

Monday Evening, December 9, 2024

Biomaterial Surfaces & Interfaces

Room Naupaka Salon 5 - Session BI1-MoE

Biomaterials/Interfaces - Characterization

Moderator: David G. Castner, University of Washington

5:40pm **BI1-MoE-1 Advanced BioAFM for Temporal Analysis, Amy Gelmi, RMIT University, Australia** **INVITED**

Electrical stimulation, a physical stimulation which can be delivered via a conductive biomaterial interface, directs human mesenchymal stem cell (hMSC) differentiation towards different cell tissue types.[1] Electrical stimulation conditioning offers a promising approach in directing stem cell fate. Conductive biomaterials are commonly used to provide either a passively conductive substrate, or actively provide 'smart' electrical stimulation of stem cells for tissue engineering. However, the mechanisms in which cells transduce these electrical signals into specific phenotype differentiation are poorly understood, restricting the intelligent design of stimulation protocols for targeted differentiation.

How the stem cells transduce an electrical signal into a biological response is explored via different classes of conductive biomaterials. Immediate changes in the stem cells during and post-stimulation is characterised, using live cell bio-AFM for morphological and biomechanical changes, complemented with standard biological characterisation. The advanced bioAFM technique delivered unprecedented intracellular biomechanical information of live cells undergoing simultaneous electrical stimulation.

For the first time we have characterised the transient mechanical response of hMSC to electrical stimulation, and related that to controlling stem cell differentiation towards osteogenesis. The knowledge gained from this study helps to further the intelligent design of stimulation parameters for targeted differentiation outcomes when using a conductive biomaterial.

[1] Gelmi, A., Schutt, C. E., Stimuli-Responsive Biomaterials: Scaffolds for Stem Cell Control. *Adv. Healthcare Mater.* 2020, 10, 2001125.

6:20pm **BI1-MoE-3 GCIB-SIMS Analysis of Skin Cancer Samples, John S. Fletcher, K. Sjögren Cehajic, K. Dimovska Nilsson, O. Zaar, D. Katasarelis, J. Paoli, R. Olofsson Bagge, N. Neittaanmäki, University of Gothenburg, Sweden**

The use of gas cluster ion beams (GCIBs) for secondary ion mass spectrometry (SIMS) analysis provides softer ejection of biomolecular ions and has created opportunities for meeting the challenges of clinical researchers who require chemical specific imaging of different sample type from cells to tissue biopsies. Here we use a J105 Buncher-ToF SIMS instrument (Ionoptika Ltd, UK) to perform in situ lipidomics of skin cancer samples. GCIB-SIMS analysis enabled detailed spatial-lipidomics that could be directly correlated with conventional histopathological analysis of consecutive H&E slides. Here we present work where melanoma cancer samples were the target in order to investigate the chemical changes associated with disease progression and also to investigate if different metastatic pathways could be distinguished based on the chemical signature of the tumours. Primary tumours were analysed along with "healthy/normal" skin from the same subject along with metastatic tumour samples that had spread via either the lymphatic system or through the blood. Significant differences in the lipid profiles were found in primary compared to metastatic melanomas, notably an increase in phosphatidylethanolamine lipids relative to phosphatidylinositol lipids and an increase in GM3 gangliosides in the metastatic samples. Furthermore, analysis of the data from in-transit versus distant metastases samples highlighted that specific glycerophospholipids, and a difference in the long versus shorter chain GM3 gangliosides, discriminated the metastatic routes. The data is also compared to other skin cancer samples including such as aggressive basal cell carcinoma. Challenges related to data processing and spectral annotation are also discussed.

6:40pm **BI1-MoE-4 Depth Correction of 3D SIMS Depth Profiling Images of Biomaterials Using Only Secondary Ion Signal Intensities, M. Brunet, B. Gorman, Mary Kraft, University of Illinois Urbana-Champaign**

We have developed a depth correction strategy for three-dimensional (3D) SIMS depth profiling images of biomaterials that solely employs secondary ion signal intensity. In this approach, the secondary ion images that were collected during depth profiling are used to create a model of the sample's morphology at the time that each depth profiling image was acquired. Then these models of the sample's morphology are used to shift the voxels in the 3D image to the correct z-position. Comparison of the morphology models created using the secondary ions and the secondary ion images the usage of secondary ion signals with high intensities tends to produce more

accurate morphology models. However, even 3D SIMS images that were depth corrected using secondary ions with relatively low intensities were more accurate than uncorrected 3D SIMS depth profiling images. This ability to use secondary ion images to depth correct 3D SIMS depth profiling images in the absence of correlated measurements of sample topography or knowledge of sputter rate expands the range of SIMS depth profiling data sets that may not be depth corrected.

7:00pm **BI1-MoE-5 Label-Free High-Resolution Molecular Imaging of Sex Steroid Hormones in Zebrafish by Water Cluster Secondary Ion Mass Spectrometry (Cluster SIMS), Kate McHardy, N. Sano, Ionoptika Ltd., UK; E. Lau, M. Bailey, University of Surrey, U.K.**

Sex steroid hormones are essential biomolecules for vertebrates and are involved in the maintenance of pregnancy, development of secondary sexual characteristics and diseases such as osteoporosis and breast cancer. Visualising the distribution of steroids contributes to further understanding of disease. However, analysis of steroids is difficult; their low polarity leads to poor ionisation efficiency, meaning they need to be derivatised for conventional analyses. Furthermore, the steroid signals overlap with a MALDI matrix background.

Water Cluster SIMS is a high-sensitivity mass spectrometry technique for imaging complex-mixture materials without derivatisation or the use of matrix. We demonstrate imaging of sex steroid hormones in zebrafish (an ideal vertebrate model organism) with a Water Cluster SIMS instrument.

An adult female zebrafish was prepared for this work. It was embedded while fresh in 0.75% HPMC and 0.25% PVP embedding media to facilitate sectioning. The whole block was flash-frozen in a dry-ice and isopropanol bath. The sample was sectioned to 20 µm at -25 °C and thaw-mounted onto a conductive indium-tin-oxide (ITO) coated glass. The section was dried while frozen in a vacuum desiccator, and then directly analysed without any matrix application for the analysis. The Cluster SIMS analyses were then performed with the J105 SIMS Cluster SIMS (Ionoptika Ltd), using a 70 keV (H₂O)_n beam, where n is in the range of 15,000-35,000, and also separately with a 40 keV C₆₀ beam. High-resolution images were acquired with a pixel size of < 1 micron.

Water Cluster SIMS uses a high-energy beam of ionised clusters of water to sputter and ionise molecules from a surface. It is far less damaging and generates far fewer fragment ions than traditional ToF SIMS, but retains many of the benefits of that technology such as high-spatial-resolution imaging. As a result, detailed images of the distribution of sex steroid hormone molecules in the zebrafish are visible. Preliminary data shows that it is possible to map the chemical distribution of steroids in the ovary area. In addition, we also detected lipid ions related to the embryo or oocyte around the ovary area as unique distributions.

Author Index

Bold page numbers indicate presenter

— **B** —

Bailey, M.: BI1-MoE-5, 1
Brunet, M.: BI1-MoE-4, 1

— **D** —

Dimovska Nilsson, K.: BI1-MoE-3, 1

— **F** —

Fletcher, J.: BI1-MoE-3, 1

— **G** —

Gelmi, A.: BI1-MoE-1, 1
Gorman, B.: BI1-MoE-4, 1

— **K** —

Katasarelias, D.: BI1-MoE-3, 1
Kraft, M.: BI1-MoE-4, 1

— **L** —

Lau, E.: BI1-MoE-5, 1

— **M** —

McHardy, K.: BI1-MoE-5, 1

— **N** —

Neittaanmäki, N.: BI1-MoE-3, 1

— **O** —

Olofsson Bagge, R.: BI1-MoE-3, 1

— **P** —

Paoli, J.: BI1-MoE-3, 1

— **S** —

Sano, N.: BI1-MoE-5, 1
Sjögren Cehajic, K.: BI1-MoE-3, 1

— **Z** —

Zaar, O.: BI1-MoE-3, 1