CHARLOTTE

CENTER FOR BIOMEDICAL ENGINEERING AND SCIENCE

PROGRAM SCHEDULE

Monday, September 15, 2025

Dubois Center, Charlotte NC

Biomedical Sciences Symposium

2025

Time	Topic	Location
8:00 AM	Registration and Coffee	Atrium
8:00 AM– 5:00 PM	**NCBiotech Synergy Suite: *Meet. Learn. Recharge.***	**Room 1105**
8:45 – 1:15 PM	Poster Session #1 Viewing Presenters at posters 12:30 – 1:15	2nd floor
8:45 - 9:00 AM	**Welcome and Opening Remarks** Dr. John Daniels, Vice Chancellor Research, UNC Charlotte Dr. Sharon Gaber, Chancellor, UNC Charlotte Tracy Dodson, COO Charlotte Regional Business Alliance	Main Auditorium
9:00 – 9:30 AM	Dr. John Hardin, Executive Director North Carolina Board of Science, Technology & Innovation **The State of Innovation and Biomedical Sciences in North Carolina**	Main Auditorium
9:30 – 9:55 AM	Dr. Dan Janies, Carol Grotnes Belk Distinguished Professor of Bioinformatics and Genomics, Co-Director CIPHER, UNC Charlotte Dr. Adam Reitzel, Associate Dean Klein College Science, Co-Director CIPHER, UNC Charlotte **Efforts of the Center for Computational Intelligence to Predict Health and Environmental Risks at UNC Charlotte**	Main Auditorium
9:55 - 10:25 AM	*Group Photo and Coffee Break*	
10:25 – 11:10 AM	**Keynote Speaker** Dr. Brad Bower Chief AI and Data Science Officer, National Institute of Biomedical Imaging and Bioengineering	Main Auditorium
11:10 – 11:35 PM	Dr. Metin Gurcan, Director Center AI Research and Clinical Image Analysis Lab, Wake Forest School of Medicine **From Images to Insights: AI Transforming Radiology and Pathology in Breast Cancer Care**	Main Auditorium
11:35 – 12:00 PM	Dr. Rob Keynton, Dean, William States Lee College of Engineering, UNC Charlotte **Advancing Bioengineering and Innovation at UNC Charlotte**	Main Auditorium
12:00 – 12:10 PM	Lightning Presentations of Posters	Main Auditorium
12:10 – 1:15 PM	*Lunch*	Atrium
1:15 – 5:00 PM	Poster Session #2 Viewing Presenters at posters 4:15 – 5:00 PM	2nd floor
1:15 – 4:00 PM	Concurrent Scientific Sessions	Check Schedule for rooms
4:00 – 5:00 PM	Reception, Poster Viewing, and Closing Remarks	Atrium

Visit the NC Biotech Synergy Suite: *Meet. Learn Recharge*

Open all day Room 1105

Afternoon Concurrent Scientific Sessions

Session Name: Regenerative Medicine I
Time: 1:15 PM – 2:30 PM
Location: Lecture Hall – 2nd Floor

Time	Topic
1:15 – 1:35 PM	Amit Mohite – Duke University **The Investigation of Hyaluronic Acid-Alginate Hydrogel as a Biomaterial Adjunct for Peripheral Nerve Reconstruction and Regeneration**
1:35 – 1:50 PM	Nan Zhao - UNC Charlotte **Modeling Angiogenesis Using Tissue-Engineered Brain Micro-vessels**
1:50 – 2:05 PM	Timothy Sganga - Wake Forest Institute for Regenerative Medicine **Physiomimetic Microwell Platform for Biomanufacturing Human Pancreatic Isletoids**
2:05 – 2:25 PM	Krishnaiah Maddeboina – Advocate Health **A Novel Multitarget Small Molecule Drug Development Platform for Cancer and Other Transcriptionally Dysregulated Diseases**
2:30 – 2:45 PM	*Break*

Session Name: Infectious Disease and Health I
Time: 1:15 PM – 2:30 PM
Location: Room 1104

Time	Topic
1:15 – 1:35 PM	Anwar Hossain – UNC Chapel Hill **First-in-Class Direct-Acting Antiviral Discovery**
1:35 – 1:50 PM	Sayal Guirles - UNC Charlotte **H5N1 Influenza A is Now Promiscuous in Host Range and has Improved Replication in Mammals**
1:50 – 2:05 PM	Alex Suptela – UNC Charlotte **Light Assisted Drying for the Thermal Stabilization of Vaccines**
2:05 – 2:25 PM	Colby Ford – UNC Charlotte **AI-Accelerated Antibody Discovery through Diffusion and Protein Language Models**
2:30 – 2:45 PM	*Break*

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Open all day Room 1105

Afternoon Concurrent Scientific Sessions

Session Name: Host-Pathogen Interactions and Health I
Time: 1:15 PM – 2:30 PM
Location: Room 506

Time	Topic
1:15 – 1:35 PM	Richard Allen White III – UNC Charlotte **Resolving T Cell Development within Chiropterans Leading to Lifelong Viral Suppression**
1:35 – 1:50 PM	Belinda Mativenga – NC State **Quantification of Empty and Full AAV Capsids using Chip-Based Molecular Diagnostics**
1:50 – 2:05 PM	Sydney Birch – UNC Charlotte **Genotype Impacts Viral and Microbial Associations in Coastal Invertebrates**
2:05 – 2:25 PM	Abigail LaBella – UNC Charlotte **Decoding Fungal Pathogens Using Codon Usage Bias**
2:30 – 2:45 PM	*Break*

Session Name: AI and Medical Imaging I
Time: 1:15 PM – 2:30 PM
Location: Room 504

Time	Topic
1:15 – 1:35 PM	Annika Marie Schoene - Northeastern University **AI Safety for Mental Health**
1:35 – 1:50 PM	Minhaj Nur Alam - UNC Charlotte **Foundational Vision Language Models for Ophthalmic Diagnostics**
1:50 – 2:05 PM	Shruti Agashe – Duke University **Deep Brain Stimulation in Generalized Epilepsies**
2:05 – 2:25 PM	Rosario Porras-Aguilar – UNC Charlotte **A Seeing More in a Single Capture: Multifunctional Microscopy for Label-free and Quantitative Bioimaging**
2:30 – 2:45 PM	*Break*

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Open all day Room 1105

Afternoon Concurrent Scientific Sessions

Session Name: Cancer and Translational Medicine I
Time: 1:15 PM – 2:30 PM
Location: Room 506

Time	Topic
1:15 – 1:35 PM	Valery Grdzelishvili – UNC Charlotte **Mechanisms of Resistance to Oncolytic Virotherapy in Pancreatic Cancer: From Molecular Drivers to Therapeutic Strategies**
1:35 – 1:50 PM	Punnya Anil Kumar Jeeja - UNC Charlotte **Modular Design of Mesoporous Silica Nanoparticles Enables Bioimaging, Dual Chemotherapy, and Combinatorial Gene Silencing in Triple-negative Breast Cancer**
1:50 – 2:05 PM	Tamanna Binte Huq – UNC Charlotte **Development of a Universal Bioreactor Platform for Regenerative Medicine Applications**
2:05 – 2:25 PM	Youjun Wu – UNC Charlotte **Activation of Interferon-Gamma Signaling Sensitizes Pancreatic Cancer Cells to Chemotherapy**
2:30 – 2:45 PM	*Break*

Session Name: Cancer and Translational Medicine II
Time: 2:45 PM – 4:00 PM
Location: Lecture Hall – 2nd Floor

Time	Topic
2:45 – 3:05 PM	Shan Yan – UNC Charlotte **Structure-function studies of APE1 in Genome Stability and Cancer Therapy Strategies**
3:05 – 3:20 PM	Cassandra Catacalos - UNC Charlotte **Repurposing an FDA-Approved Drug to Improve Oncolytic Virus Therapy in Pancreatic Cancer**
3:20 – 3:35 PM	Duhita Mirikar – UNC Charlotte **Multi-site Hsp70 Phosphorylation Regulates the Yeast DNA Damage Response**
3:35 – 3:55 PM	Renaud Warin - Biocytics **Towards a New Age for the Benefit of Cancer Patients: Development of Autologous, Reinvigorated Cancer Cell Therapies Manufactured at the Point of Care**
4:00 – 5:00 PM	*Poster Viewing and Reception* *Closing Remarks*

Visit the NC Biotech Synergy Suite: *Meet. Learn Recharge*

Open all day Room 1105

Afternoon Concurrent Scientific Sessions

Session Name: Host-Pathogen Interactions and Medicine II
Time: 2:45 PM – 4:00 PM
Location: Room 1104

Time	Topic
2:45 – 3:05 PM	Ajmal Khan – UNC Greensboro **Integrated Transcriptomics, Metabolomics, and Epitranscriptomics Reveals the Role of Microplastics in Cardiovascular Disease**
3:05 – 3:20 PM	Trevor Price - UNC Charlotte **Tau Protein Hyperphosphorylation in response to Coronavirus Infection**
3:20 – 3:35 PM	Yosauri Fernandez Figuereo - Wake Forest Institute for Regenerative Medicine **Creating a Living Intestinal Organoid Biobank: A Model System for Mechanistic Testing in Children with Autism Associated Enterolitis**
3:35 – 3:55 PM	Juan Vivero-Escoto – UNC Charlotte **A Light Activated Anti-Microbial Activity of Silver Nanoparticles against Antibiotic-Resistant Bacteria**
4:00 – 5:00 PM	*Poster Viewing and Reception* *Closing Remarks*

Session Name: AI and Medical Imaging II
Time: 2:45 PM – 4:00 PM
Location: Room 1102

Time	Topic
2:45 – 3:05 PM	William (Billy) Hempstead – UNC Charlotte **Automated Placental ROI Selection for Quantitative Ultrasound Analysis Using Boundary-Aware Thresholding**
3:05 – 3:20 PM	Maddie Kern - UNC Charlotte **Enhanced Thermal Imaging for the Detection of Blood Vessels in Soft Tissue**
3:20 – 3:35 PM	Farah Deeba – UNC Charlotte **Quantitative Ultrasound for Placenta-Mediated Disease Detection *In Utero***
3:35 – 3:55 PM	Nowlan Freese – UNC Charlotte **Single-cell RNA Seq Visualization in the Integrated Genome Browser**
4:00 – 5:00 PM	*Poster Viewing and Reception* *Closing Remarks*

Visit the NC Biotech Synergy Suite: *Meet. Learn Recharge*

Open all day Room 1105

Afternoon Concurrent Scientific Sessions

Session Name: Biomaterials and Translational Medicine
Time: 2:45 PM – 4:00 PM
Location: Room 504

Time	Topic
2:45 – 3:05 PM	Kirill Afonin – UNC Charlotte **Biomarker-Responsive RNAi Nanomachines for Precision Oncology**
3:05 – 3:20 PM	Shahed Khan Mohammed - UNC Charlotte **In Vivo Microscale Elastography for Idiopathic Pulmonary Fibrosis Detection: Design, Phantom Validation, and Preliminary Investigation**
3:20 – 3:35 PM	Md Rahatuzzaman – UNC Charlotte **Design and Simulation of Hollow Microneedle Patch for Interstitial Fluid Extraction**
3:35 – 3:55 PM	Angelo Gaitas – UNC Charlotte **Microsensors for Precision Analysis of Cellular Temperature, Mass, Mechanical Properties, and Electrical Activity**
4:00 – 5:00 PM	*Poster Viewing and Reception* *Closing Remarks*

Session Name: Regenerative Medicine II
Time: 2:45 PM – 4:00 PM
Location: Room 506

Time	Topic
2:45 – 3:05 PM	Ahmed El-Ghannam – UNC Charlotte **A Bioactive 3D-Printed SiC Scaffold for Immunomodulation and Osteoneuro Regeneration**
3:05 – 3:20 PM	Brendyn Miller - Wake Forest Institute for Regenerative Medicine **Development of a Sensor-integrated Bladder Bioreactor System for Urological Reconstructive Procedures**
3:20 – 3:35 PM	Marcus Valenta – Duke University **Understanding the Spectrum of Macrophage Activation States and Behaviors After Sciatic Nerve Injury and Repair in Mice**
3:35 – 3:55 PM	Sunil George – Wake Forest Institute for Regenerative Medicine **3D Bioprinted Autologous Vaginal Tissue Constructs for Personalized Vaginal Reconstruction**
4:00 – 5:00 PM	*Poster Viewing and Reception* *Closing Remarks*

Morning Poster Session

Viewing 8:45 AM -1:15 PM Presenters present 12:30 PM -1:15 PM

Regenerative Medicine

#1 Erika Billman Wake Forest Institute for Regenerative Medicine

E. Billman, P. Marahwa, O. Clemensen, V. Liaskonis, P.F. Lee, S. Jeon, Y.M. Ju, V. Mashanov, J. Jackson, B. Vaughan, A. Atala, J. Yoo, J.H. Kim

Introduction:

Volumetric muscle loss (VML), defined as the loss of ≥20% of skeletal muscle mass, leads to chronic functional impairments and remains a significant clinical challenge. Current treatments, such as autologous muscle grafts, are limited by donor site morbidity, immune rejection, and limited regeneration capabilities. To address these limitations, we developed a novel biomaterial platform composed of uniform, decellularized muscle fiber fragments (dMFFs, ~50 μm) that can be aligned with host muscle architecture. These fragments were conjugated with Insulin-like Growth Factor 1 (IGF-1), creating dMFF-IGF-1s, designed to promote in situ muscle regeneration by leveraging the body's innate repair mechanisms without requiring autologous cells.

Methods:

We evaluated IGF-1 release kinetics from dMFF-IGF-1s using ELISA over a 7-day period. Additionally, C2C12 mouse myoblasts were used to assess cellular responses to the dMFF-IGF-1s. Migration was measured using a transwell assay, proliferation was quantified in 3D co-culture using Cell Titer Glo, and differentiation was assessed in 3D co-culture via immunofluorescence staining for Desmin, utilizing ImageJ to quantify differentiated cell area.

Results:

ELISA results confirmed sustained IGF-1 release over 7 days. dMFF-IGF-1s significantly enhanced C2C12 migration, proliferation, and differentiation compared to dMFFs alone and negative controls. While dMFFs alone had a positive effect, IGF-1 conjugation markedly amplified regenerative responses across all assays.

Conclusion:

These findings demonstrate the potential of dMFF-IGF-1s as a functional, off-the-shelf therapeutic for VML. Ongoing in vivo studies in a rat VML model aim to validate functional muscle regeneration and long-term recovery.

#2 Adam Jones Wake Forest School of Medicine

Adam Jones, Quentin Perrier, Timothy Sganga, Brett Ritchey, Giuseppe Orlando

Islet transplantation is an effective cell therapy for treating type 1 diabetes (T1D). However, a significant proportion of islets are destroyed shortly post-transplantation due to oxidative stresses. Adenosine has been shown to decrease the metabolism of rat islets and also provide protection against ischemia-reperfusion injury (IRI). This study's objective was to assess the impact of adenosine in preventing hypoxia-associated harm on human islets viability and function. This study investigates the effect of adenosine on human islet (HI) metabolism, function, and survival under hypoxic conditions (1% O2). HI were exposed to adenosine (1 mM and 10 μM) for 24h, followed by assessments of viability, insulin secretion, and hypoxia resilience. Adenosine at 1 mM significantly reduced insulin content, an effect that was reversible within 96h, without impairing islet viability or functionality. Furthermore, hypoxia reduced islet viability compared to non-hypoxic control (72.7±6.8% vs. 91.4±0.3%, $p<0.01$), but adenosine treatment prevented the reduction in viability (81.5±5.3%, $p<0.01$ vs. hypoxia).

Hypoxia also decreased the GSIS index compared to the control (0.68±0.42 vs. 4.80±1.98, $p < 0.01$), and adenosine prevented this reduction in the GSIS index (3.41±0.80, $p<0.01$ vs. hypoxia). These findings suggest that adenosine preconditioning offers an effective strategy to enhance HI survival and function during transplantation by downregulating islet metabolism. This approach holds potential for integration into novel beta-cell replacement therapies and improving outcomes in alternative transplantation sites. In conclusion, adenosine preconditioning represents a promising avenue for mitigating IRIs in cell therapies for T1D, paving the way for more efficient and resilient beta-cell replacement strategies.

#3 Tarek Zaho Wake Forest Institute for Regenerative Medicine

Tarek Zaho, Shaelyn Walker, Adam Goff; Jay Ma, David Ornelles, Anthony Atala, and Yuanyuan Zhang

Chronic kidney disease (CKD) often progresses to renal fibrosis, a devastating condition characterized by inflammation, scarring, and eventual kidney failure. Current therapeutic options are limited and it offer limited efficacy and carry potential risks, particularly when involving viral vectors, highlighting the urgent need for innovative approaches.

Our previous research demonstrated the regenerative potential of human urine-derived stem cells (hUSCs) in kidney repair. Concurrently, we identified a correlation between decreased pigment epithelium-derived factor (PEDF) levels and impaired renal repair. PEDF is a multifunctional protein known for its anti-inflammatory, antioxidant, and anti-fibrotic properties. This study aimed to develop a novel therapeutic strategy by combining the regenerative capacity of hUSCs with the protective effects of PEDF. We hypothesized that hUSCs, efficiently transfected with a PEDF-encoding plasmid, could serve as as a more potent therapy. we investigated a novel virus-free, cell-based therapy by engineering hUSCs to overexpress PEDF using plasmid transfection. To optimize transfection efficiency and cell viability, and PEDF expression we initially transfected hUSCs with an enhanced green fluorescent protein (eGFP) reporter plasmid via Lipofectamine.

Western blot analysis confirmed significantly higher PEDF levels in hUSCs transfected with the PEDF-encoding plasmid compared to controls. While a transient decrease in total cell number was observed post-transfection, cell viability assays demonstrated that transfected cells remained healthy. Overall, we established an efficient protocol for transfecting hUSCs with PEDF-encoding plasmids using Lipofectamine, providing a foundation for a potentially safe and effective, virus-free cell therapy for renal fibrosis.

Future studies will compare plasmid DNA and mRNA transfection for PEDF delivery and explore methods for large-scale production of transfected hUSCs for evaluation in animal models of renal fibrosis. This work contributes a promising foundation for clinically translatable, virus-free cell therapy for CKD patients.

 # 4 Arash Ghalandarzadeh UNC Charlotte

Arash Ghalandarzadeh , Ahmed El-Ghannam, and Didier Dreau

Hydrogen peroxide (H_2O_2) is a key reactive oxygen species (ROS) produced predominantly by activated macrophages and neutrophils via the NADPH oxidase pathway during the inflammatory response following biomaterial implantation. At low concentrations, H_2O_2 plays vital roles in antimicrobial defense and redox signaling. However, its accumulation at the tissue–implant interface leads to oxidative stress, disrupts redox homeostasis, and adversely affects both cellular viability and the structural integrity of the implanted material. This oxidative imbalance can hinder tissue regeneration and contribute to chronic inflammation. To mitigate these effects, localized catalytic degradation of H_2O_2 has emerged as a critical strategy to reduce oxidative damage and modulate the immune microenvironment. Our previous in vivo studies highlight that bioactive silicon carbide (SiC) scaffolds release silicate species suppress pro- inflammatory

cytokines TNF-α, IL-1β secretion, promote macrophage M2 polarization, and enhance angiogenesis and bone regeneration. Thus, in this study, we investigated the catalytic activity of silicate ions in promoting the degradation of H_2O_2 under physiological conditions. Our results demonstrate a robust catalytic degradation of H_2O_2 across a range of concentrations, accompanied by measurable oxygen generation. The reaction followed pseudo-first-order kinetics, indicating that silicate ions act as stable catalytic mediators rather than being consumed stoichiometrically. In contrast, extracts from Ti-6Al-4V alloys exhibited negligible H_2O_2 degradation under similar conditions. Notably, the catalytic efficiency of silicate ions was enhanced in tissue culture medium (TCM), likely due to silanol deprotonation and synergistic interactions with enzymatic components. These findings suggest a dual functional roles for SiC ions, i.e., scavenging ROS and generating oxygen, thereby favoring immune modulation and tissue repair. Collectively, these findings support the use of SiC as a promising material for bioadaptive implants actively regulating the oxidative microenvironment to promote healing.

#5 Reid Christensen, Wake Forest Institute for Regenerative Medicine

Reid Christensen, David M. Kline, Hannah C. Ainsworth, Kevin A. Jankowski, Christopher A. Marks, Ryan M. Kelly, Alexei V. Mikhailov, Nathan L. Fearby, Kristina Stumpf, Lysette A. Mutkus, Hadi Pourhadi, Jingyun Lee, Cristina M. Furdui, Frank C. Marini, Jessica C. Cardenas, John B. Holcomb, Anthony Atala, Samuel P. Carmichael II

Introduction:

Adhesions are scar tissue networks that develop in the abdomen after 90% of operations. The innate immune system, coagulation system, and peritoneal mesothelial cells (PMC) work in concert to create a post-surgical thromboinflammatory environment (TIE) whereby coagulation drives inflammation. PMCs normally prevent the TIE by expressing an anti-friction epithelial glycocalyx (EpGL) and regulators of coagulation. Therefore, we propose that loss of the EpGL following surgical injury leads to TIE induction.

Methods:

We employed a rat model of abdominal adhesions to study tissue and peritoneal fluid at baseline, 24hrs, 72hrs, and 14d after laparotomy. Transmission electron microscopy (TEM) allowed quantification of EpGL height on PMCs. Immunofluorescent staining with confocal microscopy measured changes in PMC markers of adhesion formation and EpGL biomarkers (MSLN, αSMA, Muc16, Syndecan-1). Proteomic analysis was conducted by LC-MS/MS of the peritoneal fluid.

Results:

EpGL height decreased after injury, with interval regrowth. PMCs underwent a mesothelial-to-mesenchymal (MMT) fibroproliferative transformation. Immunofluorescence demonstrated an increase in αSMA and decrease in Syndecan-1. MSLN was elevated at 24h, and Muc16 was elevated at 14d. Mass spectrometry showed 24h increases in coagulation factor-X, fibrinogen beta-chain and fibrinogen gamma-chain. Tissue-type plasminogen activator and plasminogen activator inhibitor-1 were detectable at 24h.

Conclusion:

The thromboinflammatory response to surgical injury is promoted by changes to cellular and acellular fractions of the peritoneal cavity. Destruction of the EpGL is associated with loss of native anti-thrombotic architecture, and regeneration suggests proliferation of pro-thrombotic features. EpGL loss in the post-surgical abdomen contributes to the peritoneal TIE and promotes adhesion formation.

#6 Md Jahirul Islam UNC Chapel Hill

Md Jahirul Islam, Chengwen Li.

Preclinical Evaluation of AAV6-sPDL-1 Gene Therapy in Blue Light-Induced Dry AMD using

NRF2 Mouse Model

Dry age-related macular degeneration (dry AMD) remains a major cause of vision loss, with limited therapeutic options. An estimated 19.8 million Americans aged 40 and older are affected by dry AMD, with 1.49 million suffering from vision-threatening stages of the disease. To evaluate a novel immunotherapeutic approach, we tested the efficacy of adeno-associated virus (AAV)-mediated gene therapy in an NRF2 knockout mouse model subjected to blue light–induced retinal degeneration.

Initially, AAV serotypes 1–9 carrying a CBA-luciferase construct were intravitreally injected into C57BL/6 mice to determine retinal transduction efficiency. AAV6 exhibited the highest expression and was selected for therapeutic use. We engineered AAV6 expressing soluble PD-L1 (AAV6-sPDL-1), a checkpoint ligand with immunoregulatory activity.

NRF2 knockout mice received AAV6-sPDL-1 intravitreal injections 14 days before blue light exposure (460 nm, 15,000 lux, 3 hours/day for 3 days). Retinal structure was assessed using fundus imaging and OCT at baseline and post-exposure timepoints.

AAV6-sPDL-1 treatment significantly preserved outer nuclear layer (ONL) thickness and reduced fundus lesions compared to controls. These protective effects persisted for 4 months and were sustained after a second blue light challenge through 8 months. While NRF2 mice developed spontaneous age-related lesions by month 8, AAV6-sPDL-1–treated eyes showed attenuated progression.

Our findings show the durable efficacy of AAV6-sPDL-1 in dry AMD mouse model potentially reducing chronic retinal inflammation. Ongoing work focuses on elucidating cellular and molecular mechanisms in retinal and RPE cells following phototoxic injury.

#7 Khayzaran Qubbaj UNC Charlotte

Khayzaran Qubbaj, Bayne Albin, Prashant Adhikari, In Hong Yang

This study investigates Magnetic Stimulation (MSTIM) as a non-invasive, neuroprotective strategy for preventing Chemotherapy-Induced Peripheral Neuropathy (CIPN) which is a debilitating condition affecting up to 30-50 % of chemotherapy patients and often leading to treatment discontinuation. Currently, there are no effective therapies for CIPN beyond symptomatic pain management, highlighting a critical unmet clinical need.

MSTIM, an emerging therapeutic approach, uses magnetic fields to modulate neuronal excitability and has been clinically applied in the form of Transcranial Magnetic Stimulation (TMS) to treat neurological conditions such as depression and anxiety. While MSTIM has shown potential for promoting axon growth and regeneration, the underlying cellular mechanisms remains poorly understood. Prior research suggests that its efficacy is frequency-dependent, with low-frequency stimulation (10–1000 Hz) promoting neuronal plasticity, excitability, and growth in vitro. In this study, we explored whether MSTIM could protect against axonal degeneration and enhance mitochondrial trafficking which are considered key indicators of neuronal health, following chemotherapy exposure. Dorsal Root Ganglion (DRG) neurons were cultured in microfluidic devices that allowed for axonal isolation. We custom-built a magnetic stimulator that is capable of delivering 11 mT magnetic field across a range of frequencies (10 Hz to 10 kHz), with cells exposed to Paclitaxel which targets microtubules and Cisplatin which targets DNA replication. Fluorescent imaging using Calcein AM and MitoView Green were used to assess axonal integrity and mitochondrial dynamics.

The results revealed that low-frequency MSTIM (10–100 Hz) significantly improved axon length and mitochondrial trafficking, while reducing degeneration that was induced by both chemotherapeutic agents. In contrast, high-frequency stimulation (1–10 kHz) was detrimental, decreasing both axonal growth and organelle trafficking. Importantly, MSTIM offered neuroprotection independent of the chemotherapy's mechanism of action, indicating its wide-ranging potential for use.

Beyond its biological effects, MSTIM offers several advantages over electrical stimulation: it allows for focal delivery via engineered coil orientation, avoids biocompatibility issues, and eliminates the need for invasive procedures. These findings show that MSTIM can enhance subcellular organelle trafficking as a neuroprotective mechanism against CIPN, and they provide a strong foundation for developing effective, non-invasive neuromodulation strategies to help cancer patients complete their chemotherapy regimens without compromising quality of life.

AI, Medical Imaging and Devices and Big Data in Life Sciences

#8 Salman Jubair Jim UNC Charlotte
Salman Jubair Jim, Sina Lotfian, Robert Rohling, Farah Deeba
The key contribution of this work is the development of an interpretable deep learning model for placenta-mediated disease classification such as pre-eclampsia and small-for-gestational-age complications from B-mode ultrasound images. While there have been other studies that applied Quantitative Ultrasound (QUS) parameters to study placenta structure, our work introduces a new use of pre-trained deep learning architectures for enhancing classification accuracy.

#9 Jonathan Beaumont UNC Charlotte
Jonathan Beaumont, Javier Avalos Nunez, Ivan R. Wolf, Savannah Poston, Cynthia Vierra-Green, Martin Maiers, Danillo G Augusto
Phased de novo assemblies of two complex regions encoding Natural Killer cell receptors
The leukocyte receptor complex (LRC), located at chromosome 19q13.4 and the natural killer complex (NKC) at 12p13.1, encodes a plethora of activating and inhibitory receptors essential for cellular functions, significantly impacting immune responses and human health. Despite their critical role in disease susceptibility, the variation of these regions remains poorly characterized due to the challenges of aligning sequencing reads from several homologous genes to a reference genome that lacks the resolution needed to resolve its highly complex and atypical structural variation. Here, we developed a method using a set of over 4,850 manually curated hybrid capture probes optimized for comprehensive coverage. We generated sequencing libraries from seven samples, with an average fragment length of 9,310 bp, which were target-enriched and sequenced using PacBio technology. Our sequencing achieved a median Phred quality score of 42, with an average coverage depth of 1500×. Raw reads were aligned to GRCh38, variant called with DeepVariant, phased with WhatsHap and assemblies were generated with Canu for each haplotype. Our approach successfully phased and average of 93% of the LRC into 15 haplotype blocks and 89% of the NKC into 14.7 haplotype blocks. This method can be applied to diverse samples to create a cost-efficient larger graph assembly to allow for high fidelity variant calling. In conclusion, our novel method is cost-efficient and scalable, offering a powerful solution for overcoming current limitations in high-resolution analysis of this highly polymorphic and complex genomic region.

#10 Shounak Lahiri Campell University School of Medicine
Parkinson's Disease (PD) is a chronic neurodegenerative disorder marked by progressive motor decline. Traditional assessment of motor severity relies on in-person clinical evaluations, which can be subjective and infrequent. Leveraging voice recordings as digital biomarkers offers a scalable, non-invasive alternative for tracking motor dysfunction. This study used the Parkinson's Telemonitoring dataset comprising 5,875 voice recordings from 42 individuals diagnosed with PD. Following preprocessing to remove temporal identifiers and outliers, two predictive modeling approaches were implemented. A Random Forest Regressor was trained with optimized hyperparameters using grid search. In parallel, a Long Short-Term Memory (LSTM) neural network was developed to capture temporal dependencies in speech patterns. A

sliding window approach (5 time steps) was applied to construct the time-series input for the LSTM, and models were evaluated using RMSE and R^2 on an 80/20 train-test split. The tuned Random Forest model achieved an R^2 score of 0.99 and RMSE of 0.79. The LSTM model achieved an R^2 of 0.96 and RMSE of 1.59. Predicted vs. actual plots and residual analysis confirmed strong predictive validity in both models.Both ensemble learning and deep learning techniques effectively predicted motor symptom severity in PD using acoustic voice features. The Random Forest model provided slightly higher accuracy, while the LSTM model offered temporal modeling benefits. These findings support the potential of voice-based machine learning tools for remote, objective monitoring of Parkinson's motor dysfunction, with implications for improving disease management and accessibility of care.

#11 Musah Morro Davidson College

Musah Morro and Clyde Wright

TLR9-Mediated Inflammatory Response in Acetaminophen-Induced Neonatal Lung Injury

Patent ductus arteriosus (PDA) is a common complication in preterm infants, often treated with acetaminophen (APAP) due to its safer profile. However, emerging evidence links APAP to impaired lung development and increased risk of bronchopulmonary dysplasia (BPD). This study investigates whether APAP exposure triggers lung inflammation through Toll-like receptor 9 (TLR9), a key innate immune receptor that detects mitochondrial DNA (mtDNA) released from damaged cells.Using postnatal day 14 (P14) wild-type and TLR9 knockout (KO) mice, we examined the inflammatory response after APAP or PBS treatment. Western blotting is used to assess activation of STAT3, a transcription factor involved in inflammatory signaling. In parallel, quantitative PCR (qPCR) evaluates expression of lung injury-related genes such as IL6, CXCL1, MMP9, and BIM. By comparing molecular responses in wild-type and TLR9 KO mice, we aim to determine if TLR9 is necessary for APAP-induced immune activation in the neonatal lung. The findings could reveal a previously unrecognized pathway linking APAP metabolism to immune-mediated lung injury via TLR9. These insights may help refine PDA treatment strategies, balancing ductal closure with long-term respiratory outcomes. As a next step, we plan to analyze lung structure in the same samples—measuring alveolar number and size—and compare these structural changes with levels of TLR9 activation. This integrated approach may clarify how inflammation directly impacts lung development and guide safer clinical use of APAP in preterm infants.

#12 Paulina Wright Wake Forest University School of Medicine

Paulina Wright, Cherrie Welch, Kristen Zeller, Victoria Weis, Jared Weis

Photoacoustic Imaging to Assess Intestinal Oxygenation & Perfusion: A Pilot Pediatric Clinical Study

Background:

Necrotizing enterocolitis (NEC) is hallmarked by intestinal hypoxia, which is difficult to assess. Photoacoustic imaging (PAI) noninvasively measures oxy/deoxyhemoglobin, visualizing intestinal oxygenation and blood flow, and is promising for improved NEC detection.

Methods:

Under Wake Forest IRB approval, we used an age step-down approach to evaluate PAI safety and feasibility in eight healthy pediatric participants (12 years to birth). An iThera MSOT Acuity measured intestinal oxygenation and perfusion in each abdominal quadrant before and after a lipid-rich snack. Regions-of-interest (ROIs) were manually drawn to quantify total hemoglobin (HbT) and oxygen saturation (SO_2), averaged within each ROI.

Results:

PAI measurements were obtained at baseline and 1-hour post-prandial. Paired t-tests compared pre- and post-prandial HbT and SO_2 in the left/right upper and lower quadrants, and averaged

across all regions. Significant post-prandial increases in HbT were observed in the left lower ($p<0.05$), right lower ($p<0.05$), and averaged regions ($p<0.01$), indicating increased bowel perfusion, other regions did not reach statistical significance. Minor, transient erythema from safety goggles was the only adverse event. Thus, safety of the PAI technique was confirmed and feasibility was demonstrated. Findings suggest PAI is a sensitive tool for detecting changes in intestinal blood perfusion and oxygenation.
Conclusion:
PAI is an innovative imaging modality with clinical potential for measuring biomarkers of intestinal blood flow in neonatal patients. These findings support its potential as a noninvasive biomarker for NEC diagnosis and monitoring in neonates.

#13 Ana Espinosa-Momox UNC Charlotte
Ana Espinosa-Momox and Rosario Porras-Aguilar
Mapping Microscopy Performance for Next-Gen Biomedical Imaging
As biological questions grow more complex, microscopy must evolve beyond single-mode imaging. Conventional techniques such as brightfield microscopy offer simplicity and large fields of view but lack quantitative depth, while fluorescence and confocal methods provide molecular specificity at the expense of phototoxicity, cost, and potential perturbation of live samples. To map the strengths and limitations of core modalities, we created a benchmark of brightfield, phase-contrast, and fluorescence microscopy systems at UNC Charlotte's imaging core using calibrated microspheres (0.5–15 μm). This side-by-side comparison assessed each technique's resolution capabilities, contrast mechanisms, quantitative accuracy, and operational constraints—identifying where existing approaches excel and where critical gaps remain. By highlighting these trade-offs, the benchmark establishes clear targets for emerging methods. Quantitative Phase Microscopy (QPM) can potentially address several identified gaps by providing label-free mapping of optical path length shifts—correlating directly with refractive index and cell mass—while delivering resolution comparable to standard phase techniques. We compared core-facility images to outputs from our lab's QPM system, which operates under low-intensity illumination and single-shot capture, enabling high-resolution phase-map extraction. Through this benchmark comparison, we demonstrate how our approach obtains both phase and intensity information, pointing toward multimodal workflows. The importance of this study lies in guiding both end users and developers toward integrated imaging strategies: by systematically quantifying performance across core modalities, we lay the foundation for multimodal strategies in which QPM and conventional methods together offer richer, more quantitative insights for interdisciplinary research in biomedical imaging.

#14 Asmaa Alawbali North Carolina A&T State University
Asmaa Alawbali, Lynn Ogot, Malaz Altahir
Direct Powder Extrusion (DPE) is a 3D printing technology that is gaining popularity in the pharmaceutical industry for its single-step, solvent-free printing process, making it ideal for personalized drug product development. Eudragit® L100-55 is a pH-dependent (>5.5 soluble) anionic copolymer composed of methacrylic acid and ethyl acrylate. Processing Eudragit L100-55 through the DPE 3D printing is challenging due to its high molecular weight of 320,000 g/mol, leading to high viscosity and a short thermal processing window (with a glass transition temperature of 110 °C, and material degradation occurring within 170-200 °C). The objective of this research is to mitigate the processing challenges associated with Eudragit L100-55 by formulating it with various functional excipients to modify the thermophysical properties of the polymer. A thermoplastic printhead, along with the BioX 3D printer from Cellink, was used as the DPE 3D printing technology. The Anton Paar MCR 302 Rheometer was used for the rheological investigation. The frequency sweep and temperature oscillation ramp test were

conducted to investigate formulated blend rheology at a temperature range of 120-160°C. The Mettler Toledo DSC 3+ was used to evaluate the polymer and excipient's thermal properties at a temperature range of 25-250°C and a heating rate of 15°C/min. The Morphologi 4-ID from Malvern Panalytical was used to determine particle size to evaluate the uniformity of the formulation's particle size. The findings conclude that incorporating functional excipients significantly improved the processability of Eudragit L100-55, making it suitable for DPE 3D printing applications.

#15 Paige Kulzer UNC Charlotte

Paige Kulzer, Karthik Raveendran, Nowlan Freese, Ann Loraine

With the decreasing cost and increasing accessibility of sequencing technologies, high-throughput sequencing has become a cornerstone of modern biological research. The Integrated Genome Browser (IGB) is a free, open-source desktop genome browser designed to visualize these high-throughput sequencing datasets in the context of gene annotations. Here, we highlight new capabilities in IGB for visualizing single-cell RNA-Seq (scRNA-Seq) data. Users can now color reads by individual cell or by cluster, enabling clearer interpretation of cell-type-specific expression patterns. Additionally, reads can be filtered to display only those from selected cells or clusters, simplifying the visual analysis of complex single-cell datasets. These features make IGB a powerful tool for exploring single-cell data alongside traditional bulk sequencing, offering researchers an intuitive way to validate their alignments and generate all-new visualizations of their results.

#16 Anna Skubiz Campbell University School of Osteopathic Medicine

Anna Skubiz and James J. Cappola III

Management Challenges of an 80-year-old Man with History Cerebral Amyloid Angiopathy, Chronic Atrial Fibrillation, and Intracranial Hemorrhage Presenting with Recurrent Ischemic Stroke.

Anna Grace Skubiz, MS3, CUSOM, James J. Cappola III,M.D., FACP, Chair and Associate Professor of Internal Medicine, CUSOM

Introduction: Cerebral amyloid angiopathy (CAA) is a condition of amyloid beta-peptide deposition in the small- to medium-sized vessels of the cerebral vasculature. CAA increases the risk of transient neurologic symptoms, inflammatory encephalopathy and intracranial hemorrhage (ICH).

Patient Presentation: We present an 80-year-old man we newly diagnosed with CAA based on symptomatology and radiological findings. He had a history of hypertension, chronic atrial fibrillation and three suspected ICH. His chronic oral medications included aspirin 81 mg daily, a statin daily, lisinopril daily, levothyroxine daily and acyclovir daily. He had a Watchman left atrial appendage closure (LAAC) device placed several months previously. He was hospitalized with altered mental status with no other neurologic symptoms or deficits on exam. Brain MRI showed a punctate acute infarct in the left frontal lobe with trace subarachnoid hemorrhage, old lacunar infarcts in the basal ganglia, multiple cerebral microhemorrhages and advanced chronic small vessel disease.

Conclusions: Our patient demonstrated that in the setting of CAA and increased risk of ICH, it was not possible to modify his medical therapy to further decrease his risk of a subsequent ischemic stroke. Unfortunately, the prognosis of CAA is poor with high risk for subsequent ischemic strokes and worsening vascular dementia.

#17 Udayakumar Karuppanan UNC Charlotte

Udayakumar Karuppanan, Ana Espinosa-Momox, and Rosario Porras-Aguilar

Quantitative Phase Imaging (QPI) is an emerging, label-free optical technique that provides

quantitative measurements of optical path length variations across transparent biological samples. By enabling visualization of morphological and biophysical changes in live cells without dyes or markers, QPI holds significant promise for a wide range of biomedical applications—including cancer diagnostics, infectious disease monitoring, neurodegenerative disease research, and drug response studies.

However, the widespread adoption of QPI in clinical and research environments is currently limited by the high cost and complexity of commercially available systems. This represents a significant barrier for many clinical imaging laboratories, resource-limited institutions, and global health efforts that could benefit from high-sensitivity, non-invasive imaging.

To address this gap, our lab developed a low-cost, laser-based, common-path QPI system that operates at 633 nm and leverages photoisomerization in a custom optical element. This enables simultaneous, label-free acquisition of 3D cellular information, offering a non-invasive alternative to traditional imaging techniques.

Building on this platform, we are now working to retrofit conventional brightfield microscopes into QPI-capable systems using a white-light illumination approach. This requires careful optimization of illumination parameters such as intensity and spectral content, ensuring compatibility with both the liquid crystal components and standard brightfield optics.

By quantitatively comparing the white-light intensity and spectral characteristics of the modified system with those of standard brightfield microscopes, we assess the feasibility of clinical translation. Preliminary results demonstrate strong potential for a low-cost, scalable QPI solution suitable for routine biomedical imaging and diagnostics.

Cancer Research and Tools For Personalized Medicine

#18 Madeline Childress UNC Chapel Hill

Madeline Childress, Kristen Jeffries, Natalia Krupenko

ER-Localized p53–CerS6 Interaction Links Ceramide Metabolism to Tumor Suppressor Function

The tumor suppressor p53 is a central regulator of stress responses, promoting apoptosis in response to metabolic disruption. Our recent studies show that antifolate chemotherapy, folate depletion, or serum withdrawal activates a p53-dependent transcriptional increase in Ceramide Synthase 6 (CerS6), elevating its product, C16-ceramide (C16-Cer). This lipid binds p53's DNA-binding domain, disrupts MDM2 interaction, and enhances p53 accumulation, forming a positive feedback loop. These events contribute to cancer cell death. However, the mechanism enabling interaction between membrane-resident C16-Cer and cytosolic p53 has remained unresolved. Here, we identify a stress-inducible interaction between p53 and CerS6 at the endoplasmic reticulum (ER), visualized using bimolecular fluorescence complementation (BiFC). In this system, non-fluorescent Venus fragments fused to p53 and CerS6 reconstitute fluorescence only upon direct interaction. Treatment with p53-activating agents—including methotrexate, gemcitabine, and a synthetic ceramide analog—induces robust Venus signal co-localized with the ER marker calreticulin. No signal is observed under basal conditions or with non-p53-activating agents such as lometrexol or MG-132. Stress-induced Venus fluorescence is accompanied by formation of discrete, reversible ER aggregates enriched with CerS6, suggesting a unique ER remodeling event distinct from the unfolded protein response.

These findings reveal a previously unrecognized, ER-localized, ceramide-mediated protein–protein interaction driving p53 signaling. This mechanism offers a potential target for therapeutic modulation of p53 in cancer. Furthermore, the specificity of the BiFC response to distinct chemotherapeutics suggests utility in drug screening and stress-response profiling. Together, this work defines a novel regulatory axis linking metabolic stress, lipid signaling, and tumor suppressor function.

#19 Mohamed Amin Elaguech Virginia Tech – Wake Forest University School of Biomedical Engineering and Sciences

Mohamed Amin Elaguech, Komal Sethi and Adam R. Hall

Fast and sensitive detection of target nucleic acid biomarker sequences in complex biofluids is essential for translational diagnostics. In this work, we report on the use of a solid-state nanopore assay to quantitate sequence motifs in human plasma. Extracted DNA or RNA is annealed to a biotinylated DNA oligonucleotide probe and then subjected to single-strand-specific enzymatic digestion to decompose offtarget regions. The remaining duplex product is then bound to a protein tag that enables selective detection via resistive pulse sensing. We first demonstrate our approach on single-strand DNA and single-strand RNA spiked into human plasma and then extend the methodology to double-strand DNA, expanding the range of motifs that can be targeted. These advancements position our assay as a tool for the analysis of viral, bacterial, and human genetic markers.

#20 Sudip Kumar Dam UNC Charlotte

Sudip Kumar, Tamanna Binte Huq, Juan Luis Vivero-Escoto

Pancreatic adenocarcinoma (PDAC) is a highly aggressive form of pancreatic cancer and ranks as the third leading cause of cancer-related mortality in the U.S. Late-stage diagnosis, tumor's aggressive nature, and inherent resistance to chemotherapy significantly contribute to treatment failure. While gemcitabine (GEM) remains the standard of care for PDAC, the frequent development of resistance to these drugs poses a major clinical challenge, often limiting therapeutic success. Cisplatin (cisPt) exerts its cytotoxic effects by targeting PDAC cells, which are often sensitive to cisPt due to genetic mutations commonly associated with this malignancy. Mesoporous silica nanoparticles (MSNs) represent a promising strategy for the treatment of PDAC by enabling the precise delivery of GEM and cisPt directly to tumor sites. This targeted approach has the potential to overcome chemoresistance, enhance drug efficacy, and promote cancer cell death, thereby improving overall treatment outcomes for PDAC patients.
Resistance to chemotherapy is a common challenge in the clinical management of pancreatic ductal adenocarcinoma (PDAC). To replicate this clinical scenario, we developed gemcitabine (GEM)-resistant PDAC cell lines (KCM) by gradually exposing the cells to increasing concentrations of GEM. By the end of the induction process, the KCM cells exhibited nearly a ninefold increase in resistance to GEM. To enhance drug delivery, we synthesized mesoporous silica nanoparticle (MSN)-based nanocarriers capable of delivering chemotherapeutic agents. These MSNs were loaded with varying weight percentages of GEM (10% and 18%) and/or cisplatin (cisPt; 9% and 21%) for use in both combinatorial and monotherapy approaches. When the GEM-resistant KCM cells were treated with these MSN formulations, the combination therapies (GEM 10% or 18% with cisPt 9% or 21%) and GEM monotherapy (18%) induced significantly higher levels of cell death compared to cisPt-MSN monotherapy (9% and 21%). Similarly, cell cycle analysis revealed that both the combinatorial MSN formulations and GEM monotherapy (18%) led to a marked increase in cell cycle arrest in actively dividing GEM-resistant cells, in contrast to the cisPt-MSN monotherapy.
MSN-mediated co-delivery of gemcitabine (GEM) and cisplatin (cisPt) demonstrates significant efficacy in suppressing the uncontrolled proliferation of gemcitabine-resistant KCM cells, indicating enhanced tumor containment. The ability of GEM/cisPt-loaded MSNs to induce apoptosis in chemoresistant cells highlights their potential to address key limitations of drug resistance in current pancreatic ductal adenocarcinoma (PDAC) therapies. These findings underscore the translational promise of nanoparticle-based delivery systems in improving therapeutic outcomes and advancing precision oncology for PDAC management.

#21 Prashant Adhikari UNC Charlotte

Prashant Adhikari and Khayzaran Qubbaj

Chemotherapy-induced peripheral neuropathies (CIPNs) are common, severe sequelae of anti-cancer therapies, and there are no available treatments currently. The side-effects and complications of chemotherapy drugs have significant consequences on a patient's quality of life and can cause discomfort, nausea, cyclothymia, and withdrawals alongside other common side effects. This axonal degeneration, known as "dying-back neuropathy," commonly starts at the distal ends of peripheral nerves and can lead to reduced chemotherapy dosage or stopping the treatment. In this study, we investigated the site-specific neurotoxicity of four chemotherapeutic agents—Paclitaxel (PTX), Monomethyl auristatin E (MMAE), Vincristine (VCR), and Cisplatin (CDDP)—using compartmentalized microfluidic culture platform that isolates cell bodies from axons. PTX, MMAE, and VCR, target microtubule structures, were more toxic when focally applied to axons. In contrast, CDDP, a DNA replication inhibitor, exhibited greater toxicity when applied to cell bodies. In this research, we have shown that FDA-approved drug, fluocinolone acetonide (FA), is neuroprotective against all these chemotherapy drugs in vitro. We studied the FA-mediated neuroprotection using organelle trafficking analysis methods along axons in the microchannels. The trafficking is analyzed using AI models thus providing high-throughput screening of fluorescent microscopy images. FA co-treatment with these drugs restored anterograde mitochondrial trafficking, suggesting that enhanced organelle transport may underlie its neuroprotective mechanism. Mitochondrial trafficking analysis showed that all chemotherapy drugs significantly reduced mitochondrial movement, an important function for axonal health. These findings emphasize the importance of identifying drug-specific sites of action and targeting mitochondrial health as a therapeutic approach. This study provides a foundation for developing effective, focal treatments to CIPN based on organelle trafficking and preserving neuronal integrity during chemotherapy.

#22 Reem Ali North Carolina A&T State University

Reem Ali

Neovascularization is the process of blood vessel formation by mediating angiogenesis. Tumors release pro-angiogenic factors, such as Vascular Endothelial Growth Factor (VEGF), to disrupt blood vessel endothelial lining. This incites the proliferation of blood vessels as they adopt a permeable phenotype, enabling sprouting towards the tumor site. Tumor-mediated angiogenesis is a technique used to promote tumorigenesis for tumor vascularization and facilitate entrance into the host bloodstream. Previous work has successfully demonstrated angiogenic disruption, however we seek to facilitate angiogenic sprouting by tumor mediation. Sprouting is characterized by a tip-cell phenotype, which marks the start of the sprout. We have developed a novel segregated co-culture platform that allows for complete segregation of cell types until an extracellular matrix (ECM) is introduced on demand. The selective ECM enables examination of individual cell populations by impeding chemotaxis, thus isolating cell dynamics to the effect of cell signaling. Without a medium to migrate, it is unknown how the endothelial cells will react, such as whether they still undergo sprouting. We seek to understand the mechanism behind angiogenic dynamics and explore the role of the ECM in angiogenic sprouting. The implication of angiogenic sprouting without a migration medium can lead to angiogenic inhibiting drug therapies for cancer.

#23 Kaniz Rahman North Carolina A&T State University

Kaniz Rahman and Brandon Bell

In the pharmaceutical industry, polymeric thin films enhance drug delivery and patient compliance, while 3D printing enables customizable dosage forms, multi-drug combinations, and on-demand manufacturing. The objective of this work is to fabricate a polymeric film based on a

high-molecular-weight hydroxypropyl methylcellulose (HPMC K100M), using an extrusion-based pressure-assisted micro syringe (PAM) 3D printer and subsequently characterize it. The PAM 3D printer (BioX 3D printer from Cellink) is chosen due to its ability to handle materials at low temperatures, making it suitable for pharmaceutical applications. A viscoelastic paste, known as ink, specifically suitable for PAM 3D printer was developed by mitigating challenges (bubble entrapment, poor dispersion) of HPMC K100M. The ink also consists of a plasticizer (glycerin), a solubilizer or wetting agent (polyvinylpyrrolidone, PVP), and a cholesterol-reducing drug (Fenofibrate, FNB). Ink rheology was measured using an Anton Paar MCR 302 Rheometer through tests such as viscosity curves, amplitude sweeps, frequency sweeps, and thixotropy tests. The printed dried films were characterized for mechanical strength, drug crystallinity, and dissolution using TA.XT.plus C texture analyzer, DSC (Mettler Toledo DSC 3+), and Vision G2 Classic 6 dissolution tester, respectively. The ink rheology confirmed the suitability of the ink for extrusion-based 3D printing. The mechanical and dissolution tests ensure the film has proper strength and exhibits a slower release. The drug crystallinity in the film also remained unchanged from that of unprocessed FNB. This work presents an example of 3D fabrication of an oral thin film using HPMC K100M incorporated with the pharmaceutical drug FNB.

Neurodegenerative Disease

#24 Loren Cocciolone UNC Charlotte

Loren Cocciolone and Patricijia van Oosten-Hawle

Neuron-specific roles of Hsp90 in regulating proteostasis and aging in *Caenorhabditis elegans*

Hsp90 is a molecular chaperone that plays an integral role in protein folding and the maintenance of cellular proteostasis. In the nervous system, Hsp90 and other chaperones prevent neuronal protein aggregation implicated in neurodegenerative diseases such as Alzheimer's or Parkinson's Disease. Our lab previously demonstrated that pan-neuronal overexpression of Hsp90 in C. elegans induces Transcellular Chaperone Signaling, suppressing aggregation of human amyloid beta (Aβ) protein expressed in C. elegans muscle cells. Hsp90 is also known to influence neuronal chemosensory functions either directly or through its client proteins. Specifically, gustatory and olfactory neurons are essential for regulating developmental decisions (e.g. dauer), lifespan and organismal proteostasis. We hypothesize that Hsp90 modulates these processes by interacting with client proteins in specific neuronal subsets. To investigate the endogenous neuronal expression of Hsp90 and its neuron-specific interactome, we are employing a dual approach. First, using CRISPR-Cas9, we endogenously tagged Hsp90 fused to split-GFP. This allows us to visualize Hsp90 expression patterns in neurons and provides us insights into which neurons require Hsp90 for proper function. Second, we created a strain expressing a GFP nanobody fused to TurboID in neurons. This enables us to identify the neuron-specific Hsp90 interactome via proximity labeling. Preliminary data indicates that whole-worm Hsp90 levels remain relatively constant with age, but we hypothesize that neuron-specific expression patterns may vary and influence organismal decisions affecting healthspan and aging. By analyzing the neuronal expression and interactome of Hsp90 we aim to advance our understanding how Hsp90 regulates organismal proteostasis within the nervous system.

Host-Pathogen Interactions and Infectious Diseases

#25 Erin Mills UNC Charlotte

Erin Mills, Ian Marriott and Brittany Johnson

Staphylococcus aureus is the primary causative agent of osteomyelitis. It is now apparent that osteoblasts and osteoclasts play a significant role in the pathogenesis of such infections. Their responses can be protective or exacerbate inflammatory bone loss, mediated by the recognition of microbial motifs by various host receptors. We have reported that osteoblasts respond to S.

aureus challenge, producing type I interferons, which can reduce the number of viable bacteria harbored within infected cells. Here, we demonstrate that S. aureus viability and invasion is necessary for maximal inflammatory cytokine and type I interferon responses of osteoblasts and osteoclasts. Importantly, we show that bone cells constitutively express the cytosolic nucleic acid sensors, retinoic acid inducible gene-I (RIG-I) and cyclic GMP-AMP synthase (cGAS) and demonstrate their upregulation following S. aureus invasion. RIG-I and cGAS functional status in bone cells was confirmed by showing that specific ligands for each can elevate their expression and induce cytokine responses. We have verified the specificity of such responses and have begun to establish the biological significance of RIG-I and cGAS-mediated bone cell responses with the demonstration that their attenuation increases S. aureus burden in infected cells, suggesting a potentially protective role for these sensors in osteomyelitis.

#26 Carli Camporeale UNC Charlotte

Carli Camporeale, Cassie Catacalos, Doaa Hasan, Kaitlin Klotz, Sahiti Shomalraju, Matthew Tegowski, Kate Meyer, Arthur Hunt, Sarath Chandra Janga, and Kausik Chakrabarti

The expression of a precise mRNA transcriptome is crucial for establishing cell function. To this end, the N6-methyladenosine (m6A) modification is emerging as the most prevalent and abundant chemical modification in eukaryotic mRNAs, playing important roles in various biological processes and regulation of mRNA metabolism, ranging from 5′ end-capping, polyadenylation, and translation. Thus, this modification is of importance to eukaryotic gene expression regulation. Malaria, caused by apicomplexan parasite Plasmodium falciparum, is the deadliest vector-borne disease in the world, claiming more than 600,000 lives each year. m6A modifications have been implicated in malaria gene regulation, yet its mechanistic role in mRNA metabolism remains unknown. The survival of P. falciparum in the human host is often threatened by two important stressors – febrile temperature and antimalarial drugs, which induce oxidative stress. These stress conditions significantly decrease the sensitivity of the parasite to the drug as a survival response, but the underlying molecular mechanisms remain poorly understood. Here we seek to determine the extent of m6A modifications in the malaria epitranscriptome and investigate the induced stress response on m6A dynamicity in the malaria blood stage development. To globally map m6A modifications in P. falciparum, we used DART-seq technology to directly determine m6A sites at a single-nucleotide resolution. Additionally, we have developed an m6A mapping and detection pipeline using Oxford Nanopore-based direct RNA sequencing. These studies should shed light on the extent and dynamicity of this intrinsic RNA modification in malaria and determine m6A's potential role in stress responses in the human host.

#27 Abeoseh Flemister Cannon Research Center, Atrium Health

Abeose Flemister, Micaela F. Beckman, Abhijeet A. Henry, Thomas E. Thornburg, Michael T. Brennan, Farah B. Mougeot, Jean-Luc C. Mougeot

Objective:

Xerostomia (dry mouth) is associated with salivary hypofunction and/ or hyposalivation. Increased risk for xerostomia includes aging, autoimmune disease, medication, and radiation therapy. Xerostomia can exacerbate oral complications such as dental caries and periodontal disease. Objective: to determine differences between oral microbiome of xerostomic vs. non-xerostomic patients.

Methods:

Oral samples (saliva [S], buccal mucosa [B], and tongue swabs [T]) were collected from 27 xerostomic patients (n=81 samples) and non-xerostomic controls (n=54 samples). Next generation sequencing of the 16S rRNA gene was performed for bacterial identification. Normalized relative abundance data were square root-transformed and converted to Bray-Curtis

similarity matrices. beta-diversity was determined by PERMANOVA (Rv4.4.2) to compare xerostomic patients to controls (veganv2.7.1; 1000 permutations). Wilcoxon rank sum test was used to determine significant species-level differential features (Bonferroni correction; $\alpha=0.05$) which were confirmed via LEfSe (lefserv 1.18.0).

Results”

We identified significant microbial profile differences between xerostomic and non-xerostomic groups ($p<0.001$). LEfSe identified eight species including caries-associated species, Streptococcus mutans (padj=0.001; LDA score=2.8) and Scardovia wiggsiae (padj=0.03; LDA score=2.9) in xerostomic patients. In the non-xerostomic control group, however, LefSE identified 31 species including inflammation reducing Prevotella histicola-jejuni (padj=0.001; LDA score=-2.75).

Conclusion:

There were significant differences between bacterial communities of patients with and without xerostomia, including dominance of pathogenic species in xerostomic vs. protective species in non-xerostomic groups.

Afternoon Poster Session

Viewing 1:15 PM-5:00 PM Presenters present 4:15 PM -5:00 PM

Regenerative Medicine

#1 Isah Jain UNC Charlotte

Isah Jain, Stevie Clemens, Alex Cope, Abigail Leavitt LaBella

Why are synonymous codons that code for the same amino acids used at unequal frequencies across the genome? One reason is that synonymous codons influence cellular translational and transcriptional dynamics, impacting gene expression, protein function, and cellular health. Therefore, we know that codon usage is shaped by both neutral and selective forces and that the balance between these two forces varies between species. We are investigating the factors shaping this balance. Leveraging the Ribosomal Overhead Cost version of the Stochastic Evolutionary Model of Protein Production Rates (ROC-SEMPPR) to disentangle the effects of natural selection from mutation biases on a comprehensive dataset of 1,154 sequenced yeast genomes, we hypothesize that species-specific genomic features and gene presence significantly shape the mutation-selection equilibrium. We are testing whether the presence or absence of genes and variations in species characteristics (genotype, phenotype, environment) correlate with codon-specific mutation and selection rates. Through data visualization and statistical modeling, this work aims to analyze the extensive metadata associated with these genomes. This approach will reveal how genomic and biological features drive codon shifts, enhancing our understanding of codon evolution in eukaryotes. The findings will refine the application of codon usage metrics in evolutionary studies and optimize heterologous gene expression by accounting for species-specific and gene-specific variations in translational selection. This research addresses fundamental questions about the dynamics of codon evolution and its impact on gene expression, contributing a deeper understanding of translational dynamics across diverse eukaryotic lineages; a foundation for advancing both precision medicine and synthetic biology.

#2 Po-Feng Lee Wake Forest Institute for Regenerative Medicine

Po-Feng Lee , Adit Mehta, Eric Renteria, Frank Marini, Ji Hyun Kim, Tracy Criswell, Thomas Shupe, Anthony Atala, Joshua Hunsberger, Metin N. Gurcan, Shay Soker, Young Min Ju, James J. Yoo

Multi-functional Solid 3D Organ Bioreactor Platform for Regenerative Medicine Applications

Problem/Purpose/Objective:

Regenerative medicine is rapidly transitioning from the research phase towards the clinical phase. Many cell-based tissue-engineered products require the use of tissue-specific bioreactors for preconditioning and maturation; however, clinically usable tissue or organ-specific bioreactors are not available, and many bioreactors are custom-made which creates regulatory and manufacturing challenges. This study aimed to develop a standardized, self-contained, and modular bioreactor platform that allows for a scalable and automated process for the clinical manufacturing of solid 3D organ constructs.

Methods:

The design considerations for the solid 3D bioreactor components included biocompatibility, scalability, and functionality. Applying these design considerations, we developed a solid 3D organ-specific bioreactor prototype, consisting of a rotatable and pressurizable organ enclosure to fit and stabilize organs in different shapes or sizes. This enclosure also minimizes stress concentration from gravity influence during whole organ perfusion. The constant-pressure motion was carried out by integrating the flow pump, flow rate sensor, pressure sensor, and PID controller to minimize the delay or overshoot of the flow rate, which could lead to organ damage. Baseline tests under constant pressure and constant-flowrate perfusion modes were conducted

using a decellularized porcine kidney to confirm the functionality and reliability of the bioreactor.
Results:
Our results showed the bioreactor system's proper operation, with quantitative data displayed by the integrated sensors. Under the proportional-integral-derivative (PID)-controlled flow, we were able to perfuse multiple organs with one gear pump simultaneously, and the pressure of the renal artery during perfusion was successfully maintained for 48 hours without a flow rate overshoot observed. The design of rotable and pressurizable organ enclosure improved the organ circulation as evidenced by the dye perfusion experiment. The module was successfully used for porcine kidney conditioning to maintain scaffold integrity.
Conclusion/Significance:
The multi-functional perfusion bioreactor has been successfully validated and may be used as a standard tool for biomanufacturing tissue-engineered solid 3D organ constructs, and the perfusion system can be applied to other perfusion-based tissue bioreactors. The development of a standardized tissue-specific bioreactor platform may facilitate rapid translation of tissue-engineered medical products to the clinic.

#3 Caleb Aguayo Wake Forest Institute for Regenerative Medicine
C.A. Aguayo and P. M. McNutt
The human neuromuscular junction (NMJ) is a specialized synapse that modulates neurological control over muscle contraction While the neurophysiological properties of the NMJ have been extensively characterized in animal models, our knowledge of human NMJ neurophysiology remains limited. Compared to animal models, human NMJs are smaller, less complex, and more fragmented, with divergent molecular and cellular characteristics. Furthermore, NMJs are vulnerable entry points for pathogens and toxins that can impair motor function and propagate central nervous system infections. Despite the clinical importance of NMJ's, existing methods for studying human NMJs remain limited, hindering our ability to model disease mechanisms and develop targeted therapies. We optimized a protocol for generating functional human NMJs through directed differentiation of pluripotent stem cells via a neuromesodermal pathway, yielding cultures that recapitulate key features of native human NMJs, including tripartite cellular composition, molecular organization, synaptic architecture, and electrophysiological properties. Quantitative PCR analysis of gene expression at days 6, 15, and 25 confirmed progressive NMJ maturation through expression of neuronal (TUBB3, ChAT), muscle (CHRNA1, FBXO32), and synaptic (SV2) markers, indicating functional neuromuscular connectivity. NMJ formation was further validated by using α-bungarotoxin to label nicotinic acetylcholine receptors, and immunocytochemistry to detect mature neuronal cells (neurofilament) and skeletal muscle (myosin) markers. To validate this platform as a tool for investigating neurotoxin-induced pathologies, we characterized the effects of two neuroparalytic toxins. First, exposure to the neuromuscular blocking agent curare led to total inhibition of contraction within 5 min (n=4), by blocking nicotinic acetylcholine receptors and preventing neural activation of skeletal muscle. Second, we exposed the NMJ's to botulinum neurotoxin while evaluating synaptic transmission using multielectrode arrays. BoNT/A exposure at 10 pM (n=4) significantly decreased mean firing rate by 80% and burst frequency by 90% compared to vehicle-treated controls (n=4, $p<0.001$, two-way ANOVA followed by Dunnett's multiple comparison test), while culture viability remained unchanged. These results demonstrate that the platform expresses the key features of neuromuscular transmission. This validated human model enables mechanistic investigation of neurotoxin-induced paralysis and provides a translational platform for developing countermeasures against NMJ toxicity.

#4 Carol Bosholm Wake Forest Institute for Regenerative Medicine
Carol Bosholm, Yuanyuan Zhang, Jay Ma, Hainin Zhu
Introduction: Age-related macular degeneration (AMD) is a leading cause of vision loss in older

adults. Cell replacement therapy using retinal pigment epithelial (RPE) cells derived from induced pluripotent stem cells (iPSCs) offers a promising therapeutic approach. Urine-derived iPSCs (u-iPSCs) provide a non-invasive and accessible source of cells for regenerative medicine.
Methods and Materials: To optimize RPE cell generation from u-iPSCs, we compared two commonly used differentiation methods: Embryoid Body (EB) Differentiation and Triphasic RPE Differentiation. Both methods were evaluated for their efficiency, purity, and functional properties of the resulting RPE cells.
Results: Both methods successfully generated RPEP cells from u-iPSCs. EB Differentiation: iPSCs were aggregated into 3D spheroids-like. EBs were cultured in specific media containing growth factors and signaling molecules to induce RPEP differentiation. Triphasic RPE Differentiation: u-iPSCs were induced to differentiate into neuroectodermal cells, neuroretinal progenitor cells and subsequently RPEP cells. However, the EB method demonstrated a higher efficiency in terms of cell yield and RPEP cell purity.
Conclusion: By comparing these two methods, we aim to identify the most effective approach for generating functional RPE cells from u-iPSCs. This information will be crucial for developing advanced cell-based therapies for AMD and other retinal diseases.

#5 David Long Wake Forest Institute for Regenerative Medicine
David Long, Carlo Christine, Qian Wan, Anthony Atala, Yuanyuan Zhang
Corneal wounding and limbal stem cell deficiency (LSCD) can lead to significant visual impairment and ocular health challenges. Tissue engineering approaches using stem cells seeded on biomaterials show promise for corneal repair and offer a potential solution to restore vision and improve patient outcomes. Autologous adult stem cells isolated from various tissues such as bone marrow, fat, and corneal-limbal stroma have multipotent potential to promote corneal repair. However, obtaining these stem cells requires invasive biopsies. This study investigates the regenerative potential of human urine-derived stem cells (USCs), a non-invasive and readily available stem cell population, seeded on decellularized small intestinal submucosa (SIS) to generate autologous stratified epithelium for corneal repair.

#6 Abdulkadir Kabasakal Wake Forest Institute for Regenerative Medicine
Abdulkadir Kabasakal, Sunil K. George, Olivia Clemenson, Denethia Green, Erika Billman, Ji Hyun Kim, Sang Jin Lee, Bill Vaughan, Antony Atala, James Yoo, Young Min Ju
Burn injuries, prevalent in battlefield trauma, necessitate prompt necrotic tissue removal and wound coverage to optimize patient outcomes. Traditional grafts encounter limitations such as donor site constraints and immune rejection. We previously developed a novel treatment employing conditioned media factors (CMFs) derived from human placental stem cells (hPSCs), which demonstrated enhanced wound healing in small animal models. In this study, we investigated growth factor mimetic peptides as a potential substitute, highlighting their advantages, including reduced immunogenicity, cost-effectiveness, and enhanced stability. We assess their therapeutic efficacy in promoting cell proliferation and migration in comparison to CMFs in a preclinical large animal model.
We have developed a novel alginate/gelatin-based skin graft that incorporates either hPSC-derived CMFs or synthetic growth factor mimetic peptides, which represent key proteins from the stem cell secretome. Nine recombinant protein and mimetic peptide cocktails were initially evaluated in vitro for their effects on cell proliferation and migration. The most promising formulations were subsequently tested in a full-thickness wound model in specific pathogen-free pigs. The extent of wound healing was assessed through measurements of wound closure, contraction, and detailed histological analyses that evaluated cell proliferation, new tissue formation, and angiogenesis.
The results showed that the mimetic peptide cocktail enhances cell proliferation and migration in vitro and facilitates wound closure in vivo. The mimetic peptide treatment appears as a similar effective CMF treatment, showing a potential alternative with further development.

In summary, this study highlights mimetic peptides as a promising off-the-shelf alternative to CMF-based treatments. The alginate/gelatin skin graft, loaded with specific mimetic peptides, emerges as an advanced wound care strategy for full-thickness combat burns. This approach offers enhanced healing potential, improved formulation stability, and reduced production costs.

#7 Olivia Clemensen Wake Forest Institute for Regenerative Medicine

Olivia Clemensen, Seunggyu Jeon, Po-Feng Lee, Erika Billman, Pamela Marahwa, Vasilios Ioannis Liaskonis, Young Min Ju, John Jackson, Anthony Atala, James J. Yoo, Ji Hyun Kim

Volumetric muscle loss (VML), resulting from severe injuries, surgical resections, or progressive muscular disorders, leads to permanent functional impairment. Current gold standard treatments, such as autologous muscle flap surgery, are limited by donor tissue availability. Cell-based therapies offer promise in small-size regeneration; however, are limited by low cell survival rates and the high failure rate of volume-stable tissue formation make these approaches challenging. To address these limitations, we developed a platform technology using uniform IGF-1-conjugated decellularized muscle fiber fragments (dMFF-IGF-1, 50 μm) to promote host muscle regeneration and integration. Here, we investigate the feasibility of using this platform technology to fabricate transplantable muscle constructs as an off-the-shelf product for the treatment of VML.

A bioprinting protocol was established using dMFF-laden fibrin-based bioink and a gelatin-based sacrificial bioink. Printing parameters, including dMFF concentration, dispensing pressure, feed rate, and nozzle size, were optimized. Microscopy confirmed the preservation of dMFF morphology and uniform distribution within printed constructs. Muscle cell proliferation was evaluated using the CellTiter-Glo ATP assay.

Bioprinted dMFFs retained consistent size and morphology. Constructs containing dMFF-IGF-1 significantly enhanced muscle cell proliferation compared to serum-free and dMFF-only controls ($n = 6$, $p < 0.05$). A transplantable muscle construct with multi-layered, aligned muscle micro-bundles was successfully fabricated.

These findings demonstrate the feasibility of using dMFF-IGF-1 into a bioink for bioprinting transplantable muscle constructs. Ongoing in vitro and in vivo studies aim to validate this platform as a potential off-the-shelf therapy for VML and related conditions.

#8 Pamela Marahwa Wake Forest Institute for Regenerative Medicine

Erika Billman, Ji Hyun Kim, Vladimir Mashanov, Gyun Moo Kim, Bill Vaughan, John Jackson, Anthony Atala, and James Yoo

Development of Functionalized Acellular Muscle Fiber Fragments as an Off-the-Shelf Medical Product

Introduction: Muscle loss due to traumatic injuries, tumor resections, and degenerative diseases can lead to long-term functional impairment. Current gold-standard surgical techniques, such as muscle grafts, present with limitations, including donor tissue availability and morbidity. Alternatively, cell-based bioengineered tissues show promise for tissue regeneration; however, challenges remain in developing clinically significant functional muscle tissues. Moreover, cell-based approaches require lengthy and complex manufacturing processes. To overcome this critical challenge, this study aimed to develop uniformly sized acellular (decellularized) functional muscle fiber fragments (dMFF) as an off-the-shelf product. The processed dMFFs readily assemble into aligned muscle fibers in vivo, integrating with host muscle tissue. This study aims to establish an effective protocol to produce biologically functional, uniform-sized dMFF-IGF for efficient manufacturing.

Methods: To prepare the uniformly sized dMFFs, porcine muscle tissues were cut, dissociated, and decellularized through three freeze-thaw cycles and DNAse treatment, followed by filtration. The processed dMFFs were functionalized by conjugating with insulin-like growth factors (IGF-1) (dMFF-IGF-1) to promote host muscle cell migration and differentiation. The efficiency of dMFF production was evaluated by size measurement, DAPI staining, and scanning electron

microscopy. The IGF-1 conjugation efficiency was assessed using IGF-1 immunostaining and ELISA assay.
Results: Our protocol achieved a yield of 56% uniform-sized (50 mm length x 50 mm width) dMFFs. The decellularization process efficiently removed DNAs from the MFFs (< 50 ng/mg) while preserving their myofiber-specific aligned microstructure. We demonstrated successful conjugation of IGF-1 to the dMFFs, achieving over 90% conjugation efficiency.
Conclusion/Significance: We successfully established a dMFF manufacturing protocol, enabling the consistent production of uniformly sized, IGF-1 conjugated dMFFs. Further investigations include in vitro and in vivo studies to investigate the capability of dMFF-IGF-1 in forming aligned and functional muscle tissue The successful completion of this study holds the potential to produce an off-the-shelf, point-of-care product for treating various muscle-associated conditions, such as extensive muscle injuries.

#9 Emily Fresenko Wake Forest Institute for Regenerative Medicine
Emily Fresenko, Carol Bosholm, Sarfaraz Ahmad, Vy H. Vuong, Patrick McNutt, Jay Ma, Anthony Atala, and Yuanyuan Zhang
PEDF-Enriched Exosomes from Urine-Derived Stem Cells for Potential Corneal Repair
Purpose: Severe corneal damage and vision loss result from exposure to chemicals like alkali and mustard gas, and current treatments often fall short. In our rabbit model of alkali-induced corneal injury, we observed significant upregulation of pro-inflammatory and angiogenic markers, including Interleukin-1β (IL-1β) and Vascular Endothelial Growth Factor (VEGF), highlighting the need for therapies that can regulate these pathological responses. Therefore, this study aims to investigate a novel regenerative strategy: leveraging human urine-derived stem cells (hUSCs) to produce PEDF-enriched exosomes for potential therapeutic intervention in corneal repair.
Methods: Human urine samples (n = 3) were collected and cultured to isolate hUSCs. To optimize transfection conditions, hUSCs were transfected with either plasmids or mRNA encoding reporter proteins. Transfection efficiency and cell viability were assessed. At 90% confluence, hUSCs were transfected with PEDF mRNA using lipid nanoparticles to enhance PEDF expression. PEDF levels were measured by Western blot. PEDF-enriched exosomes were isolated from the conditioned medium and characterized for size, morphology, and PEDF content.
Results: hUSCs were successfully transfected with both plasmids and mRNA, with low nanoparticle doses preserving cell viability. PEDF mRNA transfection increased PEDF expression in hUSCs and enhanced the production of PEDF-enriched exosomes. In parallel, topical PEDF treatment in the rabbit corneal injury model reduced both VEGF and IL-1β expression, supporting the therapeutic relevance of PEDF delivery in modulating inflammation and neovascularization.
Conclusions: PEDF-enriched exosomes from hUSCs offer a promising non-invasive strategy for chemical-induced corneal repair. Further studies are needed to optimize efficacy and assess in vivo applications.

Big Data in Life Sciences

#10 Javier Avalos Nunez UNC Charlotte
Javier Avalos Nunez, Jonathan Beaumont, Veronica Calonga Solis, Ticiana Farias DL Farias, Ivan Wolf, Danillo Gardenal Augusto
Elucidating complex immune-related regions via a novel long-sequencing method
Natural killer (NK) cells mediate the innate immune response against viral pathogens and neoplastic cells. Their activation occurs via a balance of signals through inhibitory and activating receptors. The genes encoding these receptors are located in two gene families, the leukocyte receptor complex (LRC) and the natural killer cell complex (NKC). These genomic regions are exceptionally difficult to sequence and analyze at high resolution due to high levels of

polymorphism and structural variation. Here, we propose a novel method of long-read sequencing that can help elucidate the structure of these regions. DNA libraries were prepared by fragmenting high quality genomic DNA. Fragments were then end-repaired, dA-tailed, and ligated to stubby adaptors. Next, each sample was barcoded by a unique adaptor and PCR-amplified. Following quality control and pooling, the DNA libraries were enriched for the LRC and NKC regions using biotinylated probes. Enriched libraries with a size of 2800 bp were then sequenced with Oxford Nanopore technology and processed with our custom bioinformatics pipeline. We obtained 150X depth for these regions and longer reads than traditional short-read methods, which will allow us to evaluate structural variation and haplotypes of these regions in several human populations, including African and Amerindian populations. We will use this data to study aspects of evolution such as migration, mutation rates, and natural selection. Understanding the evolutionary processes and selective pressures acting on these regions can help inform NK cell biology and provide personalized medicine solutions.

#11 Trenton Thompson Davidson College

Trenton Thompson and Debbie Thurtle-Schmidt

Triodanis perfoliata, a small flowering plant native to the Americas, exhibits unique reproductive strategies that support its survival in dynamic and often harsh environments. Investigating its genome offers valuable insights into how plants maintain genetic diversity and adapt to climate change. Assembling a genome is much like reconstructing a book from scattered, sometimes repetitive pages—and in plants, this task is especially difficult due to the structural complexity of their genomes and challenges in obtaining high-quality DNA. To address this, I employed a hybrid sequencing strategy that integrates Nanopore long reads, Illumina short reads, and Hi-C chromatin conformation data to generate a high-quality de novo genome assembly. The initial assembly spans 972.4 Mb, representing approximately 83% of the estimated genome size. Benchmarking Universal Single-Copy Orthologs (BUSCO) analysis indicates high completeness at 98.8%, while QUAST analysis reports ~16.3K contigs with an N50 of 114,457 bp and a GC content of 35.26%. Further refinement using Illumina-based polishing and Hi-C scaffolding will aid in resolving ploidy level and determining chromosome number. This research advances the field of plant genomics and sheds light on the adaptive strategies of underexplored species facing environmental pressures such as resource scarcity and climate variability.

#12 Taylor Powell UNC Charlotte

Taylor Powell and Abigail L. LaBella

Over the course of hundreds of millions of years, budding yeasts of the subphylum Saccharomycotina have evolved and speciated into around 1,100 unique species, each with their own specific growth characteristics and ecological niches. Some yeasts, such as Candida sake, can thrive along the icy soil patches of Antarctica, while other yeasts, such as the cactus-dwelling Candida thermophila, prefer to live in hot, dry, desert climates. This difference in growth temperature preference among yeasts is especially important for predicting potential pathogenicity. Of particular interest is growth at 37 degrees Celsius, or human body temperature. To explore the genetic underpinnings of this thermotolerance characteristic, we employed random forest analysis and Shapley analysis. We trained random forest models to predict growth at 37C using codon optimization values for thousands of genes across hundreds of species of yeasts. Codon optimization, in short, is the process by which codons that maximize translation efficiency are evolutionarily selected for in highly expressed genes, leading to an optimization of codon usage over time. To interrogate which features from the random forest analysis were most important for determining growth at 37C, we employed Shapley analysis, which is a feature-importance analysis method used to provide significance metrics for specific target variables. Our findings suggest that using codon optimization values as input data produces a higher accuracy model than using other features, such as gene presence/absence. These results allow us

to explore the evolution of gene expression as it's related to thermotolerance in Saccharomycotina yeasts.

#13 Jack Fowler Atrium Health

Jack Fowler, Micaela F. Beckman, Abhijeet A. Henry, Thomas E. Thornburg, Michael T. Brennan, Farah B. Mougeot, Jean-Luc C. Mougeot

Salivary Proteome Analysis of Xerostomic Patients

Introduction: Xerostomia is the subjective complaint of dry mouth, impacting an individual's quality of life and oral health. It is associated with salivary flow reduction and/ or salivary gland hypofunction. Our objective was to identify differentially expressed proteins (DEPs) in saliva samples of individuals with and without xerostomia.

Methods: Saliva samples were collected from patients (N=28 total) with medication associated xerostomia (XM; n=4 samples), autoimmune disease associated xerostomia (XA; n=6) and control subjects without xerostomia (NX; n=18). Proteomic analysis was performed by nanoLC-MS/MS. Mann-Whitney U-test was used to determine DEPs of NX vs. XA groups and NX vs. XM groups with Benjamini-Hochberg correction (α=0.05). The STRING online program was used to generate protein-protein interaction (PPI) networks (CL=0.9) and to perform a pathway analysis sourced from the Kyoto Encyclopedia of Genes and Genomes (KEGG) database (α=0.001).

Results: Considering all three comparisons combined, over 5400 proteins were detected (padj<0.05). Unique protein profiles were identified when comparing NX vs. XA and XM groups combined (n=138 proteins). The GOFD2 protein (padj<0.05) was under-represented in XA group. For XM group, STRING, with an input of 138 proteins, returned a PPI network of 23 proteins. The network included microtubule structure and amyotrophic lateral sclerosis-associated proteins and TUBB (upregulated; padj=0.00016), TUBA1B (upregulated; padj=1.477e-05) and DCTN3 (downregulated; padj=0.00095), found significant by KEGG analysis.

Conclusions: These findings suggest that Xerostomia has an effect on the abundance of microtubule structural proteins in saliva, warranting further investigation regarding the origin of such observation.

Cancer Research and Tools For Personalized Medicine

#14 Suruchi Poddar Wake Forest University

Suruchi Poddar, Dorothea A. Erxleben, Rebecca J. Dodd, Heidi L. Reesink, Matthew Thomas, Anthony J. Day, Paul L. DeAngelis, Adam R. Hall

Hyaluronic acid (HA), or hyaluronan, plays vital roles in numerous physiological processes, with its biological effects largely influenced by its molecular weight. High molecular weight HA (HMW-HA) typically exhibits anti-inflammatory properties, whereas low molecular weight HA (LMW-HA) tends to promote inflammation. One key mechanism underlying the degradation of HA and the generation of LMW-HA during inflammation involves oxygen-derived free radicals (ODFRs) or reactive oxygen species (ROS). In inflammatory conditions, HA can undergo covalent modification through the attachment of heavy chain (HC) components from the inter alpha trypsin inhibitor (IαI) protein, forming a stable HC-HA complex. Literature suggests that such HC-modified HA complexes can modulate inflammatory responses during tissue injury or infection. To investigate the protective potential of heavy chain modification against HA degradation, we examined whether HC attachment shields HA from depolymerization under oxidative stress. Using high molecular weight HA (321 kDa) and an HC-HA complex of comparable size, we assessed HA fragmentation in the presence and absence of heavy chains, employing copper chloride (CuCl2) as an oxidative system combined with hydrogen peroxide (H2O2). Solid-state nanopore technology enabled us to analyze the molecular weight distribution

of HA under these conditions. Control experiments with bovine serum albumin (BSA) and IαI confirmed the specificity of HC protection. Further, we demonstrated that only covalently bound heavy chains confer this protective effect, as free heavy chains did not prevent HA degradation. Validation in equine synovial fluid samples supports the conclusion that heavy chain modification is a crucial mechanism for preserving HA integrity during inflammation-induced oxidative stress.

#15 Zahra Saghaie Dehkordi UNC Charlotte

Zahra Saghaie Dehkordi and M. Taghi Mostafavi

Ovarian cancer (OC) is one of the most fatal gynecologic cancers, mostly because of its complex nature which is usually diagnosed at a late stage. There are some traditional screening methods, like the CA-125 test, which is not reliable for ovarian cancer because of high rates of false positives. This highlights a need for more sensitive and specific diagnostic tools.

This study explores a promising alternative: analyzing microRNA (miRNA) profiles from blood serum. The main idea is that a simple blood draw could reveal the presence of ovarian cancer. Our study applied advanced machine learning and deep learning techniques to a dataset containing 700 OC and 8000 Normal samples, each with 2550 miRNA features. This non-invasive approach avoids the need for tissue biopsies, potentially making routine screening more accessible. Our findings show that the computational approaches can effectively tackle the challenges in OC diagnostics. Our computational models could distinguish between cancerous and healthy samples with 99% accuracy. Moreover, the study demonstrates a robust ability to identify the disease in its early stages, with high accuracy of 90% and a weighted F1-score of 0.90. The next step for this research would be to apply AI techniques, such as SHAP (SHapley Additive exPlanations) analyses on the trained models, to identify and rank the miRNAs most influential in the classification tasks. This research lays a strong foundation for developing a reliable blood test for early ovarian cancer detection, which, after further clinical validation, could be integrated into regular health checkups for at-risk women.

#16 Upasana Das Wake Forest University School of Medicine

Upasana Das and William H. Gmeiner

Being one of the most common cancers worldwide, colorectal cancer (CRC) treatment deals with the challenges due to systemic toxicity and drug resistance associated with the most conventional therapeutic agent, 5-fluorouracil (5FU). A next generation poly-fluorodeoxyuridine drug candidate, CF10 has been established, with improved efficacy in multiple CRC cell lines, relative to its previous versions F10 (10-mer of fluorodeoxyuridylate) and 5FU. On the other side, 5-ehtynyl-2'-deoxyuridine (EdU) is a thymidylate analogue that is commonly used to quantify proliferative cells, as it is incorporated in DNA during replication. In this study we reported synergistic interaction between CF10 and EdU in colorectal cancer cells. The EdU+CF10 combination causes cell cycle arrest at S to G2/M phase in asynchronized cells and S phase in synchronized cell population, suggesting replication stress in synergistic conditions. We showed by in situ click reaction and neutral comet assay that the presence of CF10 with EdU significantly increased the incorporation of the later into the DNA, leading to severe DNA damage. Confocal micrographs have exhibited evidence of abnormal spindle fiber formation in the combination treatments. Fluorescence in situ hybridization showed remarkable reduction in telomere signals in the synergistic combinations. Our results are consistent with CF10 enhancing the extent of EdU incorporation into DNA to cause telomere attrition and induce mitotic catastrophe in CRC cells. These suggest combining EdU+CF10 could lead to a more effective therapy for CRC treatment.

#17 Francesco Brusco Davidson College

Francesco Brusco, Y. Emily Chu, P. Brent Ferrell

Hepatocyte Growth Factor (HGF), elevated in acute myeloid leukemia (AML) – a hematologic

cancer characterized by the accumulation of immature myeloid cells. In other pathological models, HGF has demonstrated a role in promoting tumorigenesis and immune modulation. Despite the notably high levels of HGF in AML, the effect of this growth factor remains poorly characterized within the AML microenvironment. This study investigates the dual role of HGF in AML by further examining its effects against AML and CD8+ T-cells. First, we used Western Blots to validate the presence of HGF in mouse models of AML. We found that HGF was expressed in leukemic marrow of MLL-AF9 and FLT3-NPM1 models, but was absent in healthy marrow. Our lab identified CD8+ T-cell dysfunction in these mouse models of AML. Therefore, we hypothesized that HGF may directly impact CD8+ T-cell viability and proliferation. We performed cell proliferation and apoptosis assays on CD8+ T-cells in the presence of HGF concentrations at varying stages of differentiation. Our preliminary results suggest HGF impairs activated CD8+ T-cell survival and promotes AML cell growth. Expression profiling revealed heterogeneous expression of HGF specific receptor, cMET, in AML models, FLT3-NPM1 and MLL-AF9; as well as differential cMET expression across time points of activating CD8+ T-cells. Future studies include further assaying HGF effects on CD8+ T-cells, investigation of HGF affecting CD8+ T-cells from AML microenvironments, and the use of cMET inhibitors, like crizotinib. Overall, our findings highlight the HGF-cMET axis as a potential therapeutic target in AML with implications for immunotherapy.

#18 Akanksha Behl Wake Forest University School of Medicine

Akanksha Behl and William Gmeiner

The combination of chemotherapy and immunotherapy offers a promising strategy for cancer treatment, but the underlying mechanisms require further investigation to optimize therapeutic protocols. One key mechanism involves the release of danger-associated molecular patterns (DAMPs) from tumor cells undergoing stress or death. These molecules can activate immune cells, including dendritic cells (DCs), but their specific role following chemotherapy is not fully understood.In this study, we examined the effects of colorectal cancer (CRC) cells treated with CF10 and/or 5-fluorouracil (5-FU). We found that chemotherapy-treated CRC cells released elevated levels of DAMPs, including high-mobility group box 1 (HMGB1), eATP, and calreticulin. Supernatants from these cells promoted the maturation of mice and human DCs, as indicated by upregulation of MHC-II, CD80, and CD86, along with increased secretion of IL-1β, TNF-α, MIP-1α, MIP-1β, and RANTES.Importantly, DCs pulsed with these supernatants, when used as vaccines, significantly improved overall survival in tumor-bearing mice and induced a robust $CD8^+$ T cell response in the spleen, suggesting a strong systemic anti-tumor effect. These findings highlight the immuno-adjuvant potential of DAMPs released from chemotherapy-stressed cancer cells. By activating DCs and enhancing anti-tumor T cell responses, DAMPs represent a critical link between chemotherapy and adaptive immunity. This work supports the development of novel chemoimmunotherapy strategies that exploit DAMP-mediated immune activation to improve cancer outcomes.

#19 Halle Meyers UNC Chapel Hill

Halle M. Meyers, Jaspreet Sharma, Amira A. Abdellatef, Mikyoung You, David Raines, Kyle C. Strickland, Susan Sumner, Blake R. Rushing, Natalia I. Krupenko and Sergey A. Krupenko. Nutrition Research Institute, UNC-Chapel Hill; Department of Food and Nutrition and the Convergence Center for Green Anti-Aging Research, Mokpo National University, Republic of Korea; Labcorp, Durham, NC; Duke University Medical Center.

Differential expression of one-carbon pathway enzyme ALDH1L1 is linked to tumorigenicity of low-grade bladder cancer cells through metabolic reprogramming.

The RT4 bladder cancer cell line is one of the few cancer cell lineages that maintain high expression of the candidate tumor suppressor ALDH1L1. We investigated how differential ALDH1L1 expression affects the physiological characteristics, tumorigenicity, and metabotype of RT4 cells. We characterized RT4 cells and two shRNA clones (sh506/low ALDH1L1

expression; sh572/complete ALDH1L1 loss) for proliferation, migration, clonogenic capacity, and mitochondrial respiration. Further, we investigated the tumorigenic potential of the RT4 clones through untargeted metabolomic analysis. Both clones exhibited increased proliferation, enhanced motility, and higher clonogenic capacity compared to RT4 cells. Proliferation and clonogenic capacity were highest for the sh506 clone (low ALDH1L1 expression), while motility was strongest for the sh572 clone (complete ALDH1L1 loss). Both clones exhibited altered energy metabolism, as indicated by a reduced basal oxygen consumption rate and an enhanced maximal respiration rate following oligomycin treatment. Xenograft tumors derived from ALDH1L1-deficient clones were significantly larger than RT4 cell-derived tumors. Interestingly, complete loss of ALDH1L1 (sh572 clone) was less advantageous for tumor growth than partial loss of the protein (sh506 clone). Untargeted metabolomics revealed that tumors derived from RT4 clones had altered metabolism of fatty acids, amino acids, CoA, and acylcarnitines. Additional alterations were observed in several pathways, including glutathione metabolism (sh506) and TCA cycle (sh572). Our study highlights ALDH1L1 as a key metabolic regulator of proliferation and tumorigenicity in RT4 bladder cancer cells and suggests that low ALDH1L1 expression provides a metabolic advantage for the growth of aggressive tumors.

#20 Sara Scala UNC Charlotte

Sara Scala, Elyssa Moore, Didier Dreau

Modulation of CXCL12-mediated activities of metastatic breast cancer cells using a CXCL12-CXCL4 binding interface peptide

Triple-negative breast cancer is largely unresponsive to current cancer treatments, highlighting the need for new therapies. The binding of chemokine CXCL12 to its receptors CXCR4 and ACKR3 on the plasma membrane of cancer cells triggers signaling pathways that contribute to cancer progression. We previously found that the heterodimerization of CXCL12 to the chemokine CXCL4 was associated with a decrease in CXCL12-CXCR4 mediated signaling and cancer cell migration. Here, we investigated the potential activity of the CXCL4 peptide sequence mimicking the CXCL12-CXCL4 binding interface in modulating breast cancer cells' CXCR4 and ACKR3 signaling and cell migration. Our data indicate that, in the presence of the CXCL4- ß1 interface peptide, the CXCR4-CXCL12 triggered activation is altered in human breast MDA-MB-231 and MDA-MB-453 cancer cells and human breast MCF-10A epithelial cells. In particular, calcium mobilization and beta-arrestin activity, following binding and activation of CXCR4 and ACKR3 receptors triggered by CXCL12, were altered when cells were treated with CXCL12 combined with the CXCL4- ß1 interface peptide. The role of CXCR4 and ACKR3 in signaling were validated using specific pharmacological inhibitors and analysis of cell line-specific receptor expression. Importantly, in Boyden chamber assays, CXCL4- ß1 interface peptide combined with CXCL12 limited cancer cell migration compared to CXCL12 alone. Our findings suggest that targeting the chemokine CXCL12-CXCR4 signaling using a peptide mimicking the CXCL12-CXCL4 interface may hinder breast cancer progression.

#21 Amira Abdellatef UNC Chapel Hill

Amira Abdellatef, Han Suk Ryu, Da Sol Kim, Ilias P. Nikas, Sergey A. Krupenko

Breast cancer (BC) is the most common cancer in women worldwide and a major cause of cancer-related mortality. It is a heterogeneous disease characterized by several subtypes with distinct molecular profiles, clinical behaviors, and treatment responses. ALDH1L1, a key enzyme in folate metabolism, has been implicated in various cancers, but its clinical relevance in BC remains unclear. We analyzed three cohorts from Seoul National University (41 unpaired normal and invasive mammary tissue, 44 paired normal and tumor tissues, and a tissue microarray of 1003 invasive ductal carcinoma cases). ALDH1L1 immunostaining was performed on 1088 cases using tissue microarrays or whole section slides with positive cytoplasmic and

membranous reactivity. Clinical data, including tumor size, grade, lymphatic invasion, and lymph node metastasis, were retrieved from patient records. We observed that ALDH1L1 expression was significantly higher in non-tumor tissues compared to cancerous tissues ($p=0.0014$ and $p=0.0282$) and showed an inverse correlation with tumor size, disease stage, and lymphatic invasion. Elevated ALDH1L1 levels were linked to smaller tumors and lower pT stage in luminal A and HER2+ subtypes, as well as lower nuclear grade in TNBC. Higher ALDH1L1 expression was also associated with improved overall and disease-free survival, particularly in hormone receptor-positive subtypes ($p=0.0049$ and $p=0.0441$). These findings were further validated using the METABRIC dataset. Proliferation and clonogenic assays revealed potent antiproliferative effects of lentivirus-mediated ALDH1L1 expression in luminal BC cells MCF7 and T47D. Our results suggest that low ALDH1L1 expression is linked to tumor aggressiveness and poorer prognosis, particularly in luminal BC, highlighting its potential as a prognostic biomarker and therapeutic target.

#22 Elyssa Moore UNC Charlotte

Elyssa Moore, Sara Scala, Didier Dreau

Altering ACKR3-CXCR4 crosstalk to inhibit the CXCL12-CXCR4 chemokine-driven breast cancer progression

Inflammation and cell movement are key to cancer progression and are largely dependent on chemokine ligand-receptor activation and signaling. Specifically, CXCL12-CXCR4 activation is associated with the progression and metastasis of breast cancer. Recently, a signaling role of the CXCL12 scavenger receptor ACKR3 (i.e., CXCR7) has been revealed. The binding of CXCL12 to ACKR3 led to activation of beta-arrestin, MAPK and AKT pathways. Importantly, ACKR3 activation also triggers crosstalk with CXCR4 which alters CXCL12-CXCR4 signaling. How ACKR3 regulates the CXCL12-CXCR4 driven signaling and breast cancer cell migration remains poorly understood. Using pharmacological ACKR3 and CXCR4 agonist and antagonist combinations, we examined the CXCL12-driven activation of both ACKR3 and CXCR4 in triple negative breast cancer cells MDA-MB-453 and MDA-MB-231. Critically, our data indicate that breast cancer cells display marked variation in cell surface expression of chemokine receptors including ACKR3 and CXCR4. Our data suggests that cytoplasmic calcium is involved in the crosstalk between ACKR3 and CXCL12-CXCR4 signaling. Moreover, as expected agonists and antagonists to CXCR4 and ACKR3 altered signaling and for the latter appear to impact the crosstalk with CXCR4 signaling. Taken together, our data supports the potential targeting of the CXCL12-CXCR4-ACKR3 crosstalk within the tumor microenvironment to prevent breast cancer progression.

#23 Nura Brimo Duke University Pratt School of Engineering

Nura Brimo, Mingru Li, Łukasz Suprewicz, Fitzroy Byfield, Paul A Janmey, Christoph F Schmidt

Optimized Mechanical Isolation of Glioblastoma Nuclei for Biomechanical Analysis

Measuring the mechanical properties of cancer cell nuclei, especially in glioblastoma cell lines such as LN18 and LBC3, is technically challenging due to the cytoplasmic environment and the surrounding intermediate filament network (e.g., vimentin) that provides structural reinforcement. To overcome these challenges, we modified a nucleus isolation protocol to preserve nuclear integrity for downstream biomechanical analysis using optical tweezers. Unlike traditional detergent-based lysis and density gradient centrifugation, which often disrupt nuclear structure, the approach employs mechanical enucleation (1). Cells were grown on a fibronectin-coated coverslip for adhesion, treated with 2 µg/mL cytochalasin D (to depolymerize actin filaments). The coverslip was then mounted upside-down on a custom manufactured Teflon support. Centrifugation speed and duration were systematically optimized, trying 3700 RPM for 30 min, 4000 RPM for 30 min, and 4000 RPM for 40 min. Enucleation efficiency was quantified using Hoechst 34580 staining and confocal imaging (Leica SP5). For LN18, enucleation rates

improved from 33% (3700 RPM, 30 min) to 51% (4000 RPM, 30 min) and reached 87% at 4000 RPM for 40 min. Similarly, LBC3 rates increased from 31% (3700 RPM, 30 min) to 53% (4000 RPM, 30 min), achieving 81% at 4000 RPM for 40 min. The isolated nuclei appeared spherical and intact in suspension, with fluorescence confined within the nuclear envelope, suggesting preservation of structural integrity. The isolated nuclei were free of cytoplasmic remnants and suitable for rheological analysis. This protocol offers a robust strategy for isolating viable nuclei from adherent glioblastoma cells, enabling precise rheological measurements that could elucidate nuclear mechanics in cancer progression.
(1) R. D. Goldman, R. Pollack, and N. H. Hopkins. “Preservation of normal behavior by enucleated cells in culture.” In: Proceedings of the National Academy of Sciences of the United States of America 70.3 (1973), pp. 750–754. ISSN: 00278424.

#24 Doaha Awad UNC Charlotte
Analyzing the gemcitabine resistance mechanism and gemcitabine-cisplatin mesoporous silica nanoparticles (gem-cisPt MSNs) effects in pancreatic ductal adenocarcinoma (PDAC) cells.
Abstract: Pancreatic ductal adenocarcinoma (PDAC) is a highly aggressive and lethal form of pancreatic cancer, often exhibiting resistance to standard chemotherapeutic agents such as gemcitabine. Combination of drug therapies, including the drugs gemcitabine and cisplatin, have shown promise, and the use of nanoparticle-based drug delivery systems offers a novel approach to understanding and overcoming drug resistance. This study aimed to investigate the mechanisms of gemcitabine resistance in human (BxPC3) and murine (KCM) pancreatic cancer cell lines, and to evaluate the therapeutic potential of mesoporous silica nanoparticles (MSNs) loaded with gemcitabine and cisplatin (gem-cisPt MSNs). Gemcitabine-resistant cell lines were developed and analyzed using cell viability assays, western blotting, and confocal microscopy. Resistant cells exhibited a 2- to 3-fold increase in resistance compared to their respective controls, with altered expression of key proteins involved in gemcitabine uptake and metabolism, including deoxycytidine kinase (dCK), ribonucleotide reductase M1 subunit (RRM1), and human equilibrative nucleoside transporter 1 (hENT1). These findings highlight changes in protein expression associated with gemcitabine resistance, suggesting the need for a broader panel of targets and gene expression pathways to explore. Notably, gemcitabine-loaded MSNs as monotherapy demonstrated greater efficacy than the combination gem-cisPt MSN treatment, potentially due to differences in cellular uptake and drug release profiles. This study demonstrates the complexity of drug resistance in PDAC and the need for optimized nanoparticle formulations for effective combination therapy.

#25 Charlotte Johnstone UNC Charlotte
Charlotte Johnstone, Jacob Hawkins and Valery Z. Grdzelishvili
Spontaneous GFP Transgene Mutations in an Oncolytic Virus Impact Virus–Host Interaction Dynamics1
Green Fluorescent Protein (GFP) is one of the most widely used reporter genes for tracking gene expression and cellular processes due to its ability to fluoresce green under blue or ultraviolet light. Our laboratory studies vesicular stomatitis virus (VSV) as an oncolytic agent to selectively target pancreatic ductal adenocarcinoma (PDAC), a highly aggressive and treatment-resistant cancer. We use a recombinant variant, VSV-ΔM51-GFP, which carries a GFP reporter transgene to track viral replication and spread. While studying how VSV evolves in PDAC, we unexpectedly observed that two independently derived viral mutants exhibited a visibly dimmer GFP fluorescence phenotype. Genome sequencing revealed three novel non-synonymous amino acid substitutions within the GFP transgene. These mutations altered the coded amino acids, including their size and polarity, which could impact protein shape, structure, stability, and post-translational modifications. We observed less GFP in cells infected with VSV bearing mutated GFP (mutGFP) than in cells infected with VSV bearing wild-type GFP (wtGFP), which could contribute to the dim phenotype. Interestingly, viruses encoding mutGFP did not provoke as

strong an innate immune response compared to wtGFP counterparts. There was a significant decrease in the phosphorylation of STAT1, which could signify that wtGFP may enhance the immune response to VSV. We intend to characterize the molecular mechanisms underlying the reduced immune response and dim GFP phenotype. Although GFP is widely used as a supposedly inert marker in virology, our findings reveal that spontaneous mutations in the GFP transgene can alter virus–host interactions and impact viral fitness and function.

Host-Pathogen Interactions and Infectious Diseases

#26 Krishna Majithia UNC Charlotte

Globally, 1.2 million cases of meningitis are attributed to bacterial agents, contributing to 250,000 mortalities annually. Meningitis is an infection of the meninges which protect the brain and spinal cord. During bacterial meningitis, potent inflammatory responses lead to life-threatening injuries and permanent neurological damage. Previous data indicate that resident brain cells recognize bacterial motifs through host receptors, leading to the production of immune mediators. Recent data in peripheral cell types demonstrate a novel role for retinoic acid-inducible gene I (RIG-I) in identifying bacteria and stimulating type I interferons (IFNs). However, the role of RIG-I in initiating IFN production during bacterial CNS infection remains unexplored. In this study, we demonstrate upregulation of RIG-I by glial cells during infection by relevant pathogens including Neisseria meningitidis and Streptococcus pneumoniae. Additionally, we observe significant IFN production and subsequent increased expression of interferon-stimulated genes (ISGs) including interferon-induced protein with tetratricopeptide repeats 1 (IFIT1) and IFIT3 by infected glial cells. Interestingly, we show that RIG-I-mediated IFNs and ISGs contribute to restriction of N. meningitidis and S. pneumoniae in infected glial cells. Collectively, these findings highlight a protective role for IFNs during bacterial meningitis, suggesting the potential of RIG-I as a therapeutic candidate. As such, we employed RIG-I agonists to further augment protective IFN responses during infection. Consistent with our previous observations, RIG-I agonist-mediated induction of IFNs restricts bacterial burden. Our ongoing studies will determine the mechanism by which type I IFNs restrict bacterial burden and explore the role of other nucleic acid sensors in producing protective IFNs.

#27 Anjumana Jannati Nur UNC Charlotte

Anjumana Jannati Nur, Varsha Godakhindi, Juan L. Vivero-Escoto, Mariya Munir
Maximizing The Antibacterial Efficacy of Silver Nanoparticles Against Superbugs Through Sequential Light Exposure

Antibiotic resistance (AR) has become one of the leading causes of increased mortality worldwide. The primary factor for the rise of antibiotic-resistant bacteria (ARB) or superbugs is the misuse of antibiotics in healthcare and agriculture. Current approaches, such as antibiotic combinations, antimicrobial peptides, and engineered bacteriophages to eliminate ARBs face challenges like developing resistance and proteolytic degradation. Non-antibiotic approaches, such as using silver nanoparticles (AgNPs), have gained the attention of researchers for their broad-spectrum antimicrobial efficiency. The antimicrobial efficacy of AgNPs is mainly associated with the Ag+ release, which is a slow process. To enhance AgNP efficacy, we functionalized their surface with protoporphyrin IX (cysPPIX), a photosensitizer that accelerates Ag+ release under light exposure. The cysPPIX creates an oxidative environment around the AgNP, facilitating faster release of Ag+. Our study demonstrated that cysPPIX-AgNPs effectively inactivate Methicillin-resistant Staphylococcus aureus (MRSA), achieving >5 log reduction with single exposure and >6 log with sequential dual-step exposure (~1.34 log higher than single exposure) at 1.5 μg/mL. This approach enhanced the antibacterial activity of cysPPIX-AgNPs even at lower concentrations in a shorter span, offering a promising strategy for combating antibiotic resistance. The findings of this study could contribute to the development of

novel or advanced antimicrobial agents with broad applications in healthcare, agriculture, and water treatment plants for developing advanced water treatment methods. It may also provide valuable insights, contributing to designing future antimicrobial agents.

#28 Allison Stadick UNC Charlotte

Synergistic Treatment of Pseudomonas Aeruginosa Biofilms with Chlorine6 Gold Nanoparticles

Biofilms play a critical role in the rising rate of antibiotic-resistant bacteria (ARB). Biofilms consist of a complex microbial city that supports the attachment and growth of a variety of bacteria from which they work together to defend against antibiotics. From the human eye, biofilms appear as thick, slimy mucous membranes and are commonly found in infected medical devices such as implants, catheters, and surgical tools. Due to their thickness and complex environment, they prevent antibiotic penetration and effective treatment resulting in chronic infection. Since biofilms are harder to treat while maintaining structural integrity, the best way to treat biofilms is by disruption of the biofilm with an external force that is also bactericidal. The two forces that can effectively disrupt and kill biofilms is the introduction of reactive oxygen species (ROS) and heat. This project entails the treatment of Pseudomonas aeruginosa biofilm with gold nanoparticles (AuNPs) functionalized with a photosensitizer (Chlorin e6) (Ce6AuNPs). AuNPs have the advantage of strongly absorbing light and converting to heat resulting in ablation and structural damage of the biofilm. On the other hand, these NPs can also become photochemically active by functionalizing with a photosensitizer that produces ROS which will chemically interact with the biofilm components and produce irreversible oxidative damage. To determine the efficacy of this combined treatment, biofilms are grown on a plate and treated with Ce6AuNPs from which a wavelength of light will be applied. The biofilm structural integrity will be observed with confocal microscopy for visualization of biofilm integrity and bacteria viability.

#29 Kaitlin Klotz UNC Charlotte

Kaitlin Klotz, Abhishek Dey, Arpita Saha, Justin Davis, Prashant Jha, Aarti Jinwala, Bibo Li, Kausik Chakrabarti

The telomerase ribonucleoprotein (RNP) adds caps of repetitive, non-coding DNA (telomeres) to chromosome ends to prevent degradation. Telomerase is composed of the telomerase RNA (TR), which provides the code for telomeric extension, and telomerase reverse transcriptase (TERT) which catalyzes the addition of telomeric repeats. Interaction between the TR and TERT is required for telomere extension and preservation of chromosomal integrity. Protozoan parasite Trypanosoma brucei features a constantly active telomerase RNP which underpins its unlimited proliferation. Limited availability of effective therapeutics make telomerase a candidate for antiparasitic drug development.

We investigate the influence of the RNA structure on overall telomerase function. Our approach enabled direct comparison of wild-type TR with three structural mutants, each missing a defined RNA domain, within the native context of the telomerase reverse transcriptase (TERT) complex. Our structural modeling revealed that loss of individual TR domains induces distinct rearrangements in the RNA ensemble, potentially altering TR stability and disrupting key TR-TERT contacts. These conformational shifts correlate with reduced telomerase activity and suggest that specific domains act cooperatively to scaffold catalytically active telomerase complexes. Importantly, this study highlights the utility of SHAPE-MaP and ensemble deconvolution for resolving functional RNA conformations in their endogenous RNP contexts. Our findings underscore the critical role of defined T. brucei TR domains in shaping the structural architecture required for TERT engagement and enzymatic function. These insights open new avenues for targeting TR-TERT interactions as a strategy to disrupt telomerase-driven proliferation in T. brucei, the major pathogen responsible for African sleeping sickness.

#30 William McClintic Wake Forest Institute for Regenerative Medicine
McClintic, W., Gregg, Brieana M., Bollapragada, Adhirath, Stone, Adrienne B. and McNutt, Patrick M.
Cone snail α-conotoxins (α-CTXs) are potent neurotoxins that reversibly block nicotinic acetylcholine receptors (nAChRs), leading to rapid-onset paralysis and respiratory failure. There is currently no antidote, and treatment relies on supportive care, including mechanical ventilation. We evaluated two FDA-approved cholinergic agents–3,4-diaminopyridine (3,4-DAP), which enhances presynaptic acetylcholine (ACh) release, and pyridostigmine bromide (PB), which inhibits ACh breakdown–as potential post-exposure therapies. In ex vivo mouse phrenic nerve–hemidiaphragm assays, clinically relevant concentrations of 3,4-DAP and PB reversed α-CTX–induced paralysis. Using a lethal α-CTX mouse model, we demonstrated that post-symptomatic treatment with 3,4-DAP or 3,4-DAP + PB restored breathing and significantly improved survival. These findings highlight a clear therapeutic pathway, leveraging existing drugs with known safety profiles to rapidly repurpose them as medical countermeasures for α-CTX envenomation. This work lays the groundwork for clinical development of accessible, life-saving treatments for cone snail poisoning.

#31 Kayla Lenz UNC Charlotte
Kayla Lenz and Hussian Mannaki
We present the synthesis and optimization of poly(aminophenylboronic acid) nanorods (PABA) for enrichment of glycoproteins, including horseradish peroxidase (HRP), SARS-CoV-2 spike protein (SP), and acetylcholinesterase (AChE). Boronate affinity materials like PABA function as synthetic analogues to biological receptors, enabling enrichment and reversible esterification with glycoproteins. Successful enrichment requires maximizing affinity while minimizing protein degradation—two often conflicting conditions, since boronic acids typically have a pKa well above physiological pH. To achieve this, a facile one-pot synthesis of PABA was implemented to obtain flexible nanorods morphologies with similar properties to the conducting polymer, PANI, as confirmed by conductivity, UV-Vis, CV, and FTIR studies. Competitive proton uptake between secondary imines (i.e., doping) and boronic acid assists in maintaining tetrahedral hybridization state for enhanced cis dol capture in mildly acidic media. Furthermore, glycoprotein binding is greatly enhanced through multivalent interactions as a result of flexible nanoscale morphology, a high-density of functional boronic acid sites, and π-π attraction with aromatic glycan chains. Synthesis conditions were optimized, achieving uniform nanorods (3-7 μm long, 80-200 nm diameter) with high yield (>90%). PABA successfully captured HRP at pH values above 6, with a dissociation constant (kd) of <1.77 pM and a pKa of 5.3. Similar results were achieved for SP and AChE.

AI, Medical Imaging and Devices

#32 Zaynah Khan UNC Charlotte
Zaynah Khan and Farah Deeba
Ultrasound is a widely used imaging modality due to its non-invasive, real-time, and cost-effective nature. Traditional B-mode grayscale ultrasound provides qualitative images of anatomy, but emerging Quantitative Ultrasound (QUS) offers the potential for more precise tissue characterization by quantifying physical properties of tissue, including speed of sound, attenuation, density, and nonlinearity. These parameters could serve as biomarkers for conditions such as cancer, liver disease, and placenta-mediated disorders. Current QUS techniques often rely on linear spectral models and simplifying assumptions, such as the Born approximation, which ignore multiple scattering, diffraction, and nonlinear effects. Recent QUS research has explored Full-Waveform Inversion (FWI) which uses the linear acoustic wave equation to recover parameters like speed of sound and attenuation. However, FWI typically neglects nonlinear effects and energy loss mechanisms, which limits its ability to fully capture acoustic

behavior in biological tissues. In this project, we simulate forward wave propagation using the k-Wave MATLAB toolbox to model acoustic behavior in biological tissues. These simulations provide controlled test scenarios for evaluating the performance of an inversion algorithm based on the Westervelt model, a nonlinear wave equation that accounts for both attenuation and acoustic nonlinearity. By applying the inversion method to the simulated data, we assess reconstruction accuracy by comparing estimated parameter maps to known ground-truth values. This evaluation provides insights into the strengths and limitations of nonlinear wave inversion techniques. The goal is to inform the development of more accurate and efficient biomedical imaging algorithms through simulation-based validation.

#33 Jacob Ortega Cambpell University School of Osteopathic Medicine
Jacob Ortega, Anna R. Kahkoska, Anika Bilal, Richard E. Pratley
Diabetes technology such as continuous glucose monitors (CGMs) and automated insulin delivery (AID) systems offers significant potential to improve glycemic outcomes and quality of life for individuals with type 1 diabetes (T1D), yet older adults remain underrepresented in both clinical trials and real-world use. In this study, we analyzed data from the T1D Exchange Registry to assess patterns of CGM and AID adoption among adults aged 65 years and older. Among 1,382 older adults with T1D, 76 percent used CGMs and 24 percent used AID systems. Technology use was more common among those with shorter diabetes duration, higher educational attainment, and White race. Compared to non-users, AID users had significantly lower hemoglobin A1c levels (mean 6.9 percent vs 7.4 percent, $p < 0.001$). Despite growing uptake, disparities in access remain prominent, particularly among racial and socioeconomic groups. These findings highlight key barriers to device adoption and support the need for implementation strategies and regulatory frameworks that ensure equitable access to diabetes technology for aging populations. Tailored, inclusive approaches to medical device rollout in older adults with T1D may help close existing gaps and maximize the clinical benefit of these innovations.

Nanomaterials and Structure Based Drug Design

#34 Delicia Esther Cardenas Vasquez UNC Greensboro
Delicia Esther Cardenas Vasquez, Radmila Petric, Zhenquan Jia
Carbon nanodots (CNDs) are new nanomaterials widely used in biomedicine for their cost-effectiveness and low toxicity compared with other nanomaterials and applications such as bioimaging and drug delivery. While multiple in-vitro and in-vivo studies elucidated the low toxicity of CNDs during a short period of time (7 days or less), limited information exists regarding their long-term effects on in-vivo models. Specifically, we do not understand the potential toxicity of CNDs on the observable appearance, development, and behavior of an individual. We hypothesized that long-term administration of CNDs alters behavior and physiology in laboratory mice. We tested our hypothesis using C57BL/6J mice and LDLr -/- mice and evaluated behavioral and physiological responses to 2.5 mg/kg CNDs over 8 weeks. Specifically, we focused on evaluating the effects of CNDs on Ultrasonic Vocalizations (USVs) as a measure of communicative behavior. We also utilized two standardized behavioral tests, the Open Field Test and the Elevated Plus Maze Test, to analyze alterations in specific behavioral patterns induced by CNDs. Finally, we examined the influence of CNDs on the force strength of mice through a neuromuscular test. We found that CND-treated C57BL/6J mice produced fewer USVs than control mice and that CND-treated mice produced USVs with lower-end frequency and maximum frequencies. However, in LDLr -/- mice, we found no difference in calling rate between treatment groups, but CNDs treated mice produced vocalizations with different spectral characteristics. Furthermore, CNDs treated LDLr -/- mice produced calls with lower end frequency, maximum frequency, start frequency, the frequency at maximum amplitude, and minimum frequency. CNDs increased the total floor velocity in the Open Field Test in C57BL/6J

mice. We found no differences between treatment groups using the open-field or Neuromuscular tests. Together, these results suggest that the difference in behavioral tests, especially in calling rate and changes in spectral characteristics of USVs, may reveal that CNDs induce a potential stress response to C57BL/6J mice and LDLr -/- mice.

Neurodegenerative Disease

#35 Valeria Uvarova UNC Charlotte

Valeria Uvarova, Emani Foster, Patricija van Oosten-Hawle

Hsp90 is a highly conserved and essential molecular chaperone that regulates stress responses and maintains cellular proteostasis. Our lab has previously shown that tissue-specific modulation of Hsp90 expression levels in the gut and the nervous system induces a protective inter-tissue stress signaling response regulating organismal proteostasis. Here, we investigate how Hsp90 actively coordinates gut-to-neuron signaling to regulate aging. Our results show that constitutive overexpression of Hsp90 in the C. elegans gut correlates with decreased toxicity of age-associated protein aggregates in the nervous system, such as amyloid-beta and polyglutamine (polyQ40) proteins, and extends the lifespan of these neurodegenerative disease models. Interestingly, the protective effects on neuronal proteostasis and longevity are more pronounced when Hsp90 is overexpressed in the gut than in the nervous system itself. This suggests an intercellular gut-to-brain signaling mechanism that is initiated by intestinal Hsp90. Using transcriptomic and metabolic profiling, we demonstrate that gut-specific Hsp90 overexpression induces metabolic changes. These included reduced levels of triglycerides, increased lipase activity, and increased concentrations of odd-chain free fatty acids, particularly pentadecanoic acid (PA), an essential odd-chain fatty acid commonly found in dairy products. We hypothesize that Hsp90 interaction with specific client proteins in the gut underlies the rewired lipid metabolism leading to gut-to-neuron signaling and that free fatty acids may serve as intercellular signals. Supporting this hypothesis, dietary supplementation with PA extended both the lifespan and healthspan of C. elegans. Our results suggest that Hsp90-induced rewiring of lipid metabolism contributes to its downstream effect on neuronal proteostasis and aging.

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