**Poster Session 2 - July 27th 11:15-12:30**

|  |
| --- |
|  |

**42. Name:** Lynne Dieckman **Institution:** Creighton University **Email:** lynnedieckman@creighton.edu **Research area:** Other**Title:** Structure and function of complexes that regulate gene silencing

**Authors:** Jacquelyn Wright, Rebekah Rapoza, Keely Orndorff, Maggie Atkinson, Olivia Nicholson, and Lynne Dieckman
Department of Chemistry and Biochemistry, Creighton University

**Abstract:** Normal gene expression is maintained through the packaging of DNA into nucleosomes, which can occur in either open or closed structures within chromosomes. More loosely packed DNA (open nucleosome structures) represent more highly expressed, active regions of the genome, while more tightly packed DNA (closed nucleosome structures) represent silenced, inactive regions of the genome. The packaging of nucleosomes into these open and closed structures is accomplished in a DNA replication-dependent manner and requires two key proteins: CAF-1, a chromatin assembly factor that induces nucleosome formation immediately following DNA replication, and PCNA, an accessory protein that recruits and regulates a vast array of proteins involved in DNA replication and repair processes. The mechanisms by which DNA is packaged into nucleosomes immediately following DNA synthesis are not well understood. We are developing single-molecule total internal reflection fluorescence (TIRF) microscopy assays to determine the mechanism of CAF-1 recruitment to the replication fork and how PCNA distinguishes between CAF-1 and other PCNA-interacting proteins. We have identified secondary interaction sites within both PCNA and CAF-1 and, interestingly, mutant forms of PCNA that increase the affinity between these two proteins. These results suggest a novel mechanism of recruitment that has not been observed with PCNA-interacting partners previously.

This work was funded by the NIH NE-INBRE Developmental Research Project Program (DRPP).

**43. Name:** Zixuan Yao **Institution:** University of Nebraska Medical Center **Email:** z.yao@unmc.edu **Research area:** Neuroscience**Title:** The use of mobile application for self-management in patients with Parkinson’s disease: From forming diverse team to securing research support

**Authors:** Ka-Chun Siu, Zixuan Yao, Melissa Leon, Christine Toh, Kelly Gonzales

**Abstract:** This project examined the feasibility of using the Balance Capture (BACA) mobile application to promote self-management in individuals with Parkinson’s Disease (PD) in rural Nebraska. PD is a neurodegenerative disorder that results in movement-related symptoms and potential difficulty in self-managing health status. A diverse research team with nurse practitioner, physical therapist, data analyst, and informational technologist was assembled. We shared our unique expertise to target the challenge of health management in rural community and access to care barriers, coupled with PD-related movement problems. We anticipated that a mobile application could optimize self-management for patients with PD. We developed BACA to quantify balance and mobility status and piloted for the usability by both Physical and Occupational Therapists in rural Nebraska. With the diversity of our research team and topic with unmet need, we recently secured a Just-In-Time award from UNMC CENTRIC. The new research support allows us to examine the specific aspects of self-management including communication between patients and their healthcare providers, self-efficacy, patient activation, and provide additional evidence of data quality. It will help us to confirm the use of BACA for individuals with PD to regularly self-manage their chronic illness and monitor physical symptoms.

**44. Name:** Lillian Behm **Institution:** University of Nebraska Medical Center **Email:** lillian.behm@unmc.edu **Research area:** Neuroscience**Title:** Measuring the relationship between periadolescent memory ability and hippocampal functional connectivity: preliminary findings from the PRANK study

**Authors:** Lillian Behm, Connor J. Phipps, Jennifer N. Sexton, Thomas A. DeCesare, Abi M. Heller, Arthur C. Maerlender, Vaishali S. Phatak, Justin A. Cramer, James Blair, Daniel L. Murman, David E. Warren

**Abstract:** Background: Declarative/relational memory requires the hippocampus and its connections to a diverse network of brain regions. Relational memory abilities improve throughout childhood, and these improvements may be associated with changes to hippocampal brain networks. The development of such networks during periadolescence is not well characterized. Therefore, we utilized preliminary data from the NIA-funded Polygenic Risk of Alzheimer’s Disease in Nebraska Kids (PRANK) study to test whether individual differences in periadolescent hippocampal resting-state functional connectivity (RSFC) covary with declarative/relational memory ability.

Method: Analyses were conducted on preliminary data from healthy periadolescent participants (n=40). Memory performance was measured with Cambridge Cognition’s Paired Associates Learning (PAL) task. Resting-state functional MRI data were analyzed using a seed-based approach with the bilateral hippocampus as the seed region of interest. RSFC data were analyzed to determine their covariance with PAL performance.

Result: We observed patterns of hippocampal RSFC that shared territory with select portions of the default mode network. We also observed regional covariance between hippocampal RSFC and performance on the PAL task.

Conclusion: We observed that hippocampal RSFC covaries with declarative/relational memory ability among periadolescent children. Future work will utilize participants’ AD polygenic risk scores to determine whether those scores influence development of hippocampal RSFC.

**45. Name:** Connor Joseph Phipps **Institution:** University of Nebraska Medical Center **Email:** connor.phipps@unmc.edu **Research area:** Neuroscience

**Title:** Graph properties of functional brain networks and associations with cognition in periadolescence

**Authors:** Connor J. Phipps, Jennifer N. Sexton, Lillian Behm, Thomas A. DeCesare, Abi M. Heller, Arthur C. Maerlender, Vaishali S. Phatak, Justin A. Cramer, James Blair, Daniel L. Murman, and David E. Warren

**Abstract:** Network properties of the brain and memory change during the lifespan. Alzheimer’s disease (AD) can disrupt network development. Development of brain networks and cognitive abilities in early life might predispose some to AD in later life. We investigated the graph theoretical properties of brain networks and memory in periadolescent children. Data for this study was drawn from the Polygenic Risk of Alzheimer’s Disease in Nebraska Kids (PRANK) study. The goal is to evaluate the possibility that early-life brain network development may create susceptibility to AD. We studied a sample of periadolescent children (N=40) from the PRANK study. Memory was assessed using the CANTAB paired associates learning task. Brain measures were assessed with MRI utilizing protocols from the Human Connectome Project (HCP). Network properties were assessed with the HCP’s Connectome Workbench tool. Our preliminary results detected a trend between the modularity of brain networks and cognitive performance on the CANTAB task. This study measures brain network variables, cognition, and AD polygenic risk score in periadolescent children. Our analysis of brain and cognitive measures illustrate graph theoretical properties of the periadolescent brain. Future directions will be examining the association between AD polygenic risk, cognitive measures, and network properties.

**46. Name:** Janelle N. Beadle **Institution:** University of Nebraska at Omaha **Email:** jbeadle@unomaha.edu **Research area:** Clinical-translational

**Title:** Effects of Alexithymia on caregiver empathy

**Abstract:** Caregivers play a significant role in enhancing care recipients’ quality of life. However, there are key caregiver psychological factors that can influence care quality and ultimately care recipient well-being. In particular, higher levels of empathy have been linked to greater sensitivity to care recipients’ pain. Furthermore, caregivers with higher cognitive empathy (i.e., the ability to understand others’ feelings) tend to experience lower levels of stress, which in turn may help increase resilience to the challenges of caregiving. Individuals with poor emotional awareness (i.e., alexithymia), tend to experience socioemotional difficulties. The present study investigated differences in empathy and emotional awareness between caregivers and non-caregivers, and associations between psychological characteristics and prosocial behavior. The sample included 31 female caregivers and 53 female non-caregivers. Caregivers reported greater empathy and emotional awareness and showed greater prosocial behavior in an empathic context. Greater cognitive empathy was associated with lower levels of alexithymia in caregivers. Furthermore, caregivers who exhibited greater prosocial behavior had higher levels of emotional awareness. This study adds to our understanding of psychological characteristics associated with greater prosocial behavior in caregivers. Future research may investigate the degree to which these relationships extend to prosocial behaviors towards the care recipient.

**47. Name:** Lavanya Uppala **Institution:** University of Nebraska at Omaha **Email:** luppala@unomaha.edu **Research area:** Other

**Title:** Characterization of UNO-SLW2 virus infection of Pseudomonas fluorescens using RNA Sequencing

**Abstract:** The Pseudomonas genus is a large and diverse group of bacteria that occupy nearly every environmental niche. However, all members of the Pseudomonas genus are susceptible to viruses known as bacteriophages. Somewhat surprisingly, despite extensive research, both the bacteria and their bacteriophages still have many proteins and genes that are termed “hypothetical”, and as a result many of their functions are also unknown. Using novel Podoviruses that have been isolated in our laboratory and the Pseudomonas fluorescens host, we seek to elucidate the mechanisms and functions of these “hypothetical” genes and their gene products by studying gene expression changes during viral infection. These gene expression changes, will elucidate the phage genes previously unrecognized during infection of P. fluorescens over time. Novel genes will be identified using next generation sequencing, and validation using co-occurrence network analysis. This methodology identifies frameshift mutations of various Pseudomonas bacteriophages that correlate with virus pathogenicity or phenotype. By mapping the course of gene expression of P. fluorescens and an infecting bacteriophage, we will learn more about the genes and gene products of both the host and the virus. This should provide greater insight into Pseudomonas bacteria, including those that cause human disease.

**48. Name:** Thien Q. Tran **Institution:** Creighton University **Email:** ThienTran@creighton.edu **Research area:** Other

**Title:** Effects of hFWE3 on the selection of aggressive cutaneous Squamous Cell Carcinoma (cSCC) populations

Thien Q. Tran, Justin C. Rudd, Laura A. Hansen

Cutaneous squamous cell carcinoma (cSCC) is the prolific form of skin cancer and arises from the keratinocytes which compose the epidermis of the skin. Within an at-risk patient population, the metastasis of cSCC may induce other diseases or even lead to death, but the mechanism which controls the selection of aggressive populations in these lesions remains poorly defined. Flower, a gene that encodes four transmembrane proteins (hFWE 1-4), may promote the selection of aggressive cells in cSCCs. It has been proposed that aggressive cells may use subsets of hFWE 1-4 isoforms to promote the elimination of less aggressive neighbors, however, the mechanism behind these hFWE-mediated interactions is not understood. Preliminary RNA sequencing data suggested that WT cells surrounded by hFWE3 expressing neighbors decrease expression of COL8A1 (Log2FC -1.18, p-adj < 2 x 10^-5) a major constituent of the basement membrane. Subsequent RT-qPCR validated this expression pattern (p=0.069). We hypothesize that cSCC cells expressing hFWE3 drive the delamination of wild-type neighbors by forcing non-autonomous down-regulation of collagen subunits, COL8A1 and COL4A2. Here we use long-term live-cell imaging to track delamination of WT cells expressing DsRed2 surround by hFWE3-EGFP or WT-EGRP neighbors, and immunofluorescence to visualize changes in COL8As and COL4A2 expression during the delamination process. These experiments are expected to provide insights into hFWE-mediated mechanisms of cell competition.

This project was supported by INBRE and the State of Nebraska LB595.

**49. Name:** Akram Almansob **Institution:** University of Nebraska Omaha **Email:** aalmansob@unomaha.edu **Research area:** Molecular Target Discovery and Development-Nanomedicine

**Title:** Filamentation of Candida albicans in different inducing media

**Abstract:** Candida albicans is a fungal pathogen that persists in the human gastrointestinal or genital tract that can infect other organs in the host’s body (Azadmanesh et al. 2017). When C. albicans proliferates, it can cause invasive mucosal infections; the mortality rate associated with this clade of C. albicans can be as high as 40% in vulnerable populations (Pfaller & Diekema, 2007). One of the main contributions to its lethality is associated with its ability to switch between a yeast form and a filament form. According to previous work, this switch allows it to have distinct cell surface proteins by changing the composition of the cell wall (Azadmanesh et al. 2017). With this change a sticky filament is formed and C. albicans can attach to areas deep within the body. This also allows it to infect such medical appliances as pacemakers or ports (Azadmanesh et al 2017). Previous research in the lab shows that the TSC11 gene plays a role in C. albicans filamentation in the SC5314 derived strain (Azadmanesh et al. 2017).
 This study will use a transient CRISPR-CAS9 to delete the TSC11 gene in 5 isolates from distinct C. albican clades (Min, et al. 2016). This deletion of TSC11 will highlight whether TSC11 has the same effects on filament formation in our clinical strains as observed in the SC5314 derived strains (Azadmanesh et al 2017). If we observe the same pattern on filamentation as previously noted, it will mean that TSC11 may be a potential target for anti- filamentation therapies (MIN, et al. 2016). If the knockout of the TSC11gene has no effect on filamentation in our clinical strains, this will mean the gene’s role is limited in this clade; this will suggest that the role of the TSC11 gene is dependent on the genetic background.

**50. Name:** Jicheng Fu **Institution:** University of Central Oklahoma **Email:** jfu@uco.edu **Research area:** Other

**Title:** Towards a practical approach for assessing pressure relief activities for manual wheelchair users in their daily lives

**Abstract:** Wheelchair users are at great risk of pressure ulcers, which are costly to treat and can seriously affect an individual’s quality of life. To reduce the risk of pressure ulcers, Clinical Practice Guidelines (CPGs) recommend that manual wheelchair users perform repositioning activities, i.e., vertical pushups, lateral and forward leans, every 15 to 30 minutes. Despite the effectiveness of such pressure relief activities, the incidences of pressure ulcers among manual wheelchair users do not decline. Researchers hypothesize that poor compliance with CPGs could be the reason. However, no widely adopted applications are available to quantitatively evaluate whether a manual wheelchair user follows CPGs in their daily life. To fill in the gap, we have developed an iOS app that can communicate with an Apple Watch to collect the activity data of a manual wheelchair user. Based on the characteristics of sensor data specific to the iOS platform, we have developed a threshold-based algorithm to facilitate training data preparation and a neural-network-based approach to classify sensor data. Experimental results showed that our approach achieved a high classification accuracy. The outcome of this preliminary study lays a foundation for a nonintrusive and easy-to-use tool to assess a manual wheelchair user’s daily pressure relief activity.

**51. Name:** Phil Bourne **Institution:** University of Oklahoma **Email:** pcbourne@ou.edu **Research area:** Other**Title:** The protein production and characterization core facility

The Protein Production and Characterization Core Facility (PPCC) was established to support investigators participating in the NIH-funded Oklahoma COBRE in Structural Biology as well as the bioscience’s community in Oklahoma.

**Abstract:** Equipment is available for overexpression of a protein of interest, including shaking incubators, centrifuges, and an Emulsiflex cell lysis instrument. For protein purification, FPLC systems are available, including an ÄKTA pure, a BIO-RAD NGC, and an ÄKTA Start, as well as a variety of chromatography media for use in isolation of the protein of interest. SDS-PAGE and Western blotting are used to check the purity of protein samples. A imager is available to record results and, can be used to analyze both protein and DNA gels. The acquisition of a MicroCal PEAQ Isothermal Titration Calorimeter, Octet RED96 Biolayer Interferometer, and a Tensor II FTIR has expanded the biophysical characterization capabilities of the core facility.
The PPCC director provides hands-on training for all the equipment and procedures in the facility. Consultation and advice on protein expression and purification protocols are available. Users of the PPCC can produce and purify proteins either themselves using equipment available in the core or with the assistance of PPCC staff on a fee for service basis.

**52. Name:** Seth Griger **Institution:** Nebraska Wesleyan University **Email:** grigerseth@gmail.com **Research area:** Other**Title:** Comparing the courtship rituals and sexual characters of two sister species of *Schizocosa* wolf spiders

**Authors:** Seth Griger, Department of Biology, Nebraska Wesleyan University, Lincoln, NE 68504; Rowan McGinley, Department of Biology, Saint Louis University, St. Louis, MO 63103; Eileen A. Hebets, School of Biological Sciences, University of Nebraska-Lincoln, Lincoln, NE 68588

**Abstract:** This study tests for the presence of reinforcement in two sister species of wolf spider in the genus Schizocosa. In particular, it examines the degree to which secondary sexual traits are divergent in sympatric (overlapping) and allopatric (non-overlapping) populations of Schizocosa stridulans and S. uetzi. We expect that populations of S. stridulans that live among S. uetzi will produce more distinct displays compared to an isolated population of S. stridulans. To test this, we quantified the ornamentation of male S. stridulans and S. uetzi by taking measurements of the legs of males from three populations – (i) allopatric S. stridulans, (ii) sympatric S. stridulans, and (iii) allopatric S. uetzi. We also quantified aspects of the dynamic visual display from males of all three populations by analyzing videos of courting males. In particular, we measured the speed of movement, range of motion, and duration of leg movement. We will discuss our results in terms of the degree of overlap observed in both ornamentation and movement displays between S. stridulans and S. uetzi as well as between the allopatric and sympatric populations of S. stridulans.

**53. Name:** Faith Kozisek **Institution:** University of Nebraska Medical Center **Email:** faith.kozisek@unmc.edu **Research area:** Other**Title:** Physiological significance of superoxide dismutase in S. aureus

**Authors:** Faith Kozisek1, Sasmita Panda1, Vinai C Thomas1, and Sujata S Chaudhari1
1Center for Staphylococcal Research, University of Nebraska Medical Center, Omaha, Nebraska

**Abstract:** Reactive oxygen species like superoxide (O2•-), hydrogen peroxide (H2O2) and hydroxyl radicals (OH•) are adventitious byproducts of aerobic metabolism that readily damage cellular macromolecules. The human pathogen Staphylococcus aureus expresses two superoxide dismutase (SOD) enzymes, SodA and SodM, that can reduce O2•- mediated oxidative stress. Although both SODs have been shown to play important role in countering host-derived O2•-, their role in protection from endogenously produced O2•- has not yet been elucidated. Here, we reveal that both SodA and SodM are important for the optimal growth of S. aureus under aerobic conditions. The sodAsodM double mutant produced higher levels of O2•- and exhibited a decreased growth yield relative to the parental strain. The enhanced sensitivity of the sodAsodM mutant to endogenously produced O2•- was effectively reduced upon anaerobic growth. The deleterious effects of O2•- on growth yield of the sodAsodM mutant resulted from decreased activity of multiple enzymes of the TCA cycle. Finally, we provide evidence that supports a regulatory, rather than a direct effect of O2•- in reducing activity of TCA cycle enzymes in the sodAsodM mutant. Collectively, our study highlights a physiological role for staphylococcal SODs in promoting metabolic activation of the TCA cycle during growth.

**54. Name:** Diane Smith **Institution:** Mount Marty University **Email:** diane.smith@mountmarty.edu **Research area:** Other

**Title:** *Wicozani Waste*: A healthy lifestyle for rural American Indian youth through cultural and physical activities: A community-based participatory research study

**Authors:** Fellows Malaya Heine and Mia Salas with Mentor Dr. Diane L. Smith, PhD, RN Mount Marty University & Sheridan Parker Graduate Student Investigator with Dr. Brian Knarr PhD Department of Biomechanics from the University of Nebraska Medical Center at Omaha

**Abstract:** In the summer of 2021 a collaborative community-based participatory research study under South Dakota INBRE BRIN and NIGMS administrative supplemental funding, Mount Marty University South Dakota INBRE BRIN researchers and IDeA-CTR researchers from the University of Nebraska Omaha’s Engineering Department assessed health disparities including obesity, Type II diabetes, and violence related to human trafficking by investigating and evaluating cultural and physical activity interventions with youth ages 8 to 19. An activity actigraph monitoring device and InBody 570 were used to collect the data during cultural and physical interventions provided by Coach Rozy’s Performance Program in Niobrara/Santee, NE and the Protect the Sacred youth events by the Great Plains Action Society with Indian Youth of America. The cultural traditional games activities evaluated were lacrosse; doubleball; archery; hand games; moccasin game; tipi set up and protocols; nature hike; powwow dancing, women’s self-defense training and boxing. Through these interventions in collaboration with the rural American Indian communities, the INBRE BRIN researchers joined forces in an attempt to prevent future health complications, and to achieve health equity or as the American Indian culture would rather say achieve a culture of equality, harmony, and Wicozani Waste-a healthy lifestyle.

**55. Name:** Kevin Rice **Institution:** University of Nebraska-Lincoln **Email:** kevin.rice@huskers.unl.edu **Research area:** Other**Title:** Mining metagenome-assembled genomes to quantity bacterial Dimethylsulfoniopropionare (DMSP) synthesis potential

**Authors:** Rice Kevin, Cooper Reilly, Cressler Clay, Department of Ecology and Evolution, University of Nebraska-Lincoln, Lincoln, NE 68505

**Abstract:** The organosulfur compound dimethylsulfoniopropionate (DMSP) is the main precursor to dimethylsulfide (DMS), a molecule that contributes significantly to Earth’s sulfur cycle and climate regulation. While pathways for DMSP biosynthesis have been well-described in plants and cyanobacteria, only recently have bacterial DMSP pathways been described. In some -Proteobacteria, a DMSP pathway consisting of four key enzymes has been characterized. However, it is unknown how widespread this specific DMSP biosynthesis pathway is among bacteria and environments. To address this, we mined a set of 52,515 published metagenome-assembled bacterial genomes (MAGs) using custom-built profile HMMs of the genes involved in this pathway. Our results indicate that many more bacteria than the previously described -Proteobacteria, particularly aquatic species, encode for DMSP biosynthesis. We identified 251 unique bacterial MAGs with all four enzymes. Within these MAGs, the copy number of each gene in the biosynthetic pathway varied across environments. However, the copy number for MSMT did not vary significantly, with MAGs having at most two copies, potentially suggesting a more conserved function compared to the other pathway genes. Our findings indicate that DMSP biosynthetic potential is a rare bacterial function but can be found readily in some aquatic bacteria. This work can serve as a basis for future targeted inquiries into bacterial DMSP biosynthesis in aquatic ecosystems.

**56. Name:** Rhiannon McCracken **Institution:** Creighton University **Email:** rbm71897@creighton.edu **Research area:** Other**Title:** Structural and functional analysis of *Crassostrea gigas* OAZ1-PK RNA

**Authors:** Rhiannon McCracken1, Spencer Thompson1, Siddharth Venkatraman1, Juliane Strauss-Soukup1,2
1Creighton University, Department of Chemistry and Biochemistry
2Creighton University School of Medicine, Department of Medical Microbiology and Immunology

**Abstract:** A riboswitch is a non-coding RNA sequence that regulates the expression of a downstream gene when it is bound to a metabolite. When the riboswitch interacts with a specific metabolite, it undergoes a conformational change, which leads to a change in gene expression. Ultimately, gene expression is altered so as to inhibit the production of this same metabolite within its metabolic pathway. The Soukup lab is currently researching a potential mammalian riboswitch in the Ornithine Decarboxylase Antizyme pseudoknot (OAZ-PK) RNA segment. Previous work in the lab revealed that OAZ-PK RNA in mouse undergoes conformational changes in the presence of a specific polyamine. A polyamine is an organic compound that influences cell growth and differentiation. Since riboswitches have such a profound influence on metabolic pathways in bacteria, this provides an outlet for new antibiotic treatments. Identification of similar noncoding RNAs in eukaryotes will open up possibilities for new antibiological agents.

My project focuses on studying a potential riboswitch in Crassostrea gigas, a species of oyster. More specifically, I am performing In-Line Probing (ILP) experiments to analyze the secondary structural changes of this RNA segment when it interacts with various concentrations of natural and non-natural polyamines. Preliminary data from ILP experiments suggest that the OAZ-PK RNA in oyster is undergoing conformational changes in the presence of different concentrations of spermine. In the future, more ILP experiments will be performed, along with the use of Selective 2'-Hydroxyl Acylation analyzed by Primer Extension (SHAPE) to further study the polyamine concentration-dependent conformational changes in OAZ-PK RNA.

Acknowledgements: I would like to thank the Soukup lab, Creighton University Center for Undergraduate Research and Scholarship, and the NIH INBRE Program of the National Institute for General Medical Science (5P20GM103427) for the support and funding of my project.

**57. Name:** Seth Harriet **Institution:** University of Central Oklahoma **Email:** sharriet@uco.edu **Research area:** Other**Title:** Design, fabrication, and mechanical testing of bioresorbable PCL flow diverters

**Authors:** Seth Harriet1, Vishal Barot1, Andrew Bauer2, Melville Vaughan3,4 and Mohammad R Hossan1,4
1Department of Engineering and Physics, Department of Biology2and 3Center of Interdisciplinary Biomedical Education and Research, University of Central Oklahoma, Edmond, OK 73034
2Department of Neurosurgery, University of Oklahoma-health science center, Oklahoma City, OK

**Abstract:** Flow diverters (FDs) have become a promising endovascular device for the treatment of aneurysm. This research presents a novel Polycaprolactone (PCL) FDs that will degrade after dissolution of aneurysm. Non-braided FDs with 60% to 70% porosity were designed and fabricated with computer-aided design, Python programming, and a fused deposition modeling system. The in-house system was built with a micromotion stage, rotary robotic arm, and electromelt nozzle. FDs were fabricated from medical grade PCL and characterized using SEM and 3D profilometer. The radial compression, longitudinal tension, and bending strengths of the FDs were evaluated using a universal testing machine. The SEM surface characterization showed that the struts were connected without deviation from the CAD design. Nanometer-scale roughness was observed in 3D profile measurement. However, surface roughness was improved after mild sonication of FDs in an acetone bath. The radial, longitudinal, and bending flexibility were found to be 0.64 N/mm, 4.34 N/mm, and 0.373 N/mm respectively which are comparable to the conventional coronary stents. PCL FD was fully recovered from the repeated radial compression and returned to the original shapes without compromising mechanical integrity. This study is a step forward in the development of bioresorbable FDs for the endovascular treatment of aneurysms.

**58. Name:** Shaoning Jiang **Institution:** University of Oklahoma Health Science Center **Email:** Shaoning-Jiang@ouhsc.edu **Research area:** Obesity Diseases**Title:** Fetal liver peroxisomal defects in response to maternal high fat diet

**Authors:** Mary-Ellen Jensen, Steven D Chernausek, and Shaoning Jiang

**Abstract:** Adverse maternal environments, such as obesity and diabetes, can increase child’s lifelong risk of metabolic diseases, including non-alcoholic fatty liver diseases (NAFLD). Peroxisomes are oxidative organelles that are functionally required for fatty acid oxidation, homeostasis of reactive oxygen species, and metabolism of bile acids in liver. Despite implication of peroxisome defect-induced oxidative stress in obesity and diabetes, the effects of maternal environments on fetal peroxisomal remodeling and the roles of fetal peroxisomal defects in offspring’s long-term metabolic diseases remain unknown. Using a mouse model of maternal obesity, we demonstrated that maternal high fat diet (HFD) feeding resulted in increased adiposity and fatty liver in the offspring. Targeted proteomic analysis of proteins related to oxidative and glycolytic metabolism in fetal liver revealed that proteins dysregulated by maternal HFD were mostly related to peroxisomal function, including peroxisomal fatty acid transport and peroxisomal β-oxidation, such as Abcd3 and IDH1. In addition, the level of peroxisome antioxidant catalase was significantly lower in the fetal liver of obese dam. Together, those findings provide novel evidence of peroxisome as a component of early life events, which potentially result in oxidative stress and aberrant lipid and metabolites accumulation, leading to offspring development of NAFLD.

**59. Name:** Katrina Jensen **Institution:** Black Hills State University **Email:** katrina.jensen@bhsu.edu **Research area:** Other**Title:** Adapting enantioselective photoredox reactions to catalysts with earth abundant metals

**Authors:** Katrina H. Jensen, Adrienne Roller, Abie McCollar, Gabriella Nowodworski, Sierra Ward, Michael R. Hurst, and Thomas G. Trimble
School of Natural Sciences, Black Hills State University, 1200 University Street, Spearfish, SD, 57793

**Abstract:** Photoredox reactions are useful tools in the chemical synthesis of small organic molecule targets. These reactions use light to generate new products through electron transfer reactions, and are most frequently catalyzed by complexes of precious metals, such as ruthenium and iridium. Our group has been working to develop alternative catalysts based on earth abundant metals, such as copper, with the goal of developing photoredox catalysts that are both less toxic and less expensive. Specifically, we have been examining the use of copper(I) bisphenanthroline complexes in reactions involving the α-alkylation or α-benzylation of aldehydes. These reactions involve a second, chiral catalyst (known as MacMillan’s catalyst), and result in the enantioselective formation of chiral products. We have worked towards optimizing the reaction conditions, evaluated the scope of the aldehyde and bromide reaction partners, and measured the enantiomeric excess of the products via HPLC with a chiral stationary phase. We are evaluating a series of copper(I) complexes, varying the ligand structure through the synthesis of various 1,10-phenanthroline derivatives. In an effort to improve catalyst efficiency, we are studying how changes to ligand structure are correlated with the photophysical properties of the complexes.

**60. Name:** Kaitlyn Tidwell **Institution:** The University of Central Oklahoma **Email:** Ktidwell4@uco.edu **Research area:** Other**Title:** Biocompatibility analysis of Polycaprolactone (PCL) flow diverters for brain aneurysm treatment

**Authors:** Kaitlyn Tidwell (1), Seth Harriet (1), Andrew Bauer (2), Melville Vaughan (3,4), and Mohammad R Hossan (1,4)
1) Department of Engineering and Physics, 3) Department of Biology, and 4) Center of Interdisciplinary Biomedical Education and Research, University of Central Oklahoma, Edmond, OK 73034
2) Department of Neurosurgery, University of Oklahoma-health science center, Oklahoma City, OK

**Abstract:** Flow diverters are the endovascular devices that have become popular in the treatment of brain aneurysms. This research presents a biocompatibility study of bioresorbable Polycaprolactone (PCL) flow diverters with human umbilical vein endothelial (HUVEC) cells.  PCL FDs were developed using in-house fused deposition modeling. In-vitro degradation analysis was performed in phosphate buffered saline (PBS) with a pH of 7.4 at 37°C and at 47°C for accelerated degradation. HUVEC cells were seeded with PCL FDs for 24-, 36-, and 48-hours. Cytotoxicity analysis of LDH release and NO production of HUVECs with PCL FDs were studied using colorimetric assay kits. The degradation rate for 5 weeks was found to be 0.312% and 0.315% for 37°C and 47°C, respectively. Cell studies show that adhesion and proliferation of endothelial cells on the PCL FD surface increases over time. Cell morphologies of endothelial cells on FD surface were analyzed under SEM. Endothelial cells were elongated to cover the FD surface and developed an endothelial monolayer. Cytotoxicity level was decreased with PCL FDs compared to the control and no statistical difference was found in NO production. This study shows that PCL FDs can be a viable material for bioresorbable flow diverters for brain aneurysm treatment.

**61. Name:** Alvaro Moreno Lozano **Institution:** University of Nebraskas Lincoln  **Email:** alvaro@huskers.unl.edu **Research area:** Other**Title:** Optimizing techniques to quantify neurite length in rat DRG explants in vitro

**Authors:** Alvaro Moreno Lozano, Fei San Lee, Rebecca A. Wachs. Department of Biological Systems Engineering, University of Nebraska-Lincoln, Lincoln, NE 68588

**Abstract:** Low back pain affects up to 80% of the population at some point in their lifetime, with intervertebral disc degeneration being highly correlated1. At least 40% of the cases of chronic low back pain exhibit ingrowth of sensory neurites into deep layers of lumbar discs2-3. These neurites from nearby dorsal root ganglion (DRG) can be sensitized and cause chronic pain4-6. Therefore, retracting sensory neurites or inhibiting their growth in the disc could alleviate disc-associated low back pain. In vitro DRG explant cultures can be used as a screening tool for potential therapeutics; however, neurite length analysis methods need to be optimized. Current methods using ImageJ (SimpleNeuriteTracer) to quantify changes in neurite length7 are inefficient due to manual tracing and limitation in the number of neurites that could be feasibly quantified. Sholl analysis is a faster semi-automated method in neurobiology to analyze the complexity of dendritic arbors by creating concentric rings and quantifying the number of intersections. This method could be applied in quantifying neurite growth or retraction in vitro8-9. The goal of this project is to optimize the Sholl analysis method for an automated higher throughput analysis for screening neuroinhibitory biomaterials and neurite retraction compounds using DRG explant cultures.

References: 1. Andersson et al 1999 2. Binch et al 2015 3. Freemont et al 2008 4. Choi et al 2009 5. Freemont et al 2007 6. Garcia-Cosamalon et al 2010 7. Romereim et al 2019 8. Sholl et al 1953 9. Binley et al 2009

**62. Name:** Nashanthea Roland **Institution:** University of Nebraska Medical Center **Email:** nashanthea.roland@unmc.edu **Research area:** Neuroscience

**Title:** Method for studying Cholinergic neurons in terms of Alzheimer's Disease

**Abstract:** Alzheimer’s Disease (AD) is the most common form of dementia worldwide. This detrimental ailment is characterized by the formation of extracellular senile plaques and intracellular neurofibrillary tangles (NFT) formed from β-amyloid peptides and hyper-phosphorylated tau, respectively. Many studies have shown that cholinergic neurons, which are responsible for the production of acetylcholine in the brain, are the most susceptible to damage during the progression of this disease. Targeting this mechanism has proven to ameliorate symptoms in the early stages of the disease; however, the mechanisms for why these neurons are more vulnerable have not yet been fully explored. We aim to improve and determine techniques to isolate and observe these neurons in both aging and AD models. Through antibodies against choline acetyltransferase (ChAT), and animal models that enhance the pull-down and visualization of these neurons and their individual cellular components, we look to elucidate ways to better study cholinergic neurons. Better ways to study these neuronal populations in vivo with AD-specific environments will aid in understanding the multiple factors that characterize this disease.

**63. Name:** Leoanrd Thomas **Institution:** University of Oklahoma **Email:** lmthomas@ou.edu **Research area:** Other**Title:** The University of Oklahoma Biomolecular Structure Core: Oklahoma COBRE in Structural Biology

**Authors:** Leonard M. Thomas1, Fabiola Janiak-Spens1 and Blaine H.M. Mooers2
1Department of Chemistry and Biochemistry
University of Oklahoma, Norman, OK 73019
2Department of Biochemistry and Molecular Biology
University of Oklahoma Health Sciences Center, Oklahoma City, OK 73104

The Biomolecular Structure Core (BSC)\* (https://www.ou.edu/structuralbiology/cobre-core-facilities) offers services and training to facilitate macromolecular structure determinations, with assistance ranging from obtaining preliminary crystallization conditions to full structure determinations.

**Abstract:** The BSC houses instrumentation and resources for crystallization, X-ray diffraction, and structure determination of macromolecular molecules. High-throughput crystallization screening is available using an SPT Labtech Mosquito or an ARI Gryphon with an LCP adapter crystallization robots. A Formulatrix Rock Imager 1000 provides automated imaging of the crystallization experiments with UV and Multi-Fluorescence Imaging (MFI) technologies, and a Rigaku Minstrel Imager for imaging of crystallization trays at 4 C. Each location houses Rigaku 007HF MicroMax X-ray generators with dual optics and detectors for the collection of X-ray diffraction data. The BSC also coordinates data collection at the Stanford Synchrotron Radiation Lightsource. Computational resources are available for data processing, structure determination, structure analysis, and molecular graphics.

Since the inception of the BSC, over 50 research groups have utilized the facility, resulting in 32 publications and the awarding of 45 external grants from both federal and state entities ($23 M total) for structure biology projects.

\*The BSC is supported, in part, by a COBRE grant P20GM103640 (PI: Ann West).

**64. Name:** Se-Ran Jun **Institution:** University of Arkansas for Medical Sciences **Email:** sjun@uams.edu **Research area:** Clinical-translational**Title:** A real-time genomic surveillance for infection control and antibiotic stewardship

**Author:** Se-Ran Jun, Assistant Professor
Department of Biomedical Informatics, University of Arkansas for Medical Sciences

**Abstract:** Background: Antibiotic resistance has become a widespread problem in the US, and worldwide, and is a great challenge to public health. Nosocomial infections caused by antibiotic resistant pathogens are a significant cause of morbidity and mortality especially in immunocompromised cancer patients and elderly. The adoption of genomic surveillance of antibiotic resistance for infection control and antibiotic stewardship would be a revolution in clinical medicine and public health.
Results: We present 2 cases of vancomycin-resistant Enterococcus faecium bacteremia with development of daptomycin (DAP) resistance in 2 patients with acute myeloid leukemia and myelodysplastic syndrome. Using real-time nanopore sequencing, mutations in liaSR genes known to be associated with DAP-nonsusceptible phenotype were identified in all strains of the study, including those with a minimum inhibitory concentration <1 µg/mL collected before daptomycin therapy. Real-time nanopore data analysis revealed that those DAP resistance mutations could be observed within five hours. Comparative analysis of whole genome using our k-mer based alignment-free method, FFP (feature frequency profile) revealed clonality of all the isolates from two patients distinguishing their hosts. Further, epidemiologic integrative investigation of electronic health record (EHR) and genomic data suggested nosocomial outbreak.
Conclusion: Our method, FFP showed the power of high-resolution phylogenomic analysis to track even clonal isolates for infection control. The study highlighted the need of genomic surveillance for infection control and antibiotic stewardship. Our results support the proof of concept of real-time genomic surveillance which would provide timely assistance in breaking transmission routes of antibiotic resistance infection and optimizing antibiotic treatment for precision medicine.

**65. Name:** Maddy Sladky **Institution:** Doane University **Email:** maddy.sladky@doane.edu **Research area:** Other

**Title:** Using bred to identify essential genes that affect the lysogenic life-cycle found in a bacteriophage’s genome

**Abstract:** A bacteriophage is a virus that infects a specific bacterium. With the epidemic of antibiotic-resistant bacteria, understanding how bacteriophages infect bacteria and what genes are specific to that process is crucial for the future treatment for bacterial infections. Using the Bacteriophage Recombineering of Electroporated DNA (BRED) can help identify genes found in bacteriophages that can be useful for phage therapy. I have selected a bacteriophage named Jabith that infects the host bacteria Mycobacterium smegmatis. Jabith is lysogenic, meaning it incorporates its DNA into the host bacteria’s genome for replication. By engineering Jabith’s genome using BRED, by deleting a gene, could change the phage infection to lytic. I hypothesize that if we deleted an essential gene, the bacteria infected would not produce plaques. The phage DNA was isolated for transformation for electroporation. We identified important genes for lysogenic growth in Jabith’s genome. We will use this gene to construct oligos. The next steps are to use BRED to delete a gene. This will illustrate what genes are vital for lysogenic growth and specific genes that kill M. smegmatis. By finding what genes cause a change from lysogenic to lytic behavior using BRED, can help with the availability of phage therapy treatment.

**66. Name:** Nathan de la Montanya **Institution:** Black Hills State University **Email:** Nathan.delamontanya@yellowjackets.bhsu.edu **Research area:** Molecular Target Discovery and Development-Nanomedicine**Title:** A general method for deubiquitination assay

**Authors:** Nathan DelaMontanya, Teagen Hartley, Aaron Schone, Jordan Brooks, Olivia Clarke, Vincent Leahy, Aidan Baker, and Yun-Seok Choi

School of Natural Sciences, 1200 University St, Unit 9008, Black Hills State University, Spearfish, South Dakota, 57799-9008

**Abstract:** Deubiquitinase (DUB) is an enzyme responsible for the removal of ubiquitin (Ub) conjugated on proteins, generating free Ub (i.e. unconjugated Ub) as the reaction product. The human genome encodes nearly 100 DUBs playing important roles in cell cycle control, DNA damage repair, and disease pathways. The deregulation of DUBs has an impact on human diseases, like cancer, neurodegeneration, and inflammation, which highlights the therapeutic potential for pharmacological modulation of DUB activities. Although the kinetic data of DUB are important to understand DUB functions, there is no practical method for deubiquitination assays with physiological substrates. Free Ub is the common product of DUB assays, and so measurements of free Ub would be a general method of DUB assay. We developed Atto532-tUI2 which has a strong binding affinity (Kd: 1.2 nM) with free Ub while it shows no binding to hundreds micromolar conjugated Ub. We successfully obtained the kinetic data of Usp2 catalytic core, a DUB, with Ub-GB1 as the substrate in presence of Atto532-tUI2. This method with Atto532-tUI2 can be a general method for DUB assays with physiological substrates.

**67. Name:** Vinay Swami **Institution:** University of Central Oklahoma **Email:** vswami2@uco.edu **Research area:** Other**Title:** Identification of brain signaling from post-traumatic brain injury shock

**Authors:** Vinay Swami, Vivek Swami, Helga Progri, Roman Wolf, Mohiuddin Ahmad, PhD, & Morshed Khandaker, PhD

**Abstract:** Post-traumatic brain injuries (TBI) in mice involve brain injuries that can be stimulated through shock. Brain histology can be utilized to assess whether injuries have taken place. It allows sectioning of mice brains to be done with an addition of staining protocols to contrast between TBI and control. Cell morphology can also be used to contrast between healthy and unhealthy mice. To analyze brain activity, we utilized a vibratome, GFAP expression, and confocal imaging. The vibratome was used to obtain 40-micron sections. The brains were categorized into blast (7 days or 24 hours) and control (7 days or 28 days). Confocal was used to obtain images in the hippocampus to identify expression of cells between control and TBI brains. We immunostained fixed brain sections with GFAP and lbaI prepared from control and TBI animals to investigate reactive astrogliosis and morphological changes induced by TBI. Our preliminary data show that GFAP expression increases in the hippocampus of mice at 24 hours following TBI. We also examined reactive changes in other cells in the brain, including the expression of Iba1 in microglia and the accumulation of hyperphosphorylated tau in neurons. as part of examining the morphological changes induced by TBI. The above histopathology result confirms that our developed blast equipment can successfully generate moderate TBI injury on mice brain.

**68. Name:** Andrew Trease **Institution:** University of Nebraska Medical Center **Email:** andrew.trease@unmc.edu **Research area:** Neuroscience

**Title:** Mitochondrial homeostasis and function is altered by modulation of Parkin activity in a mouse model of aging

**Abstract:** Parkinson's disease, the second most common age-related neurodegenerative disorder, is characterized by progressive loss of nigrostriatal dopaminergic neurons, as well as cognitive and motor deficits in afflicted patients. Molecularly, aberrations in mitochondrial maintenance are implicated in disease onset and progression, however, precise initiating and sustaining mechanisms are somewhat controversial. With this is mind we investigated the importance of Parkin expression/activity in vivo for controlling mitochondrial fidelity and homeostasis in the context of aging as a risk factor. Using the progeroid PolgD257A mutator mouse model to accelerate the mitochondrial aging phenotype in combination with parkin deletion or hyperactivity we used biochemistry, molecular biology, and bioenergetics to evaluate parkin as a potential therapeutic target. We observed age- and parkin-dependent differences in body weight compared to wild-type (WT) animals that primarily affected males. In females, only progeroid mice lacking parkin exhibited reduced body weight. In contrast to body weight, we observed a near ubiquitous increase in heart mass in males and females compared to WT animals independent of parkin status. Finally, we observed age- and parkin-dependent alterations in synaptic bioenergetics that correlated with alterations is mitochondrial biomass.

**69. Name:** Kade Wehrs **Institution:** Doane University **Email:** kade.wehrs@doane.edu **Research area:** Other

**Title:** SATB1 forms homodimers independent of DNA

**Abstract:** Chromatin reorganization is one of the many factors that influence gene regulation, and Satb1 is one of the few proteins that has been implicated in this process. This conformational change is used to switch cell behavior in a number of important ways, including being a factor in determining whether embryonic stem cells differentiate. Satb1’s mode of activity is uncertain, but it contains three DNA-binding domains that bind to AT-rich sequences. Many DNA-binding proteins dimerize in order to recognize longer stretches of DNA, but there is conflicting evidence whether this is true for Satb1. Here we show that a fluorescently-tagged Satb1 is able to drag a nuclear-import deficient mutant of Satb1 into the nucleus. This demonstrates that Satb1 forms homodimers in a DNA-independent manner and that they are stable enough to persist through nuclear import. Truncations of Satb1 are currently being tested to identify which region of Satb1 is responsible for homodimerization.

**70. Name:** Rachel Armfield **Institution:** University of Central Oklahoma **Email:** rarmfield@uco.edu **Research area:** Other

**Title:** Differential gene expression and smooth muscle differentiation in a murine model of maternal Phenylketonuria

 **Abstract:** Maternal Phenylketonuria (MPKU) affects embryos exposed to high concentrations of phenylalanine (Phe) in utero due to Phenylketonuria in the mother. MPKU leads to craniofacial, cardiac and cognitive disabilities. The mechanism of MPKU is unknown, but due to early diagnosis and treatment of PKU, cases are increasing.
Cranial neural crest cells from Mus musculus were exposed to Phe concentrations that occur in utero. mRNA was extracted and converted to cDNA. Quantitative Real-Time PCR (qRT-PCR) was performed on a total of 89 genes involved in Retinoic Acid signaling. Data were analyzed using Ct method, with expression changes given as a log2 fold change. 13 genes were significantly upregulated on exposure to Phe.
Some of these upregulated genes affect smooth muscle differentiation in the embryo. The regions affected by MPKU contain neural crest-derived smooth muscle. The same cell line was treated with three clinically relevant concentrations of Phe, and immunostained for smooth muscle actin. The treated cells demonstrate a dose-dependent delay in differentiation, along with an alteration in phenotype when compared with the control cells.
This is the first gene expression investigation using a mouse model of MPKU, and the first to determine that phenylalanine alters differentiation of neural crest into smooth muscle.

**71. Name:** Sarah Altman **Institution:** University of Nebraska Medical Center **Email:** saltman@unmc.edu **Research area:** Clinical-translational**Title:** MUC4 autoantibody signatures for refining vaccine design and patient stratification in pancreatic cancer.

**Abstract:** Pancreatic cancer (PC) is a lethal malignancy with a grim 5-year survival rate of 10%1. PC treatment is challenging due to late diagnosis, poor resectability, and poor response to therapeutics2. In contrast to other malignancies (melanoma and lung cancer), immunotherapy is relatively ineffective for PC due to its poor immunogenicity. Due to its differential overexpression, aberrant glycosylation, extensive splicing and functional role, Mucin 4 (MUC4) has emerged as a promising candidate for vaccine development3. We hypothesize that antibodies are surrogate biomarkers of: a) vaccine efficacy in animals immunized with MUC4 vaccine; and, b) compromised immune tolerance in PC patients. Unpublished studies from our lab suggest that autoantibodies against certain overlapping MHC I and B-cell epitopes can predict survival of PC patients in an isotype-dependent manner. We predicted overlapping MHC II and B-cell epitopes of MUC4 and synthesized peptides to correlate the humoral response with the efficacy of a MUC4 vaccine. Further, we are developing Luminex xMAP multiplex assays to enable the high-throughput isotype analysis of epitope-specific MUC4 autoantibodies in PC sera. These studies will allow us to interrogate anti-MUC4 antibody signatures to determine the association of epitopes and antibody isotypes with vaccine efficacy and clinical outcomes.

Citations:
1. Survival Rates for Pancreatic Cancer. Cancer.org. Accessed June 21, 2021. https://www.cancer.org/cancer/pancreatic-cancer/detection-diagnosis-staging/survival-rates.html
2. Why is pancreatic cancer so hard to treat? Mskcc.org. Published November 8, 2016. Accessed June 21, 2021. https://www.mskcc.org/news/why-pancreatic-cancer-so-hard-treat
3. Gautam SK, Kumar S, Dam V, Ghersi D, Jain M, Batra SK. MUCIN-4 (MUC4) is a novel tumor antigen in pancreatic cancer immunotherapy. Semin Immunol. 2020;47:101391. doi:10.1016/j.smim.2020.101391

**72. Name:** Ronit Gandhi **Institution:** UNL/UNMC **Email:** rgandhi3@huskers.unl.edu **Research area:** Other**Title:** Utilizing Markov chains to estimate allele progression through generations

**Authors:** Ronit Gandhi and Austin Eide, both of University of Nebraska - Lincoln

**Abstract:** All populations display patterns in allele frequencies over time. Some alleles cease to exist, while some grow to become the norm. These frequencies can shift or stay constant based on the conditions the population lives in. If in Hardy-Weinberg equilibrium, the allele frequencies stay constant. Most populations, however, have bias from environmental factors, sexual preferences, other organisms, etc.
 We propose a stochastic Markov chain model to study allele progression across generations. In such a model, the allele frequencies in the next generation depend only on the frequencies in the current one.
 We use this model to track a recessive allele through successive generations. Eventually, the allele will be “cancelled out” by the genotype of an organism becoming homozygous dominant. We estimate the number of generations it will take for this allele to be "cancelled out" by computing a hitting time in the Markov chain. This will allow us to efficiently communicate the trends of allele frequencies and estimate the speed of growth or decay of alleles.

**73. Name:** Melville B. Vaughan **Institution:** University of Central Oklahoma **Email:** mvaughan4@uco.edu **Research area:** Other

**Title:** In vitro aging enhances the Dupuytren’s Contracture myofibroblast phenotype

**Authors:** Melville B. Vaughan, Gang Xu, Austin Segrest, Chanock Lee, Juyoung Cho

**Abstract:** Dupuytren’s Contracture (DC) is the buildup of scar tissue in the hand that causes one or more digits to flex, reducing utility. Due to lack of appropriate animal models, scientists often use 3D in vitro models to study DC. This disease in vivo has a high recurrence rate after scar tissue removal, thus short telomeres from repeated cell divisions may play a role in the pathology of recurrent DC. We used this rationale to study phenotypic differences of DC cells from 3 different patients aged in vitro (early and late passage, more specifically population doublings (PD)). Cells were treated with TGF-beta to induce myofibroblasts. 2D assays with immunocytochemistry and western blotting were conducted to study proliferation, migration, focal adhesion formation and alpha smooth muscle actin expression. 3D collagen matrix assays were conducted to observe compaction, contraction, proliferation, and alpha-smooth muscle actin expression. Our overall results showed that aging DC cells in vitro increase their TGF-beta responsiveness through myofibroblast differentiation. These results may provide insight for therapies targeting the recurrent DC disease or provide momentum to develop an appropriate DC animal model.

**74. Name:** Jordan Rasmussen **Institution:** University of Nebraska Medical Center **Email:** jrasmussen@unmc.edu **Research area:** Other**Title:** MnTnBuOE-2-PyP5+, a Superoxide Dismutase mimic, induces vasodilation in hypertension: A mechanistic investigation

**Authors:** Jordan Rasmussen, Sarah L. Schlichte, Elizabeth J. Pekas, Taylor J. Bruett, Elizabeth A. Kosmacek, Rebecca E. Oberley-Deegan, Song-Young Park, Matthew C. Zimmerman

**Abstract:** It is well established that the accumulation of reactive oxygen species (ROS), particularly superoxide (O2•-), contributes to the pathogenesis of hypertension. Decades of evidence obtained from experimental animal models of hypertension clearly demonstrate that scavenging of O2•- via overexpression of superoxide dismutase (SOD) or administration of SOD mimics decreases elevated blood pressure. However, the translation of these observations to the clinical setting have been limited for various reasons. One particular SOD mimic that has advanced into clinical trials is MnTnBuOE-2-PyP5+ (BuOE). This manganese porphyrin is being clinically investigated as a radioprotector in cancer patients receiving radiation therapy. Considering BuOE’s SOD-like action, our lab recently examined its ability to decrease hypertensive blood pressure. In a mouse model of hypertension, we have shown that BuOE induces a significant transient decrease in blood pressure. Additionally, we have shown that BuOE directly induces vasodilation, which likely contributes to its hypotensive response. For the current INBRE scholar summer research project, we hypothesize that BuOE scavenges O2•- in the vasculature resulting in an increase in the bioavailability of nitric oxide (•NO), a well-known vasodilator. Superoxide and NO• levels in arterial tissue samples collected from normotensive and hypertensive mice will be measured using electron paramagnetic resonance (EPR) spectroscopy. This study will provide insight into the mechanism(s) by which BuOE induces vasodilation and decreases hypertensive blood pressure.

**75. Name:** Scott P. Mattison **Institution:** University of Central Oklahoma **Email:** smattison1@uco.edu **Research area:** Other**Title:** Cochlear mechanics of the developing chicken embryo

**Authors:** Gianella Albines Chavez and Scott P. Mattison

**Abstract:** Damage and degeneration of hair cells within the inner ear is the most common form of hearing loss and its prevalence greatly increases with age. Current treatments for sensorineural hearing loss are unable to fully correct or compensate for the damage to the inner ear. A key challenge in development of treatment methods is the incomplete understanding underlying the passive and active biomechanics of the inner ear. Using a technique known as Optical Coherence Vibrometry, we can quantitatively measure the nanometer scale mechanical motion of the inner ear in response to auditory stimuli. Using an ex ovo model, we are quantifying the passive mechanics of the avian cochlear ducts throughout a key stage of cochlear development. The coupling efficiency of vibrational motion between the basilar membrane and the tectorial membrane of the cochlear duct of developing chick embryos was measured using Optical Coherence Vibrometry between ages E10 and E13 of development. Here, we present our initial findings of this project.

**76. Name:** Alexis Burke **Institution:** Doane University  **Email:** lexi.burke@doane.edu **Research area:** Other**Title:** Using Raman spectroscopy to view carbon monoxide bonded to heme on gold nanoparticle platforms

**Abstract:** Heme is the iron complex in the blood, a specific part of hemoglobin that bonds to both oxygen and carbon dioxide and is crucial to the respiratory system’s function. Using Raman spectroscopy, a type of spectroscopy utilizing vibrations to record and visualize bonds within molecules, the iron of heme bonding with oxygen and cyanide can be examined. While heme, by itself, has a too weak Raman signature, so we would be recording reliable data, it can be mixed with gold nanoparticles (AuNPs), acting as an amplifier that enables the Raman spectra to pick it up; this technique is called surface-enhancing Raman spectroscopy (SERS). A home-built Raman spectrometer was used to collect the SERS spectra at an excitation of 785 nm. The SERS spectra demonstrates the successful binding of AuNPs to the heme compound. We are beginning to collect data on different carbon monoxide solutions in an aqueous solution. Carbon monoxide bonds very quickly with the heme, so using a deoxygenating agent can break the iron’s bond with the oxygen and bond the iron with carbon monoxide. Additionally, we will be working with bigger molecules that contain heme, such as myoglobin and hemoglobin.

**77. Name:** Lyle G. Best **Institution:** Turtle Mountain Community College **Email:** lbest@restel.com **Research area:** other

**Title:** Maternal risk of pre-eclampsia: Influence of fetal rs1205 genotype

**Authors:** Lyle G. Best,1 Crystal Azure,1 Hailey Davis,1 Craig Poitra,1 Tyler Parisien1, 1Turtle Mountain Community College

**Abstract:** Background and Purpose:

 We have previously identified three C-reactive protein (*CRP*) gene variants, the maternal genotypes of which, increase the risk of pre-eclampsia (PE). These findings have been replicated in two non-American Indian populations. Most analyses of genetic PE risk assume that maternal genotype confers risk, whereas the fetal genotype may be determinative, and the maternal genotype is simply correlated with fetal genotype.

Method:

 We enrolled only offspring of mothers known to be heterozygous for the rs1205 variant of *CRP* and experiencing either PE affected or normal pregnancies. Thus, eliminating the maternal genetic influence of this variant. Offspring were then genotyped to determine if fetal rs1205 genotype was associated with PE.

Results:

 Offspring of 9 of 15 normal pregnancies and 1 of 4 PE pregnancies carried the rs1205 T allele in a dominant genotype (Pearson's chi square p=0.213, continuity correction p=0.495). Logistic regression analysis gives an odds ratio of 0.222, p=0.236, 95% CI 0.018-2.67.

Conclusion:

 Although only 19 of 50 planned offspring have been genotyped, the trend indicates a reduced risk of PE among those pregnancies with fetal T allele dominant genotypes. This is in accord with previous findings of reduced risk associated with maternal T allele genotype.

**78. Name:** Patricia Soto **Institution:** Creighton University **Email:** patriciasoto@creighton.edu **Research area:** Neuroscience**Title:** Cellular prion protein gene polymorphisms linked to differential scrapie susceptibility correlate with distinct residue connectivity between secondary structure elements

**Authors:** Patricia Soto[1], India A. Claflin[2], Alyssa L. Bursott[3], Aimee D. Schwab-McCoy[4], Jason C. Bartz[5]

[1] Physics department, [2] Biology department, [3] Neuroscience program, [4] Math department, [5] Medical microbiology and immunology department

**Abstract:** The conformational conversion of the cellular prion protein (PrPC ) to the misfolded and aggregated isoform, termed scrapie prion protein (PrPSc), is key to the development of a group of neurodegenerative diseases known as transmissible spongiform encephalopathies (TSEs). Although the conversion mechanism is not fully understood, the role of gene polymorphisms in varying susceptibilities to prion diseases is well established. In ovine, specific gene polymorphisms in PrPC alter prion disease susceptibility: the Valine136-Glutamine171 variant (Susceptible structure) displays high susceptibility to classical scrapie while the Alanine136-Arginine171 variant (Resistant structure) displays reduced susceptibility. The opposite trend has been reported in atypical scrapie. Despite the differentiation between classical and atypical scrapie, a complete understanding of the effect of polymorphisms on the structural dynamics of PrPC is lacking. From our structural bioinformatics study, we propose that polymorphisms locally modulate the network of residue interactions in the globular C-terminus of the ovine recombinant prion protein while maintaining the overall fold. Although the two variants we examined exhibit a densely connected group of residues that includes both -sheets, the 2-2 loop and the N-terminus of -helix 2, only in the Resistant structure do most residues of -helix 2 belong to this group. We identify the structural role of Valine136Alanine and Glutamine171Arginine: modulation of residue interaction networks that affect the connectivity between -helix 2 and -helix 3. We propose blocking interactions of residue 171 as a potential target for the design of therapeutics to prevent efficient PrPC misfolding. We discuss our results in the context of initial PrPC conversion and extrapolate to recently proposed PrPSc structures.

Acknowledgment: This work was made possible partly by grants from the National Institute for General Medical Science (NIGMS) (5P20GM103427), a component of the National Institutes of Health (NIH), and its contents are the sole responsibility of the authors and do not necessarily represent the official views of NIGMS or NIH.

**79. Name:** Samuel Streeter **Institution:** Nebraska Wesleyan University **Email:** samstreeter000@gmail.com **Research area:** Other**Title:** The role of viruses in ocular surface tumors

**Authors:** Sam Streeter and Peter Angeletti

**Abstract:** The countries of Sub-Saharan African not only have very high incidence rates of ocular surface tumors, but also lack many important diagnostic and prognostic tools. Ocular surface tumors consist of a variety of abnormal growths on the cornea and conjunctiva and may be either malignant or benign. Various viruses, especially HIV, have been found to correlate with the incidence of these cancers. However, the underlying roles of these viruses has yet to be elucidated. Samples from Zambian individuals with ocular surface tumors were collected and their HIV status was tested. The presence of other viruses in the patients was then determined by genetic analysis. A significant focus was placed on making the investigation replicable in low-income locations, such as the aforementioned Sub-Saharan Africa.

**80. Name:** Trey Farmer **Institution:** University of Nebraska Medical Center **Email:** trey.farmer@unmc.edu **Research area:** Neuroscience**Title:** Characterization of Pink1/Parkin double knockout rats: A novel animal model for Parkinson’s disease

**Authors:** Trey Farmer1, Mohannad A. Almikhlafi1,2,3, Benjamin G. Lamberty1, Steven Totusek1, Howard S. Fox1, Kelly L. Stauch1
1 University of Nebraska Medical Center, College of Medicine, Department of Neurological Sciences, Omaha, Nebraska, USA
2 University of Nebraska Medical Center, College of Medicine, Department of Pharmacology and Experimental Neuroscience, Omaha, Nebraska, USA
3 Taibah University, Collage of Pharmacy, Department of Pharmacology and Toxicology, Saudi Arabia

**Abstract:** Animal disease models are important for mechanistic studies in the neuroscience field in general and in Parkinson’s disease (PD) in particular, which is characterized by the loss of dopaminergic (DA) neurons in the substantia nigra pars compacta (SNpc) and the associated terminals in the striatum, leading to motor impairments. Here, we describe the generation and phenotypic characterization of a combined Pink1/Parkin (mitochondrial control proteins) double knockout (DKO) rat, which reproducibly exhibits PD-relevant pathology in males. Synaptosomes from 3-month-old Pink1/Parkin DKO rats demonstrate reduced mitochondrial maximal respiration and spare respiratory capacity. Pink1/Parkin DKO rats exhibit significant nigral degeneration at 6 months of age, followed by a loss of DA neurons in the ventral tegmental area at the 8 months. Motor dysfunction, specifically gait abnormalities and decreased rearing frequency, were uncovered in Pink1/Parkin DKO rats starting at 3 and 6 months respectively. Further, PINK1/Parkin DKO rats show elevated levels of alpha-synuclein protein levels starting as early as 1 month of age. Altogether, the Pink1/Parkin DKO rats exhibit phenotypes like what is seen with patients that have PD, thus highlighting the suitability of this model for studies on PD pathogenesis and treatment.