Study of the Viscosity of Room Temperature Ionic Liquids on the Electrochemical Performance of Redox Active Species

Danny M. Hristov (1), Hugo Y. Samayoa-Oviedo (1), Sekhon Jagdeep-Kaur (2), Edward L. Quitevis (2), Julia Laskin (1)
(1) *Purdue University*, (2) *Texas Tech University*

Studying the electrochemical behavior of ion species has led to significant discoveries of new and more efficient ways to run electrical systems, that support society and everyday life. Present studies have focused on including solvents with low environmental toxicity, high conductivity and stability to improve the performance of batteries. Room temperature ionic liquids (RTILs) satisfy those conditions, given that they are stable over a wide electrochemical window. We characterized the role of the length of the side alkyl chains of selected RTILs in the electrochemical performance of selected redox active species. Such performance was evaluated by calculating the electron transfer rate and diffusion of three redox active species of different initial charge states. Cyclic voltammetry (CV) is an electroanalytical technique in which the current produced by an electrochemical system is monitored as a function of the applied potential. The different RTIL solvents were scanned via CV to measure each potential window of stability and the electrochemical measurements of each dissolved analyte. Parameters were calculated using data points from the cyclic voltammograms, specifically anodic and cathodic peaks. These parameters included the diffusion coefficient and electron transfer rate constant of each analyte in solvent to assess the overall electrochemical performance of a system. Experimental data shows that the complexity of the chemical structure of each RTIL affects the diffusion of the analytes. Conclusive results from this experiment can be utilized to find the most efficient and sustainable solvent/analyte electrochemical system for wide dissemination.

B20

Taking the Edge off from Particle Collision Electrochemistry: Recessed Electrodes Improve Analytical Performance

Michael Pence (1), Joaquín Rodríguez-López (1)
(1) *University of Illinois at Urbana-Champaign*

Redox blocking methods offer a straightforward approach for electrochemical sizing of suspended particles in solution at ultralow concentrations.[1] When insulating particles collide with a microelectrode they block flux of redox mediator to the electrode, resulting in a current step. The magnitude of this step is representative of the size of the particle, however electrode geometry can introduce high levels of uncertainty. Particle collisions at the edge of a typical micro-disk UME cause a much larger current response than collisions at the center due to a non-uniform flux profile across the surface of the electrode.[2] Deng et. al used hemispherical Hg UMEs to decrease edge effects, however this requires electrodeposition of toxic Hg and these electrodes are anodically unstable.[3]

We hypothesized that using recessed electrodes would create a uniform flux profile at the electrode surface, thus decreasing the measurement error when analyzing collision transients. COMSOL simulations showed that a more uniform flux profile is achieved when the recession length is equal to the electrode diameter. Particle collision experiments with 1.1 um polystyrene beads were carried out at 10 um Pt electrodes with varying recession length in standard mediator solutions. When plotting standard deviation of observed current steps versus recession length, an exponential decrease was observed, matching the results of simulations. The new method improves the analysis of particle size and creates new opportunities to integrate photolithographic methods, which inherently result in recessed electrodes, to the design of collision detecting devices.

References
1. Quinn et al. J. Am. Chem. Soc. 2004, 126, 27, 8360â€“8361
2. Fosdick et al. J. Am. Chem. Soc. 2013, 135, 16, 5994â€“5997
3. Deng et al. Anal. Chem. 2018, 90, 21, 12923â€“12929

POSTER SET-UP

11:45 AM - 1:30 PM, LARK ROOM

POSTER SESSION

GROUP B

B21

Linear and non-linear analysis of NIR spectra can quantify acetaminophen, enabling detection of substandard pharmaceuticals

Olatunde Awotunde (1), Nicholas Roseboom (1), Marya Lieberman (1)
(1) *University of Notre Dame*

Portable spectrophotometers are in commercial use for detection of substandard and falsified pharmaceuticals (SFPs) but there is little published evidence for how well these devices perform, particularly for the task of detecting substandard products. Here, we spiked pure acetaminophen (AC) with lactose (LA) and/or ascorbic acid (AA) to simulate the presence of adulterants and/or excipients. We collected 100 NIR spectra of each of the three pure compounds and 100 spectra of each of 9 binary and 4 ternary mixtures of these compounds. A range of algorithms was then applied to the combined data set (n = 1200 spectra) to distinguish between the different mixtures. An approach combining PLS, SIMCA, and SVM classification and regression not only grouped the lab-formulated samples correctly, but accurately differentiated five different commercial acetaminophen dosage forms from two major brands. We studied the robustness of the combined approach with 100 spectra generated from blinded samples to ascertain its ability in detection of substandard formulations. The analysis of the confusion matrix showed excellent prediction ability as well as the ability to detect when an API was not in the training set. Our end goal is to integrate NIR with the chemical functional group analysis performed by our already widely accepted paper analytical device; together, these technologies will be a more powerful tool for field screening of pharmaceutical and illicit drugs.

B22

Impact of Dry Intrusion Events on Composition and Mixing State of Particles During Winter ACE-ENA Study

Kevin Jankowski (1), Jay M. Tomlin (1), Daniel P. Veghte (2,3), Swarup China (3), Peiwen Wang (4), Matthew Fraund (5), Johannes Weis (5), Guangjie Zheng (6,7), Yang Wang (7,8), Felipe Rivera-Adorno (1), Shira Raveh-Rubin (9), Daniel A. Knopf (4), Jian Wang (6), Mary K. Gilles (5), Ryan C. Moffet (10), Alexander Laskin (1)
(1) *Purdue University*, (2) *The Ohio State University*, (3) *Pacific Northwest National Laboratory*, (4) Stony Brook University, (5) *Lawrence Berkeley National Laboratory*, (6) *Washington University in St. Louis*, (7) *Brookhaven National Laboratory*, (8) *Missouri University*, (9) *Weizmann Institute*, (10) *Sonoma Technology*

Long-range transport of continental emission has far reaching influence over remote regions resulting in substantial change in the size, morphology, and composition of the local aerosol population and cloud condensation nuclei (CCN) budget. Here, we investigate the physiochemical properties of atmospheric particles collected onboard a research aircraft flown over the Azores during the winter 2018 Aerosol and Cloud Experiment in the Eastern North Atlantic (ACE-ENA) campaign. Particles were collected within the marine boundary layer (MBL) and free troposphere (FT), after long-range atmospheric transport episodes facilitated by dry intrusion (DI) events. Chemical and physical properties of individual particles were investigated using complementary capabilities of computer-controlled scanning electron microscopy and X-ray spectro-microscopy to probe particle external and internal mixing state characteristics in the context of real-time measurements of aerosol size distribution, cloud condensation nuclei (CCN) concentration, and back trajectory calculations. While carbonaceous particles were found to be the dominant particle-type in the region, changes in the percent contribution of organics across the particle population (i.e. external mixing) shifted from 68% to 43% in the MBL and from 92% to 46% in FT samples during DI events. This change in carbonaceous contribution is counterbalanced by the increase of inorganics from 32% to 57% in the MBL and 8% to 55% in FT. The quantification of organic volume fraction (OVF) of individual particles derived from X-ray spectro-microscopy, which relates to the multi-component internal composition of individual particles, showed a factor of 2.06±0.16 and 1.11±0.04 increase in the MBL and FT, respectively, among DI samples. We show that supplying particle OVF into the Kähler equation can be used as a good approximation of field measured in-situ CCN concentrations. Our observations suggest that entrainment of particles from long-range continental sources alters the mixing state population and CCN properties of aerosol in the region. The work presented here provides field observation data that can inform atmospheric models that simulate sources and particle composition in the Eastern North Atlantic.

POSTER SET-UP

11:45 AM - 1:30 PM, LARK ROOM

POSTER SESSION

GROUP B

B23

Why it's hard to monitor population iodine deficiency; metabolites that interfere with the Sandell-Kolthoff reaction

Ornella Joseph (1), Madeline Eberle (1), Marya Lieberman (1)
(1) *University of Notre Dame*

Urinary iodine is indicative of dietary iodine intake and its regular assessment at the population level is required to guide iodine supplementation programs. The Sandell-Kolthoff (S-K) reaction, where iodine acts as a catalyst for the reaction between cerium(IV) and arsenic(III), is the most widely used analysis to quantify parts per billion (ppb) levels of iodine, such as those found in human urine. The S-K reaction is susceptible to interference from a large number of species present in urine and therefore requires that urine samples be digested with a strong oxidizing agent such as ammonium persulfate. The literature describes interference by ascorbic acid, but there are over 2,000 other compounds in urine; some with the potential to interfere.

The goal of this study is to determine which of the metabolites in urine interfere with the S-K reaction. For this purpose, 31 of the most abundant metabolites in urine were selected and tested at biologically relevant concentrations, by spiking them into aqueous iodide samples of known concentrations from 0-300 ppb. The S-K reaction was carried out in a microplate format which increased throughput and reduced waste. The accuracy of the S-K analysis protocols was validated under an external quality assurance program conducted by the Centers for Disease Control and Prevention.

Of the metabolites screened, cysteine, citric acid, glycolic acid, ascorbic acid, and urea were found to cause either positive (increased apparent iodine concentration) or negative (decreased apparent iodine concentration) interference according to Welch's t-test. For each interferent, the lowest interfering concentration was determined, and the interferents impact at high and low iodide levels was evaluated to probe possible interference mechanisms. This knowledge allows for more focused future work in developing a convenient and field-friendly technique for interferent removal.

B24

Gold Nanoparticles Indirectly Impact Human Monocytic Cell Line (THP-1) Chemotaxis

Maxwell G. Tetrick (1), Catherine J. Murphy (1)
(1) *University of Illinois at Urbana-Champaign*

Nanoparticles are increasingly being incorporated into medical and consumer products. Therefore, it is important to understand the interactions between nanoparticles and biology in order to safely utilize advances in nanotechnology. However, while there is a large body of research on direct interactions between nanoparticles and living systems, such as toxicological studies, few studies have examined the indirect effects nanoparticles have on biological systems. Due to their large surface area, nanoparticles adsorb biomolecules in the extracellular matrix, making these molecules less bioavailable. A decrease in bioavailability can impact cell behaviors such as chemotaxis which is directed cell migration in response to a concentration gradient of a molecular species. Recently, our group showed that by adsorbing monocyte chemoattractant protein-1 (MCP-1) in the extracellular matrix, gold nanoparticles (AuNPs) functionalized with polystyrene sulfonate decreased the chemotactic ability of a human monocytic cell line (THP-1). Previous research has shown an increased affinity between MCP-1 and sulfonated receptor protein residues. We aim to expand upon this finding by investigating the impact of a variety of other sulfonated AuNPs. By introducing AuNPs into the extracellular matrix and monitoring cell migration via brightfield microscopy we can analyze the impact of various surface chemistries on the adsorption of MCP-1 and the subsequent impact on cellular chemotaxis.

POSTER SET-UP

11:45 AM - 1:30 PM, LARK ROOM

POSTER SESSION

GROUP B

B25

Study of the role of countercations in the electrochemical performance of well-defined electrode-electrolyte interfaces

Hugo Y. Samayoa Oviedo (1), Julia Laskin (1)
(1) *Purdue University*

Ion soft-landing enables surface modification using mass-to-charge selected gaseous ions thereby generating well-defined interfaces. Soft-landing is defined as the deposition of intact ions onto surfaces with or without retention of ionic charge. This approach is advantageous to study the electrochemical performance of electrode-electrolyte interfaces (EEI) in the absence of solvent and impurities. It also enables the study of the role of counterions in the electrochemical performance of redox-active analytes.

In this work, we present a systematic study of the effect of tetrabutylammonium (TBA+) cation on the electrochemical performance of Keggin Molybdenum polyoxometalate (MoPOM3-) anion. By controlled codeposition of TBA(+) and MoPOM(3-) onto an ionogel membrane grown on a screen-printed electrode, we created interfaces with defined molar ratios of these two ions. While under vacuum, we used square wave voltammetry (SWV) to characterize the soft-landed EEI, which provides a high faradic-to-capacitive current ratio. With this technique, we are able to observe 6 well-defined redox peaks for the soft-landed EEI and determine the electron transfer coefficient for each one. Our observations show that by increasing the TBA:MoPOM molar ratio, the electron transfer coefficient increases which indicates that the presence of the cation stabilizes MoPOM(3-) and increases the reduction rate of MoPOM(3-) to MoPOM(2-). This statement agrees with the observed shift in standard redox potential towards more reductive voltages as the amount of TBA(+) is increased on the interface. We propose that TBA(+) forms an ion-pair with MoPOM(3-) which results in the stabilization of the oxidation strength of the anion.

In conclusion, we show that ion soft-landing can be used to create well-defined EEIs to study the role of TBA(+) as countercation on the electrochemical performance of redox-active Molybdenum polyoxometalate. In conjunction with SWV, we determined that the countercation stabilizes the (3-) charge state of the MoPOM, therefore increasing the electron-transfer rate of the reduction step. This finding is of relevance for the design of novel materials with efficient electron transfer to be used in charge storage systems.

B26

Understanding Single Human Erythrocyte Mechanical Variation of Multiple Sclerosis Disease through Scanning Ion Conductance Microscopy

Yunong Wang (1), Lane A. Baker (1)
(1) *Indiana University*

Cardiovascular and central nervous related syndromes (e.g., multiple sclerosis) are often accompanied by significant changes in mechanical stress of erythrocytes. Early results have illustrated the significance of changes in deformability of red blood cells when in the presence of multiple sclerosis. A possible hypothesis for this observation is the leakage of hemoglobin protein in the blood from erythrocytes, causing varying frangibility and stiffness, with many downstream diseases. Mechanical mapping with conventional techniques (e.g., atomic force microscopy (AFM)) to physically characterize these changes is a challenging proposition due to a host of experimental difficulties. To obtain real-time spatial variation of cell stiffness, we have developed a high-speed pressurized scanning ion conductance microscopy (SICM) platform. SICM, a noncontact, nondestructive imaging platform allows safe and high-resolution spatial mapping of the cell. Pressure sensing was achieved by applying a time-varying force on the sample from pressure-induced nanofluidic flow through the pipette, and extraction of quantitative results from approach curves. We will describe our results in the context of different erythrocyte samples and underscore future applications of this technology.

POSTER SET-UP

11:45 AM - 1:30 PM, LARK ROOM

POSTER SESSION

GROUP B

B27

Bacterial Growth Monitored by 2D MS/MS

Lucas J. Szalwinski (1), L. Edwin Gonzalez (1) Brett M. Marsh (1) R. Graham Cooks (1)
(1) *Purdue University*

Lipids play integral roles in the cellular function of bacteria. Methods in obtaining the lipid composition of cells has progressed significantly. Although colorimetric and spectroscopic measurements broadly detect lipid composition, the most definitive method of acquiring the lipid content of a cell is by liquid chromatography tandem mass spectrometry (LC-MS/MS). This method typically requires some sample preparation followed by a long chromatographic run where the elute is monitored over time by a mass spectrometer.
The mass spectrometer is most commonly operated by data-dependent acquisition where only the most abundant ions are fragmented to determine structural information needed for adequate identification. The obvious drawback is low-abundance species are ignored in the analysis. Although many lipids are identified by this method, the sample throughput of chromatographic methods is severely limited. 2D MS/MS is a method where all precursor ions and their subsequent product ions are identified. This avoids chromatographic separation increasing sample throughput.

B28

Modulation of Ion Transport in Nanopores by Nafion

Kristen Alanis (1), Rachel Lucas (2), Zuzanna Siwy (2), Lane Baker (1)
(1) *Indiana University*, (2) *University of California - Irvine*

The control of ion transport is an important tool with wide technological applications. Desalination, electrolytic production of chemicals, capillary electrophoresis, and iontophoresis are examples of the importance of selective, controllable ion transport.Here, a synthetic nanopore system is developed from a silicon nitride membrane that utilizes a film of Nafion to modulate the ion transport across nanopores in a controllable manner. The Nafion film act as a cation reservoir that sources the nanopore with a flux of cations dependent on the applied transmembrane potential. As a result, ion concentration polarization is induced which leads to rectified current-voltage behavior analogous to a diode. Scanning ion conductance microscopy (SICM) was implemented to study the transport properties across the nanopore due to the Nafion film. SICM allows concentration effects at small distances (~100s nm) from the nanopores to be explored.

POSTER SET-UP

11:45 AM - 1:30 PM, LARK ROOM

POSTER SESSION

GROUP B

B29

High-Throughput Nanoelectrochemistry: Individual Nanoelectrodes investigated via the Array Microcell Method (AMCM)

Sasha E. Alden (1), Lingjie Zhang (1), Nickolay V. Lavrik (2), Yunong Wang (1), Lane A. Baker (1)
(1) *Indiana University*, (2) *Oak Ridge National Laboratory*

Electrochemical measurements at individual nanoelectrodes within a nanoelectrode array are performed with the array microcell method (AMCM). AMCM employs the meniscus, in contact with a single nanoelectrode, at the tip of a solution filled glass micropipette (inner diameter ~30 µm) as a micro electrochemical cell. Instrumental advancements reported include automated movement/positioning of the pipette coordinated to electrodes within an array, and feedback controlled pipette approach to the surface. These improvements allow for high-throughput electrochemical analysis at hundreds of single nanoelectrodes, where the electrochemical conditions can be varied for each electrode. Characterization of individual metal disk nanoelectrodes with diameters ranging from 150 nm to 800 nm is performed via voltammetry with automated AMCM.

Acknowledgements: Nanoelectrode fabrication was conducted by Dr. Nickolay Lavrik at the Center for Nanophase Materials Sciences, which is a DOE Office of Science User Facility part of Oakridge National Laboratory.

B30

Molecular characterization of the Fe(III)/nitrocatechol complexes formed in the atmospheric aqueous phase

Alison R. Reed (1), Ana C. Morales (1), Matthew A. Varas (1), Christopher P. West (1), Alexander Laskin (1)
(1) *Purdue University*

Atmospheric aerosols influence the Earth's radiative balance by scattering or absorbing light, resulting in a cooling or warming effect, respectively. Organic aerosols (OA) produced by biomass burning (BB) are known to have a significant impact on global and regional air quality, public health, and climate. One group of compounds present in biomass burning-related OA is brown carbon (BrC), a class of light-absorbing absorbing molecular components. Of these, nitroaromatic compounds (NAC) are known to contribute substantially to the overall light absorption by OA. Although the formation and physicochemical properties of NAC have previously been investigated, the subsequent multiphase reactions of these species are not fully understood. Conjointly, biomass burning fumes frequently interact with mineral dust in the atmosphere, the most abundant particulate of which is iron. BrC and iron form metal-organic complexes on SOAs, but the impact they have on climate change and their formation under light is largely understudied. Here we study an NAC, 4-Nitrocatechol (4NC), and iron in both light and dark environments to mimic ageing of atmospheric clouds and fogs in the BB impacted areas.. We employ high-performance liquid chromatography (HPLC) equipped with a photodiode array detector (PDA) and high-resolution mass spectrometry (HRMS) techniques to investigate the changes in optical properties of the solution at a molecular level. We found that the optical properties are dependent on pH and that visible particles are formed in light environments under unbuffered conditions- indicating a need for further research. This study provides insight on the multiphase reactions of BrC in atmospheric aerosols.

POSTER SET-UP

11:45 AM - 1:30 PM, LARK ROOM

POSTER SESSION

GROUP B

B31

Microfluidic Devices for Tracking the Effects of Divisome Proteins on Z-ring Dynamics in Bacillus subtilis

Laura C. Lastra Gonzalez (1), Yuanchen Yu (1), Daniel B. Kearns (1), Stephen C. Jacobson (1)
(1) *Indiana University*

FtsZ is a tubulin-like protein that polymerizes into a ring structure (the Z-ring) at the site of future cell division. This ring constricts as the cell undergoes cytokinesis, but more importantly, provides the framework for interactions between many divisome proteins and for assembly of the division machinery. Fluorescently labeled FtsZ can be used as a visual indicator of the progression of cell division. Molecular interactions between divisome proteins have been widely studied; yet, how spatiotemporal regulation of the ring is achieved is not well understood. Here, we track FtsZ parameters and localization of the Z-ring in Bacillus subtilis, at both the single cell and population levels in response to deletions of divisome proteins, EzrA and MinD. We make use of a hybrid glass-poly(dimethylsiloxane) device with an integrated microchannel array that confines bacterial growth to a single dimension, while allowing for extensive control over the environmental conditions. Our microfluidic device serves as a reliable platform to study interactions between the divisome proteins and how their interaction regulates Z-ring dynamics throughout the cell cycle. These phenomena are not easily tracked with agarpad-based microscopy methods. Both MinD and EzrA act as negative Z-ring regulators, preventing Z-ring formation at aberrant positions. When deleted, each protein leads to the formation of Z-rings at the cell poles, but only a MinD deletion results in productive cell division and minicell formation. Our data parallel differences in FtsZ dynamics that might explain why polar Z-rings do not mature in ezrA null, unlike the MinD mutant, and suggest the involvement of EzrA in the progression of cell division beyond its role as Z-ring inhibitor.

B32

Probing Atmospheric Aerosol by Multi-modal Mass Spectrometry Techniques: Revealing Aging Characteristics of its Molecular Components

Kyla Siemens (1), Demetrios Pagonis (2), Hongyu Guo (2), Pedro Campuzano-Jost (2), Jose-Luis Jimenez (2), Alexander Laskin (1)
(1) *Purdue University*, (2) *University of Colorado*

Atmospheric organic aerosols (OA) are either directly emitted from various emission sources as primary organic aerosol (POA) or formed as a result of complex multi-phase chemistry, converting atmospheric organic species into airborne particles of secondary organic aerosol (SOA). Once in the atmosphere, POA and SOA undergo rapid external and internal mixing which blurs their original identity. Over atmospheric lifetime, POA components react away, while SOA components build-up, therefore modifying composition of real-world OA. Due to the complexity and variability of atmospheric OA, current methods used to attribute aging characteristics to specific molecular species are limited. Here we demonstrate the novel implementation of multi-modal mass spectrometry techniques to reveal aging characteristics of individual molecular components of OA. In this case study, OA from wildfires in northwestern US were analyzed in-situ using a high-resolution time of flight aerosol mass spectrometer (HR-ToF-AMS) and an extractive electrospray ionization mass spectrometer (EESI-MS) deployed onboard the NASA DC-8 research aircraft. Additionally, bulk samples of OA were collected for offline laboratory-based analysis using high performance liquid chromatography interfaced with photodiode array and electrospray ionization high resolution mass spectrometry (HPLC-PDA-ESI-HRMS). HR-ToF-AMS is a technique frequently employed to detect and follow the evolution of common OA-type classes. EESI-MS is a novel technique employed to probe time-resolved quantitative contributions of individual aerosol components. These techniques are complementary, as the broad class-specific description of OA provided by HR-ToF-AMS guides investigation of time-resolved molecular components detected by EESI-MS, to determine the quantitative evolution of specific species of interest. However, mass resolution of the real-time MS datasets is inadequate to confidently identify species of interest. To compensate, offline HPLC-PDA-ESI-HRMS is employed to elucidate species of interest using MS and MSn techniques. In this work, HR-ToF-AMS highlighted enhanced unusual organic-sulfur species. HPLC-PDA-ESI-HRMS was employed to identify these as organic sulfonate species. We also identified organic sulfates, nitroaromatics, and oxygenated aromatics. We used EESI-MS to determine the aging characteristics of these species.

POSTER SET-UP

11:45 AM - 1:30 PM, LARK ROOM

POSTER SESSION

GROUP B

B33

Intraoperative Assessment of IDH Mutations and Tumor Infiltration in Glioma

Hannah Marie Brown (1), Rong Chen (1), Diogo Garcia (2), Mark Jentoft (2), Erik Middlebrooks (2), Kaisorn Chaichana (2), Alfredo Quiñones-Hinojosa (2), R. Graham Cooks (1)
(1) *Purdue University*, (2) *Mayo Clinic - Jacksonville*

Maximizing surgical resection in gliomas, while avoiding compromising non-infiltrated tissue, is associated with survival benefit. Current methodologies are suboptimal in providing rapid, intraoperative molecular characterization of tissue. We address this unmet need by using desorption electrospray ionization mass spectrometry (DESI-MS) for the intraoperative molecular assessment of gliomas.
This prospective study uses intraoperative DESI-MS analysis of fresh tissue to evaluate IDH mutations via 2-hydroxyglutarate intensity and TCP via measurement of N-acetylaspartic acid (NAA) intensity and characteristic lipid profiles in less than three minutes. Blinded review of the tissue smears by a neuropathologist is used to validate IDH mutation status and TCP estimates.
Presently, 529 biopsies from 85 enrolled patients have been collected and analyzed at two institutions. TCP assessment based on NAA intensity in 203 biopsies at the first institution yielded sensitivity, specificity, and accuracy values of 91, 76, and 83%, whereas TCP estimates via characteristic lipid profiles yielded 76, 85, and 81%, respectively. Assessment of IDH mutation status of 71 core biopsies yielded sensitivity, specificity, and accuracy values of 89, 100, and 94%. Ongoing validation of the methodology is being performed at a second institution, where we have recruited 39 patients and have collected 282 biopsies from 36 patients. IDH mutation assessment of core biopsies from the first 15 patients indicate 100% sensitivity, specificity, and accuracy.
This study represents the first and largest study using DESI-MS for the intraoperative evaluation of IDH status and TCP measurement in gliomas. Prospectively, we propose to modify our DESI-MS methods to allow for intraoperative subtyping of gliomas. We envision molecular analysis by DESI-MS as a complementary technique to histopathologycapable of providing additional clinical information in near real-time.

POSTER SET-UP

11:45 AM - 1:30 PM, LARK ROOM

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