Wednesday Morning, October 30, 2013

Applied Surface Science
Room: 204 - Session AS+BI+IS-WeM

Ambient Ionization Mass Spectrometry

Moderator: C. Szakal, National Institute of Standards and Technology, K. Artyushkova, University of New Mexico

8:20am **AS+BI+IS-WeM2 Rapid Evaporative Ionization Mass Spectrometry - Principles and Applications**, *Z. Takats*, Imperial College, London, ***J. Balog***, MediMass Ltd., Hungary **INVITED**

Development of ambient ionization methods lifted some of the constraints on the applications of mass spectrometry regarding sample pre-treatment and accessibility. However, even these techniques failed to offer a general solution for in-vivo analysis. Rapid Evaporative Ionization Mass Spectrometry (REIMS) has been developed to fill this gap and bring metabolic/lipidomic phenotyping into interventional medical environment. Origins of REIMS technique were based on the observation that thermal evaporation of tissues during surgical intervention produces gaseous ions corresponding to complex lipid species. Furthermore, these complex lipid fingerprints were found to show excellent histological specificity, similarly to those obtained by MALDI or DESI. Following the development of REIMS-based intra-surgical tissue identification technology, the mechanism of the technique was studied in details, and a wide variety of further applications were proposed. Observations strongly suggest that the REIMS technique – similarly to sonic spray ionization – transfers pre-formed ions from solution to gas phase. Electric current and power setting studies revealed minor dependence of the ionization efficiency on the AC frequency, while increasing power (and hence current) settings improved ion yield in the studied ranges. Studying the effect of atmospheric interface settings led to the conclusion that gaseous ionic species detected in the mass spectrometer are formed in the intermediate vacuum regime via cluster-surface collision phenomena. The assumption was further supported by cluster pick-up experiments where various parts of the ion optics were labelled with low volatility compounds (Rhodamine 6G, arginine) and surface re-ionization was studied during REIMS process. Based on these observations, a new type of atmospheric inlet was built, featuring a target surface for surface-induced dissociation of large molecular clusters accelerated by free jet expansion. The ions formed on collisions are collected by a ring electrode trap which is coupled to the ion optics of the mass spectrometer. Based on the results of mechanistic and earlier surgical studies, a number of new applications were developed ranging from the analysis of arbitrary liquid samples through identification of bacterial strains to imaging analysis.

9:00am **AS+BI+IS-WeM4 A Microplasma VUV Photoionization Source for Ambient Mass Spectrometry**, ***J.M. Symonds***, *R.D. Gann, F. Fernández, T.M. Orlando*, Georgia Institute of Technology

Microplasma ionization sources have been shown to be simple, effective tools for ambient mass spectrometry. Microplasmas have the advantages of being cheap to operate and manufacture, and require only modest gas flows and power sources. One of the challenges in ambient mass spectrometry is to produce sample ions from a wide variety of sample molecules without excessive fragmentation. Due to the chemically-specific nature of ionization, this remains a challenge for any new source. In this work we attempt to mitigate both of these problems by using high energy photons to ionize our samples. We have created a microplasma source that employs a mixture of neon and hydrogen to produce vacuum ultraviolet (VUV) light which can ionize samples at atmospheric pressure. Traditionally, VUV light has been both difficult and expensive to produce, which limits its use for applications like ambient mass spectrometry. With the development of our microplasma VUV source, we are able to take advantage of the VUV photon's capability as a broadly-applicable, low-fragmentation photoionization source, while retaining the low cost and simple operation which makes ambient mass spectrometry so appealing. By combining this ionization technique with laser desorption, we investigate the use of this source for mass spectrometric imaging.

This work was supported by the National Science Foundation under award number 0923179.

9:20am **AS+BI+IS-WeM5 Advances in Pulsed-Plasma Sources for Surface Analysis by Ambient Mass Spectrometry**, ***J.W. Bradley***, *K. McKay, A. Bowfield*, University of Liverpool, UK, *T.L. Salter*, National Physical Laboratory, UK, *J.W. Walsh*, University of Liverpool, UK, *M.R. Alexander, D.A. Barrett*, University of Nottingham, UK, *I.S. Gilmore*, National Physical Laboratory, UK

The potential benefits of using atmospheric pressure "cold" plasma sources as a means of both desorption and ionisation of material in ambient mass spectrometric analysis of surfaces has been recognized by a number of researchers worldwide. Plasma sources include dielectric barrier jets (PADI [1] and LTP [2]) operating at mid-frequency and also RF corona needle discharges.

Here we develop further strategies to pulse modulate such sources (jet and needle) and investigate the influence of duty cycle on the production of chemical species in the source plasma and the composition of the ionised desorbed species from a range of test surfaces (polymeric, pharmaceutical and biological). For the plasma plume study we use a time resolved (5 μs) Hiden Analytical molecular beam MS (HPR-60) unit, while detailed information on the spatial distribution of surface species from the chosen material samples was done using a Thermo Velos LTQ Orbitrap MS.

The influence of source-sample and sample-instrument distances on the signal intensities is investigated for both sources. We observe that as the duty cycle of the pulse is decreased the positive ion yield shifted towards higher mass clusters, due to a decrease in gas temperature enabling increased hydration reactions. The negative ions also display similar trends with the yield of larger negative ions increasing with shorter duty cycles. From time-resolved ion intensities it is clearly seen that positive ions are produced in the on-phase of the discharge, and decay in the off-phase. Negative ions, in contrast, are produced mainly in the off-phase of the discharge and decay during the on-phase. With increased distance between source and instrument we observe that the yield of large positive ions increases, at the expense of smaller positive ions which are lost before they reach the orifice. Negative ions, on the other hand, show an increase in yield as distance is increased.

Preliminary analysis of common pharmaceutical products suggest that a decreased duty cycle gives improved identification of negative ion surface compounds however, where surface compounds undergo ionisation to form positive ions, larger duty cycles allowed for better identification. The gas-phase plasma chemistry for different arrangments will be discussed.

1] Ratcliffe LV, Rutten FJ, Barrett DA, Whitmore T, Seymour D, Greenwood C, Aranda-Gonzalvo Y, Robinson S, McCoustra M, Anal Chem. (2007) 79 (16) 6094

2] Zhang, JI, Costa, AB,Tao, WA, Cooks, RG, Analyst, (2011), 136, 15, 3091

9:40am **AS+BI+IS-WeM6 Comparison of Ambient Pressure Ionization Sources by Determining Useful Yields of Forensic Compounds of Interest**, ***T. Brewer***, *C. Szakal, E. Sisco, S. Muramoto, T. Forbes, G. Gillen*, NIST

The detection of illicit drugs and trace explosives represents one of the most significant challenges for law enforcement and forensic communities. Of particular interest to the forensic analyst is the ability to rapidly identify suspected illicit drug materials and explosives residues in their native state (powder, tablet or liquid form), under atmospheric conditions and with a high level of specificity and sensitivity. To that end there are numerous ambient pressure ionization techniques such as atmospheric pressure glow discharge (APGD), low temperature plasma (LTP), and desorption electrospray ionization (DESI) that can be used to interrogate forensic compounds. However, a method of comparing between the different ambient ionization sources does not exist. Here, useful yields are determined for a series of forensic compounds using different ambient pressure ionization sources as a means of comparison. Using a precision inkjet deposition system a well-defined array of microdrops is produced with each deposit containing a known number of analyte molecules. The individual deposits were removed or desorbed until consumed while monitoring the integrated characteristic molecular secondary ions for each analyte. The ratio of integrated counts to the number of molecules in the deposit defines the useful yield of the experiments. The results here highlight a way to compare the different ambient ionization sources for the analysis of forensic compounds of interest.

10:40am **AS+BI+IS-WeM9 Atmospheric Pressure Ionization Mass Spectrometry: Fundamentals, Simulations, and Applications**, ***Th. Benter***, University of Wuppertal, Germany **INVITED**

Almost for a century now, mass spectrometric instrumentation is generally designed to establish linear analyte concentration – ion signal responses. Deviations from linear relationships are tolerated to a certain extent but such observations usually raises doubts on the performance of the method applied. Surprisingly, Atmospheric Pressure Ionization (API) techniques have swiftly led to the frequent usage of terms such as "matrix effects", "ion suppression", or "non-linear response". This is particularly true for ambient ionization methods. In fact, the various API methods not only target different analyte properties, e.g. gas phase acidities, they also frequently generate new ion signals which are then somehow related to the neutral analyte precursor. On the other hand API mass spectra may also show unexpected fragmentation patterns – despite the often claimed "soft" nature of the ionization processes involved.

In this contribution we are attempting to highlight some of the key processes operating on the primarily generated analyte ion population en route from the origin of ion formation to the collision free analyzer region. For this purpose, we are defining *chemical domains* such as the initial reagent ion generation domain (in ambient ionization often plasmas), the chemical ionization domain, or the thermal ion transport domain, among others. These domains exhibit distinct features, which are significantly changing the chemical matrix in which ions and neutrals are moving towards the collision free - and thus chemically non-reactive - analyzer region.

Primary ionization pathways, subsequent thermal ion molecule chemistry, and electrical fields are discussed as potential drivers of chemical transformation processes, which may render the interpretation of API mass spectra quite difficult. This is particularly true for the analysis of complex mixtures using API MS without chromatographic pre-separation of the neutrals. Ambient ionization methods are generally designed to do exactly that: Analyze samples (e.g., human urine, drug tablets, surface contaminations, to name but a few) without sample preparation and preferentially in real time.

Examples are given to illustrate the extent of selected transformation processes. Among other issues it is discussed why the generation of Helium metastable atoms (He^M) results in protonation in API MS, or why aromatic hydrocarbons ionized with the exact same primary excitation scheme yield almost exclusively radical cations in classical mass spectrometers but often deprotonated molecules in API systems.

11:20am **AS+BI+IS-WeM11 Ambient Mass Spectrometry for Structural Analysis of Organic Monolayers**, ***H. Zuilhof***, Wageningen University, Netherlands

For the analysis of covalently bound organic monolayers a variety of surface-sensitive techniques has been developed, including XPS, AES, IR, contact angle measurements and X-ray reflectivity. While each of these has its own merits, none of them provide **structural** information. In addition, via e.g. XPS it is sometimes possible to follow A -> B reactions on a surface, but A -> x% B + y% C is already nearly impossible to properly analyze. Similar restrictions apply to the study of diluted monolayers (e.g. 10% of a bioactive compound surrounded by 90% inert surface-covering monolayer), while dilution may actually be essential for the proper biological functioning of the monolayer! Therefore novel analysis techniques are still in demand, and here we present the application of DART ambient mass spectrometry as a generic and highly powerful technique for the analysis of such monolayers. Using a variety of tailor-made, covalently attached organic monolayers on silicon nitride and other substrates we show that MS can be used to study: 1) the progress of four sequential surface-bound organic reactions, 2) surfaces with a mixture of halogens on them, 3) the progress of incomplete reactions, and 4) the stability of biofunctional groups. In the current presentation we summarize our recently published work in this area (ChemComm 2013, 922) and present new, as of yet unpublished data that outline the tremendous potential of this novel analysis technique!

11:40am **AS+BI+IS-WeM12 Differentiation of Microbial Species & Strains in Coculture Biofilms by Multivariate Analysis of Laser Desorption Postionization Mass Spectra**, *C. Bhardwaj, Y. Cui*, University of Illinois at Chicago, *H.C. Bernstein, R.P. Carlson*, Montana State University, ***L. Hanley***, University of Illinois at Chicago

The metabolic states of microbial biofilms vary with growth conditions such as host surface, culture media, or antibiotic concentration. 7.87 and 10.5 eV vacuum ultraviolet (VUV) photon energies were used in laser desorption postionization mass spectrometry (LDPI-MS) to analyze microbial biofilms comprised of binary cultures of interacting microorganisms grown on polymer membranes. Principal components analysis (PCA) was applied to the MS data to differentiate species in *Escherichia coli-Saccharomyces cerevisiae* coculture biofilms. PCA of LDPI-MS also differentiated individual *E. coli* strains in a biofilm comprised of two interacting gene deletion strains, even though these strains differed from the wild type K-12 strain by no more than four gene deletions each out of approximately 2000 genes. PCA treatment of 7.87 eV LDPI-MS data separated the *E. coli* strains into two "pure" groups and a distinct mixed region. Furthermore, the "pure" regions of the *E. coli* cocultures showed greater variance by PCA when analyzed by 7.87 eV photon energies than by 10.5 eV radiation. Comparison of the 7.87 and 10.5 eV data is consistent with the expectation that the lower photon energy selects a subset of low ionization energy analytes while 10.5 eV is more inclusive, detecting a wider range of analytes. These two VUV photon energies therefore give different spreads via PCA and their respective use in LDPI-MS constitute an additional experimental parameter to differentiate the metabolite states of microbial biofilms growing on different surfaces.

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