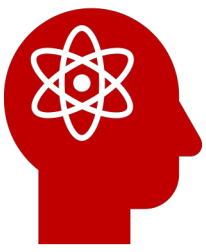
RUTGERS

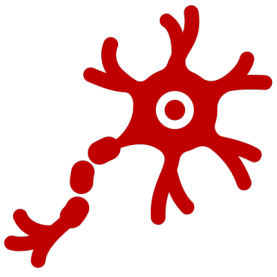
THE STATE UNIVERSITY OF NEW JERSEY

Summer Undergraduate Research Fellowship (SURF)

Final Presentations

July 24, 2025





Week	SURF Weekly Activities
1	Orientation (Lab Notebook keeping, Reading Manuscripts, & Safety Training)
	Advice from SURF Alumni
	Responsible Conduct of Research
2	Chemicals in our Environment with Sean Stratton
3	Hot Topic: Plastics in our Lives: From Nano to Macro
4	Getting Noticed and Building Your Brand on LinkedIn
5	Careers, Networking, and Painting
	What is She Talking About? Communicating Science Effectively
6	Careers in Pharma with Dr. Gary Grover
	What's in My Personal Care Products? Are They Safe?
7	The Art of Compelling Abstracts
8	Bristol Myers Squibb Field Trip
	Research Blitz with Pharmacy Research Students
9	Chemicals in Our Environment: Drinking Water Results
10	Final Symposium

Session I Presentations (11:00 a.m. – 12:00 p.m.)	
Presenter	**Mentor**
Christina Kolman	Brian Buckley
Eric Luo	Mathew McBride
Monica Ragheb	Wei-Wing Zong
Harjeet Sandhu	Andrew Gow
Yuchi Zhang	Lei Yu
Collin Drazek	Luigi Brunetti
Daniel Kim	Luigi Brunetti
Lily Tews	Mary Bridgeman
Julia Yang	Lauren Aleksunes

Session II Presentations (12:15 p.m. – 1:15 p.m.)	
Presenter	**Mentor**
Kaizen Lee	Debra Laskin
Jaden He	Rama Malaviya/ Debra Laskin
Ashley Zheng	Laurie Joseph/ Sara Campbell
Sean Chen	Steven Zheng
Fan Li	Eileen White
Brock Shahinian	Troy Roepke
Fathima Syed	Hilary Groso Jasutkar
Kelly Huang	Gary Aston-Jones
Lindsey Buchanan	Manny DiCicco-Bloom

Session III Presentations (1:30 p.m. – 2:15 p.m.)	
Presenter	**Mentor**
Daniel Heltberg	Emily Barrett
Madisyn Moore	Shuo Xiao
Taylor Troncoso	Grace Guo
Felise Coulon	Kyle Murphy
Sara Hoffman	Phoebe Stapleton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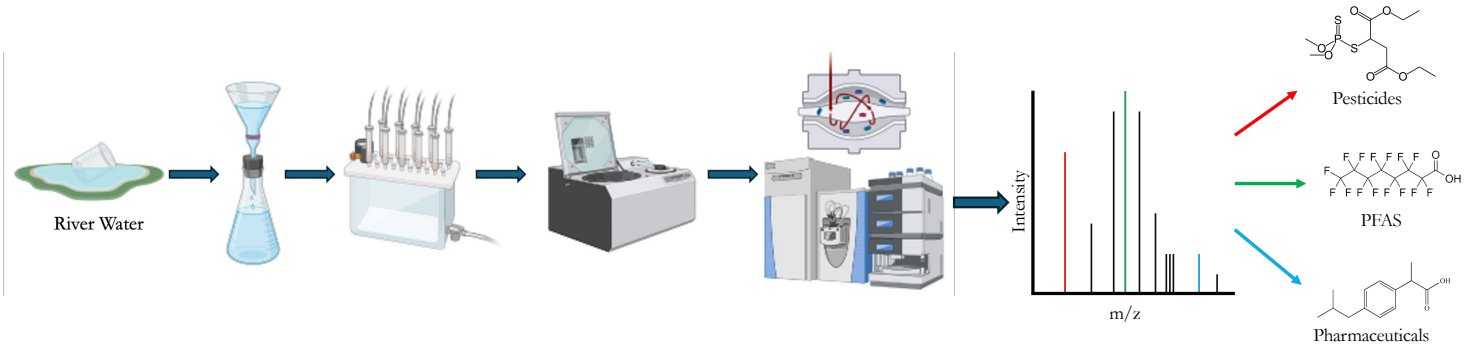
Small Molecule Extraction Optimization and Analysis from River Water Using Liquid Chromatography Coupled to Mass Spectrometry

Christina Kolman, Rachel Buckley, Ill Yang, Brian Buckley
Rutgers University, Environmental and Occupational Health Sciences Institute – Piscataway, NJ

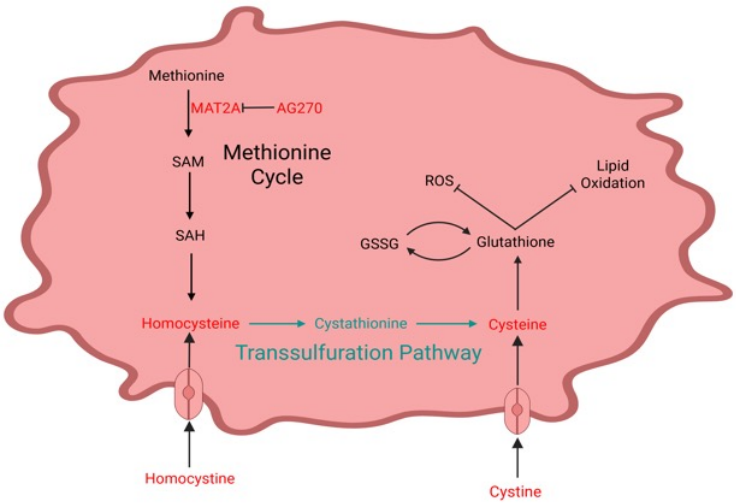
The purpose of this study was to improve protocols for small molecule isolation and concentration from environmental water samples to maximize the identification of unknown compounds. The primary objectives were to optimize evaporation of organic solvents and the subsequent evaporation of solubilized analytes in aqueous solution. The EPA Method 537.1, which utilizes solid-phase extraction (SPE), was the foundation of our protocol. A Speedvac was implemented to replace a slower nitrogen blowdown system for organic solvent evaporation. Samples containing organic solvents were evaporated at room temperature under varying pressures, and recovery ratios were calculated. To replicate SPE elution solvents, water was added to samples prior to evaporation. A segmented evaporation approach was developed to first remove organic solvents, followed by aqueous content. Surface water samples collected from the Rutgers University golf course were analyzed using the modified Method 537.1 for an untargeted assay. Liquid chromatography-mass spectrometry, combined with untargeted data analysis using Mzmine and Compound Discoverer were used. Recovery of standard spikes in organic solvents decreased at lower pressures, likely due to rapid evaporation leading to analyte loss. The optimized single-step method of organic solvents, 25℃ at 30 torr for 30 minutes, yielded 63-73% recovery of internal standards. The segmented evaporation method in which organic solvents were first evaporated at 30 torr for 30 minutes followed by aqueous solutions at 5.1 torr for 2 hours, improved recovery ratios to 63-84%. Preliminary field data analysis revealed several compounds, including zeranols, tramadol, and PFBS. Future work will expand this method to profile small molecules across multiple New Jersey surface waters. Supported by NIH R25ES020721

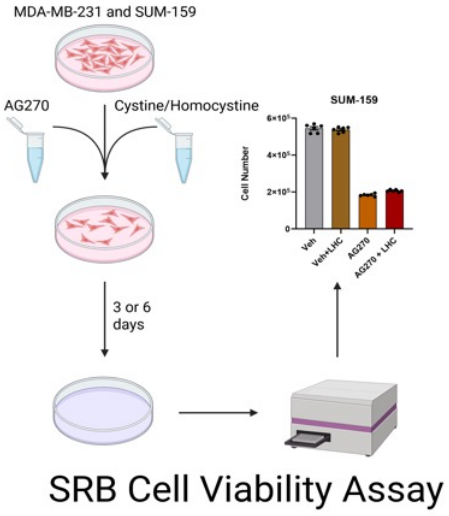


Depletion of S-adenosylmethionine Synthesis Reduces Triple Negative Breast Cancer Cell Proliferation Independent of Oxidative Stress

Eric Luo, Md. Salman Shakil, Matthew J McBride
Rutgers, The State University of New Jersey

Triple-negative breast cancer (TNBC) is a type of aggressive breast cancer with a poor prognosis. TNBC is characterized by the lack of estrogen, progesterone, and human epidermal growth factor 2 (HER2) receptors, making hormonal or HER2-targeted therapies ineffective. Currently, methionine adenosyltransferase 2A (MAT2A) inhibitors are under clinical investigation for their efficacy as a potential therapeutic target in many cancer types, including TNBC. MAT2A is responsible for S-adenosylmethionine (SAM) production, which is the substrate for methylation reactions and is a precursor to the transsulfuration pathway. The transsulfuration pathway produces cysteine, which is the precursor to the major antioxidant glutathione (GSH). Data from the McBride Lab shows that treating TNBC cells with the MAT2A inhibitor AG270 causes a potent decrease in cell proliferation and decreased levels of SAM, transsulfuration pathway metabolites, and GSH, which indicates elevated oxidative stress. Thus, we aimed to investigate whether the cell death was caused by this oxidative stress induced by MAT2A inhibition. We performed add-back experiments in AG270-treated TNBC cells, supplementing cell culture media with different metabolites in the transsulfuration pathway, and reducing lipid oxidation with a ferroptosis inhibitor, and then measured cell proliferation with Sulforhodamine B assays. Restoring transsulfuration pathway metabolite levels and reducing lipid radical levels failed to rescue the anti-growth effects of AG270. We conclude that the anti-proliferative effect of MAT2A inhibition in TNBC cells is independent of disrupting the transsulfuration pathway to induce oxidative stress, and we look to confirm that it is due to SAM-mediated methylation in the future. Supported by NIH R25ES020721, NIH 1R35GM154956, and the New Jersey Health Foundation.

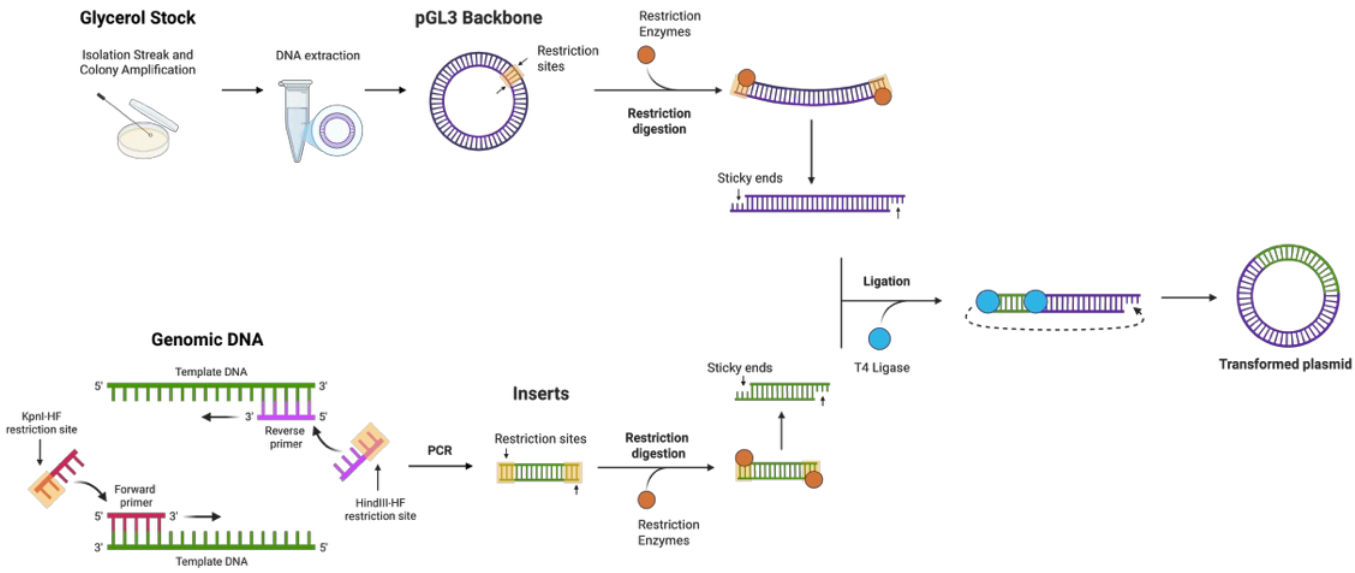




Construction of a Luciferase Reporter Vector for Characterizing the Expression of Plcd4 driven By Zbtb24

Monica Ragheb, Rongrong Li, Wei-Xing Zong
Rutgers, The State University of New Jersey

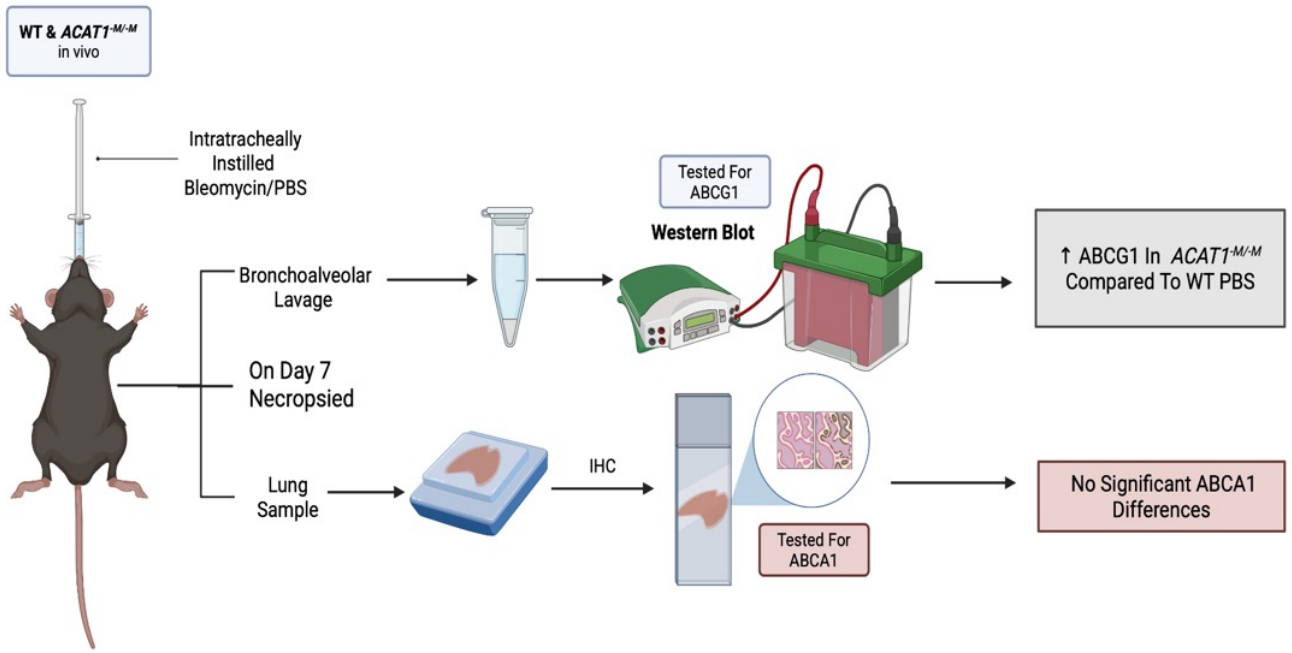
B-cell lymphoma constitutes 90% of non-Hodgkin's lymphoma, the seventh most common type of cancer in North America. Our lab previously identified Zbtb24, a zinc finger transcription factor, as a potential tumor suppressor in B-cell lymphoma via whole-genome CRISPR/Cas9 screening. Previous searches for Zbtb24's tumor suppression mechanisms via chromatin immunoprecipitation sequencing (ChIP-seq) and RNA-sequencing (RNA-seq) identified Plcd4, a phospholipase C enzyme, as a potential transcription target of Zbtb24. We hypothesize that Plcd4 is a direct transcription target of Zbtb24. To test this hypothesis, Zbtb24 binding motifs were mapped in the Plcd4 promoter region, and subsequent cloning of this region into a luciferase reporter vector was conducted using restriction enzyme cloning. Cloning of the Cdca7 promoter region, a known transcription target of Zbtb24, was also conducted as a positive control for Zbtb24-driven gene expression in a future luciferase assay. The pGL3 basic luciferase reporter vector was used as the cloning backbone and dual restriction enzymes within the multicloning site were chosen. Restriction recognition sites were designed in primers to amplify mouse Plcd4 and Cdca7 genes using polymerase chain reaction (PCR). Restriction-digested amplicons were ligated into the backbone and transformed into competent cells via bacterial transformation. Colonies were then screened to confirm correct constructs. At this time, screening for the constructs is in progress and is anticipated to yield the correct constructs. Once obtained, these constructs will be used to perform a dual luciferase assay, which along with other results would validate if Plcd4 is a direct transcription target of Zbtb24. Supported by NIH R25ES020721.



Macrophage Lipid Metabolism in the Absence Of Cholesterol Esterification

Harjeet S. Sandhu, Tony Hu, Elena Abramova, Andrew Gow
Rutgers, The State University of New Jersey

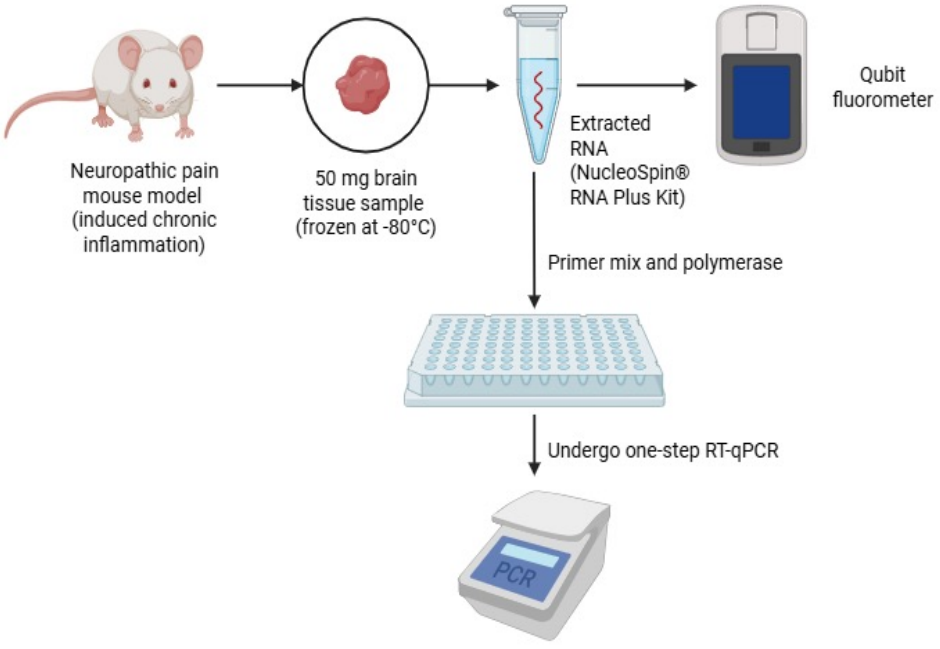
Acute Lung Injury (ALI) is characterized by lung inflammation. Acyl-CoA:Cholesterol acyltransferase (ACAT1) is an enzyme that esterifies free cholesterol into cholesterol esters and is critical in lipid handling. ACAT1 inhibitors, like K-604, reduce lung injury. To study their role in macrophages a myeloid specific ACAT1 knock out mouse (Acat1-M/-M) has been generated. We hypothesize that loss of ACAT1 in lung macrophages reduces intracellular cholesterol ester accumulation, leading to upregulation of cholesterol efflux transporters such as ABCA1 and ABCG1, thereby promoting lipid efflux and lowering inflammation. To test this WT and Acat1-M/-M mice were intratracheally instilled bleomycin to induce lung injury or PBS as control. On day 7, at the peak of inflammation, mice were necropsied and bronchoalveolar lavage (BAL) cells and lung tissue collected. Western blot of BAL cells was used to determine ABCG1 protein expression and immunohistochemistry (IHC) to visualize ABCA1 expression. Western blot analysis showed a baseline increased ABCG1 in BAL macrophages from Acat1-M/-M mice compared to the WT, but WT expression increased to match Acat1-M/-M after bleomycin treatment. ABCA1 showed no difference between treatments through IHC, indicating possible less reliance on ABCA1 for cholesterol efflux in Acat1-M/-M. Future work will examine cholesterol uptake mechanisms, like CD36, and cholesterol signaling pathways, such as LXR, to fully understand macrophage cholesterol handling. Supported by NIH R25ES020721, CEED ES005022, and the American Society for Pharmacology and Experimental Therapeutics.



Chronic Inflammation in Painful Diabetic Neuropathy: CCR2 and other Chronic Pain Candidate Genes

Yuchi Zhang, Anveshi Prakash, Ivana Albert, Leah Chang, Lei Yu, Robert McLaughlin
Rutgers, The State University of New Jersey and Kean University

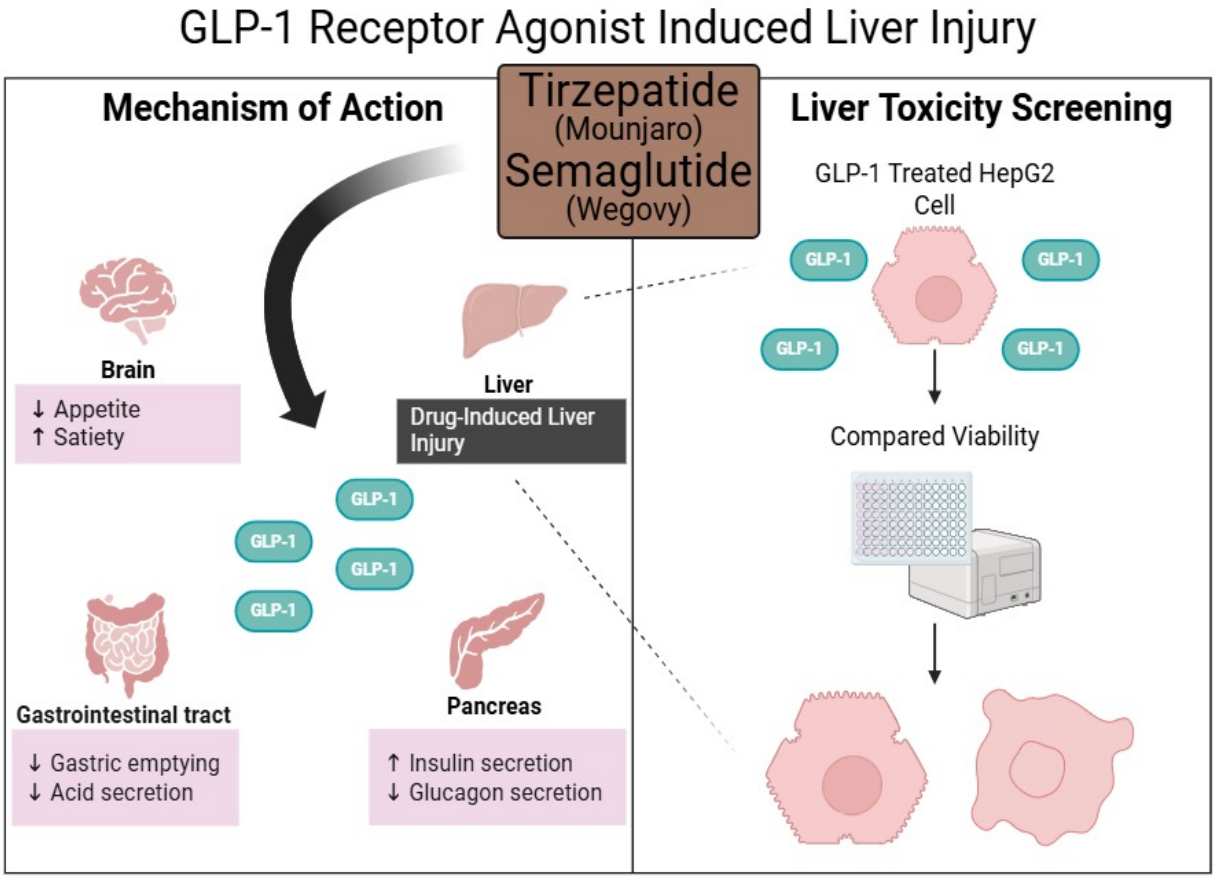
Painful diabetic neuropathy (PDN) is a diabetes complication involving pain in extremities from peripheral nerve damage. A major CCR2 chemokine receptor isoform, CCR2A or CCR2B, may be an underlying contributor to PDN. Previous experiments with normal human blood samples suggested a consistently higher CCR2B level, indicating potential functional consequences. The purpose of this study was to assess CCR2 expression among mice with neuropathic pain, with the future goal of assessing specific CCR2 isoform expression. Quantitative reverse-transcriptase PCR (RT-qPCR) was used, alongside primers designed for multiple mouse genes involved in neurological disease: CCHCR1, SNAP29, GOLGA2, APP, as well as CCR2. Mouse brain and spinal cord tissue samples were collected from neuropathic pain mouse models. A protocol was developed for extracting RNA from frozen mouse brain tissues; isolated RNA was quantified and tested for purity using fluorometric assays before undergoing TaqMan-based fluorogenic RT-qPCR with designed primers and a GAPDH internal control. Current testing has been done only on control mouse samples to streamline the RNA extraction and one-step RT-qPCR protocol for higher efficiency and to resolve inconsistencies in qPCR results. It was found that running qPCR at an annealing temperature of 58°C has produced consistently higher amplification from RNA extracted from brain tissue samples approximately 50 mg in size. In the immediate future, an optimized protocol for RNA extraction and RT-qPCR will allow for reliable results from experiments conducted with tissue from PDN mice, enabling direct assessment and comparison of expression levels of CCR2 and other neuropathic pain-related genes. Supported by NJ ACTS NIH R25TR004777 CREST Program, NIH R43NS120617, and New Jersey Commission on Science, Innovation and Technology.



Hepatocyte Viability after Treatment of Weight Loss Drugs

Collin Drazek, Katherine Otersen, Luigi Brunetti
Rutgers, The State University of New Jersey

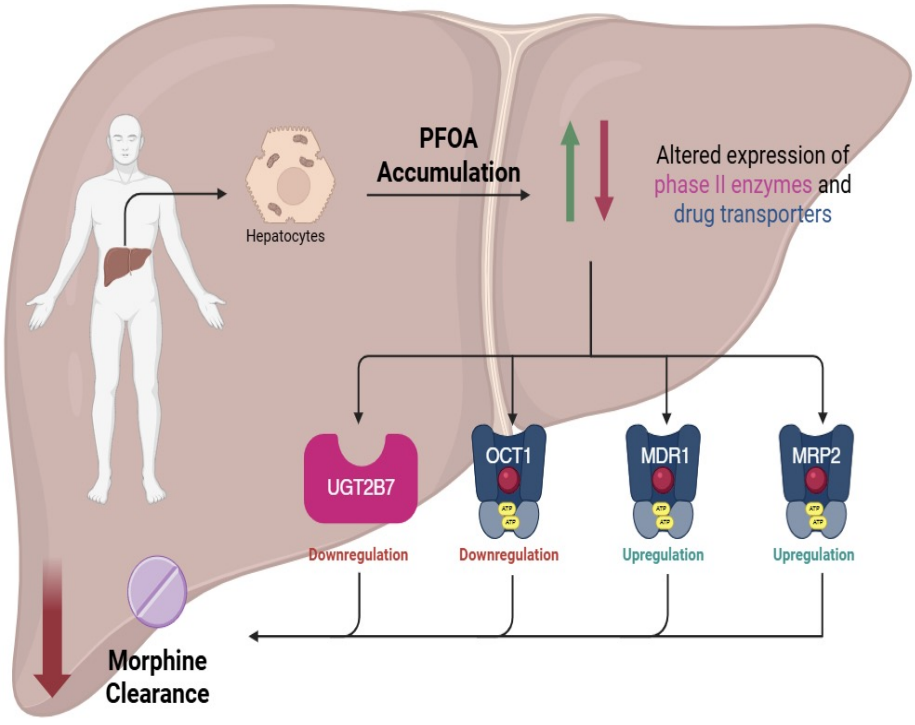
Glucagon-like peptide-1 (GLP-1) receptor agonists such as Tirzepatide and Semaglutide are commonly prescribed for treating type 2 diabetes mellitus and obesity. These agonists mimic the effects of endogenous GLP-1, an incretin hormone that enhances glucose-dependent insulin secretion, inhibits glucagon release, delays gastric emptying, and promotes satiety. While GLP-1 receptor agonists have demonstrated hepatoprotective effects, there are around 140 cases of drug-induced liver injury among patients taking these medications. This study aims to evaluate the cytotoxic effects of Tirzepatide and Semaglutide in a dose-dependent manner using HepG2 cells, a well-differentiated hepatocellular carcinoma, and an established in vitro model for assessing hepatotoxicity. HepG2 cells were treated with clinically relevant increasing concentrations of Tirzepatide and Semaglutide for 24, 48, 72, and 96 hours. Cell viability was assessed using Cell Counting Kit-8 (CCK-8) assays. Sorafenib, a known hepatotoxic agent, was used as a positive control, while HepG2 media was the negative control. We report no impairment in HepG2 cell viability with concentrations of the Tirzepatide and Semaglutide treatment groups up to 25 uM and 2.5 uM, respectively. In future studies, we aim to evaluate the effects of Tirzepatide and Semaglutide on a cholangiocyte cell line, given that cholangiocytes express GLP-1 receptors and GLP-1 receptor agonists have been implicated in the development of cholestasis. Supported by NJ ACTS NIH R25TR004777 CREST Program.



Evaluating the Influence of Environmental Chemicals on the Regulation of Genes Governing the Pharmacokinetics of Morphine in the Human Liver

Dohyun Kim, Katherine Otersen, Moriah Anthony, Tingying Xie, Luigi Brunetti
Rutgers, The State University of New Jersey

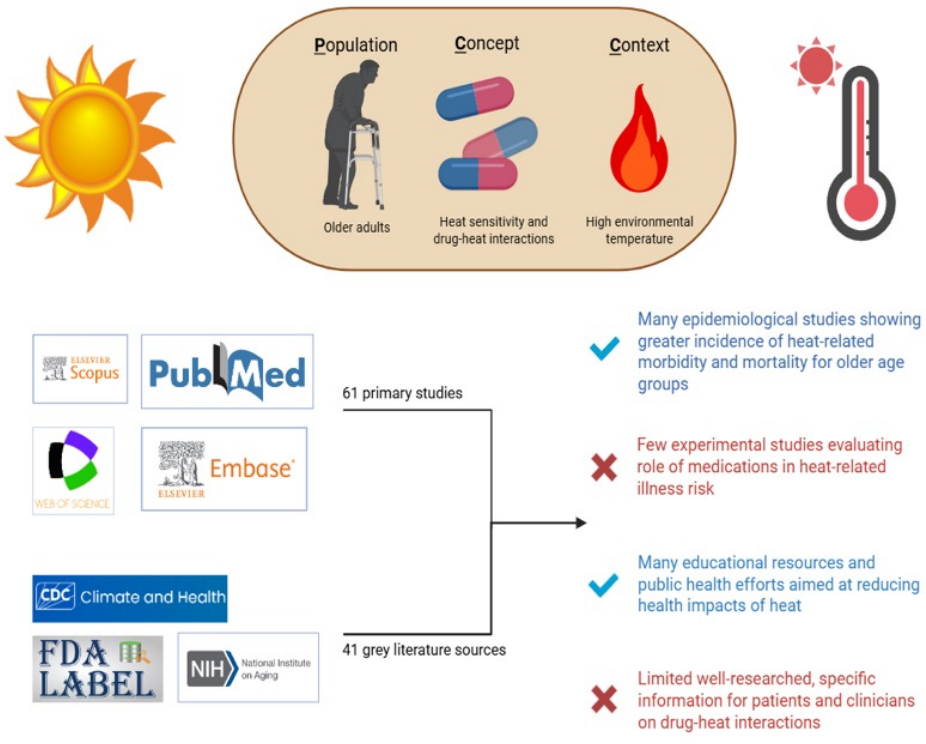
Over 70% of morphine is metabolized in the liver by the UDP-glucuronosyltransferase 2B7 (UGT2B7) to form glucuronide conjugates, which are excreted into bile via efflux transporters, Multidrug Resistance Protein 1 (MDR1) and Multidrug Resistance-associated Protein 2 (MRP2). The uptake transporter Organic Cation Transporter 1 (OCT1) facilitates morphine entry into the liver. Perfluorooctanoic acid (PFOA), a widespread environmental contaminant found in human serum at concentrations up to 12 µM in the U.S., inhibits HNF4α and activates NRF2 signaling, leading to downregulation of UGT2B7 and OCT1, and upregulation of MDR1 and MRP2. This study aimed to quantify changes in expression of UGT enzymes and drug transporters in HUH7 human hepatoma cells after exposure to PFOA. Cells were exposed to 12 concentrations of PFOA (0.1–100 µM) for 24, 48, and 72 hours to identify the impact of dose and duration of exposure on cell viability using CCK8 assay. These data were then used to identify the optimal dose and exposure for quantitative PCR studies focused on mRNA expression of UGT2B7, OCT1, MDR1, and MRP2. At both acute and chronic exposure to the selected PFOA doses consistent with reported human serum concentrations, no significant reduction in cell viability was observed. We expect a time-dependent downregulation of UGT2B7 and OCT1, and an upregulation of MDR1 and MRP2 at physiologically relevant PFOA levels. These findings will improve our understanding of how PFAS chemicals interfere with hepatic clearance of morphine and may support the use of PFOA exposure levels as a potential biomarker for personalized drug dosing. Supported by the Rutgers School of Graduate Studies and Ernest Mario School of Pharmacy..



Recognizing and Mitigating the Impact of Medications on Heat-Related Illness in Older Adults: A Scoping Review

Lily M. Tews, Mary Barna Bridgeman, Daniel T. Abazia, Hayley Blackburn, Kiri Carmody
Rutgers, the State University of New Jersey

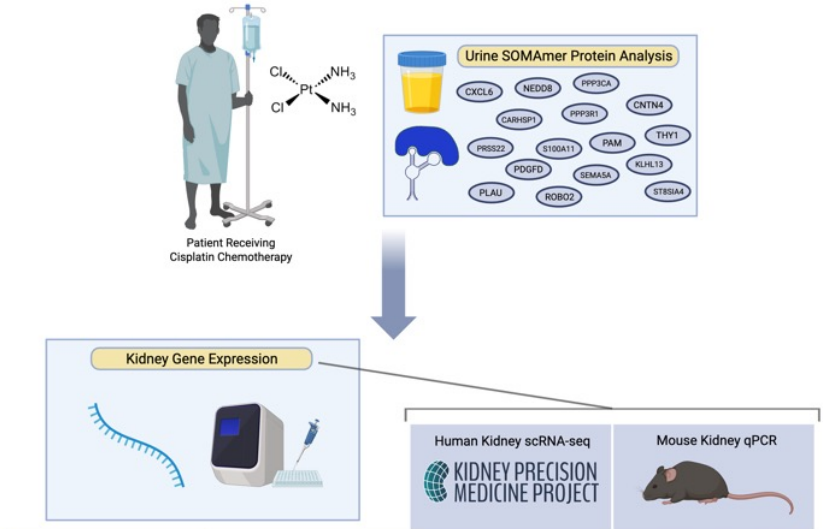
Older adults are uniquely susceptible to heat-related illness, including hyperthermia due to thermoregulatory impairment, dehydration, and electrolyte abnormalities. It is generally recognized among clinicians that medication use plays a role in heat susceptibility; however, both accelerating climate change and increasing rates of medication use accentuate the need for additional research. The objective of this scoping review was to investigate current literature regarding the heightened risk of medications and heat-related illness in older adults and to reveal areas of future research need. Investigators queried the databases PubMed, Embase, Web of Science, and Scopus; English-language primary studies and case reports published between January 2000 and June 2025 were considered for inclusion based on a predefined Population, Concept, Context (PCC) pertaining to the research questions. Additionally, a grey literature search was conducted to map existing mitigation strategies in the United States. Two reviewers independently screened studies for eligibility using Covidence and one reviewer extracted data. A total of 61 primary studies and 41 grey literature sources were identified. An abundance of epidemiological studies demonstrate greater incidence of heat-related morbidity and mortality for older age groups, but few experimental studies evaluating the role of medications exist. There are many educational resources and public health efforts aimed at reducing health impacts of heat, yet limited well-researched, specific information is available for patients and clinicians on managing drug-heat interaction. This scoping review highlights a need for more studies investigating the confluence of age, multimorbidity, medication use, and heat-related illness in order to inform future mitigation efforts. Supported by NIH R25ES020721.



Discovering and Validating New Biomarkers for Drug-Induced Kidney Toxicity in Cancer Patients

Julia Yang[1], Xia Wen[1], Christine Kim[1], Melanie Joy[2], Lauren Aleksunes[1]
[1]Rutgers, the State University of New Jersey and [2]University of Colorado

Cisplatin is a chemotherapeutic drug used in the treatment of many solid tumors, but its clinical utility is limited by nephrotoxicity. Current methods of detecting cisplatin-induced acute kidney injury (AKI) are only effective when a significant amount of kidney damage has already occurred. To identify more sensitive novel biomarkers for cisplatin-induced AKI, an untargeted, SOMAmer-based proteomic analysis was conducted on urine samples from 20 patients before and 48 hours after cisplatin treatment. The purpose of this study was to prioritize 53 potential biomarkers for validation using: 1) the human AKI dataset in the Kidney Tissue Atlas and 2) kidneys of mice treated with cisplatin. Total RNA was extracted from frozen kidneys of saline-treated control mice (n=4) and cisplatin (20 mg/kg, ip)-treated mice (n=8) at 72 hrs. cDNA was generated and qPCR was performed for 16 genes. Cisplatin treatment produced kidney mRNA expression changes in 7/16 genes, with 5/16 going in the same direction as the Kidney Tissue Atlas data. One of these 5 genes, Cxcl5, the mouse ortholog of human CXCL6, exhibited an 80-fold increase. This data can be utilized in further validating these identified potential biomarkers of interest in larger sample sizes of patient urine using additional protein assay techniques. Supported by NIH R25ES020721 and the American Society for Pharmacology and Experimental Therapeutics.

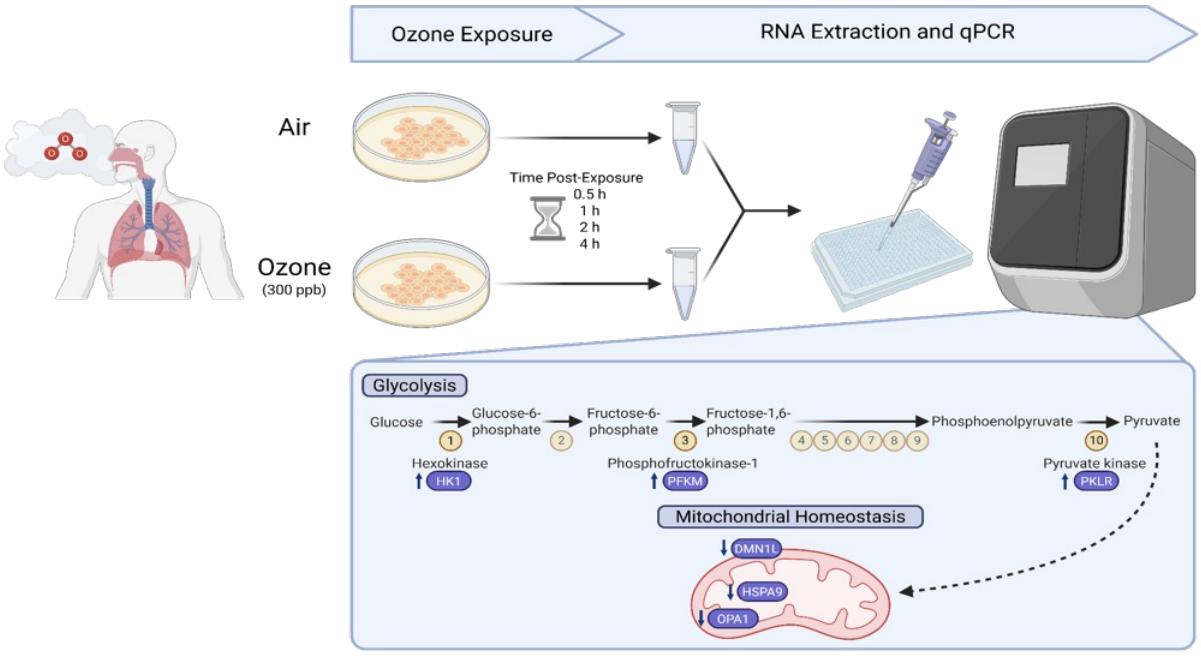


Gene Name	Function	Expression Change	Expression Change
Cxcl5	Immunity/chemokine	↑	↑
Carhsp1	RNA-binding	↑	↑
S100a11	Growth/differentiation	↑	↑
Prss22	Serine protease	↑	↑
Klhl13	Protein breakdown	↑	↓
St8sia4	Cell-Cell interaction	↑	↓
Thy1	Cell adhesion	↓	↓

Effects of Ozone Exposure on Macrophage Glycolysis and Mitochondrial Integrity and Homeostasis in RAW 264.7 Macrophages

Kaizen Lee, Jessica R. Rodriguez, Debra L. Laskin
Rutgers, the State University of New Jersey

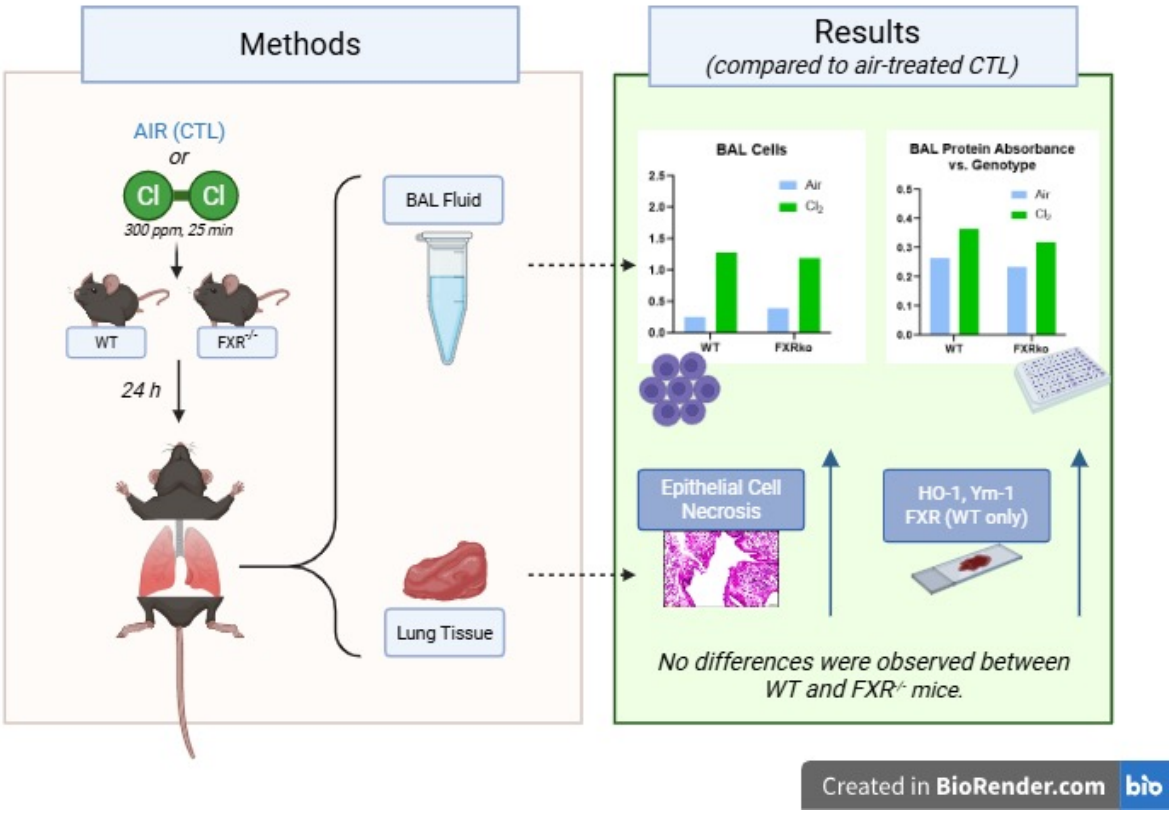
Ozone is a cytotoxic oxidative air pollutant known to induce lung epithelial injury, leading to the recruitment of macrophages to the lungs. Evidence suggests that ozone negatively affects mitochondrial function in macrophages, leading to decreased ATP production through oxidative phosphorylation. We hypothesized that ozone exposure upregulates glycolysis in macrophages as a compensatory mechanism in response to ozone-induced mitochondrial dysfunction. RAW macrophages were exposed to ozone (300 ppb) or air for 30 min; RNA was extracted 0.5 h, 1 h, 2 h, or 4 h post-exposure. Gene expression of rate-limiting glycolytic enzymes (Hk1, Pfkm, Pklr) and mitochondrial homeostasis, fusion, and fission proteins (Hspa9, Opa1, Dmn1l) were assessed by qPCR. Hspa9, Opa1, and Dmn1l expression was reduced 1 h following ozone exposure compared to air controls and returned to baseline after 2 h. In contrast, the expression of glycolytic genes Hk1 and Pfkm was upregulated 1 h post-exposure, followed by a decrease to control levels at 4 h. Unexpectedly, Pklr expression increased 0.5 h post-exposure, but returned to baseline at 1 h. These findings suggest that glycolysis increases in response to mitochondrial dysregulation caused by ozone exposure. Given its role in modulating metabolic proteins and driving cells towards recovery or apoptosis after oxidative stress, the integrated stress response (ISR) may contribute to this effect. Future studies will use pathway inhibitors to examine the role of the ISR in regulating mitochondrial bioenergetics and morphology. Supported by NIH R25ES020721, ES004738, ES005022, and the American Society for Pharmacology and Experimental Therapeutics.



Role of Farnesoid X Receptors in Chlorine-Induced Pulmonary Injury

Jaden He, Khushi Desai, Elena V. Abramova, Kinal Vayas,
Rama Malaviya, Jeffrey D. Laskin, Debra L. Laskin
Rutgers, the State University of New Jersey

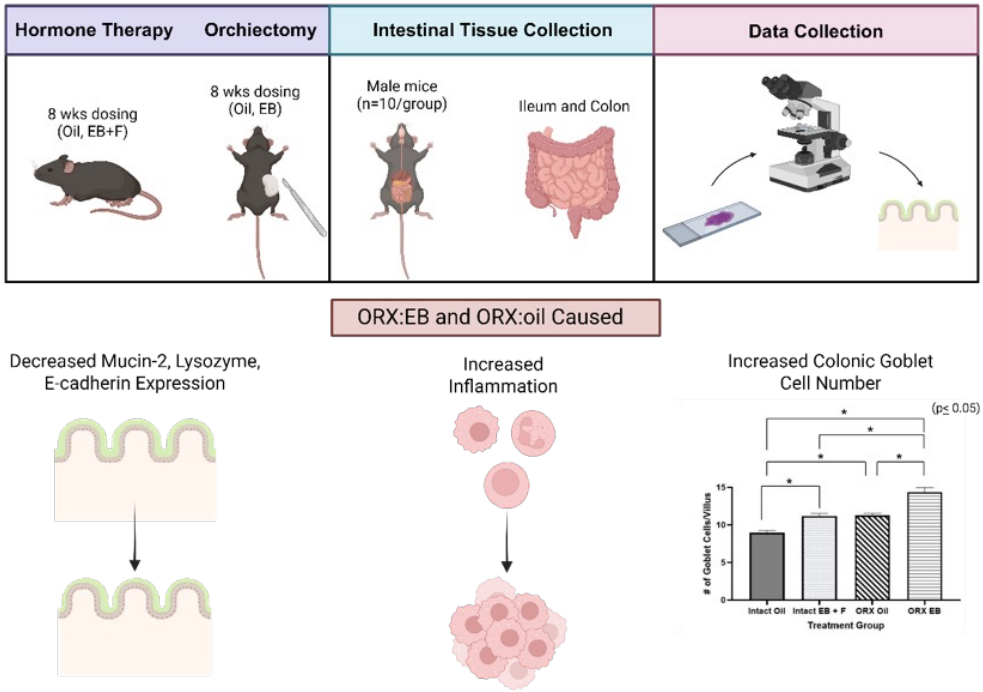
Chlorine (Cl2) gas is a highly toxic irritant that causes acute injury to the respiratory tract. Farnesoid X Receptor (FXR) is a nuclear receptor involved in lipid metabolism; it exerts anti-inflammatory activity. In these studies, the role of FXR in Cl2-induced injury and inflammation was assessed. Male WT and FXR-/- mice were exposed to air or Cl2 (300 ppm, 25 min) in a whole-body exposure chamber. Bronchoalveolar lavage (BAL) and lung tissue were collected 24 h later and analyzed for markers of injury and oxidative stress. Cl2 exposure caused necrosis of proximal bronchiolar epithelial cells and an accumulation of epithelial cell debris in in the lungs of both WT and FXR-/- mice; proximal peribronchial edema and mononuclear inflammatory cells were also observed. These structural changes were associated with increases in total BAL protein and cell content, demonstrating alveolar-epithelial barrier dysfunction. Immunohistochemistry revealed that Cl2 upregulated FXR expression in alveolar macrophages in lungs of WT mice. Oxidative stress, assessed by expression of heme oxygenase (HO)-1 and Ym-1 were also increased in WT as well as FXR-/- mice. However, no differences were noted in the response of FXR-/- and WT mice to Cl2. These findings suggest that FXR does not play a role in acute lung injury or oxidative stress induced by inhaled Cl2. Supported by NIH Grants U54AR055073, P30ES005022, R25ES020721, and the American Society for Pharmacology and Experimental Therapeutics.



Orchiectomized Male Mice Supplemented with Estrogen Display Increased Perturbations in Gut Mucosa Compared to E-GAHT

Ashley Zheng, Ali Yasrebi, Kaitlyn M. Synder, Daniel D. DeSio, Isabel George, Prabhjit Sandhu, Kyeongseo Kim, Troy A. Roepke, Sara C. Campbell, Laurie B. Joseph
Rutgers, The State University of New Jersey, Piscataway, NJ

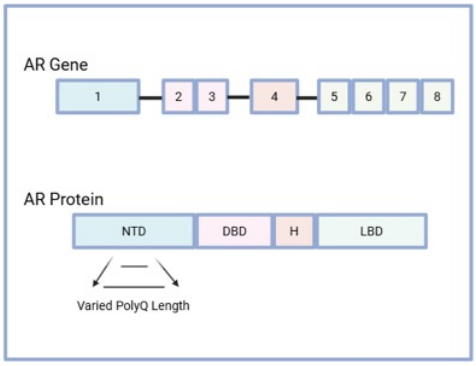
The effects of estrogen gender affirming hormone therapy (E-GAHT) on gut homeostasis is unknown. We determined whether E-GAHT or orchiectomy (ORX) induced changes in the gut of 8-week-old mice. Forty C57BL6 male mice were grouped (n=10/group) as follows: 1) intact with oil (CTL), 2) intact with estradiol benzoate (EB, 150 µg/kg) and finasteride (F, 0.25 mg/kg), 3) orchiectomized with oil; and 4) ORX with EB (150 µg/kg), and orally dosed daily for 8 weeks. Ileum and colon were collected and sectioned for immunohistochemistry to visualize gut proteins. F4/80, lysozyme, and E-cadherin (E-cad) were measured in the ileum. Colonic goblet cell numbers were quantified using Alcian Blue Periodic Acid-Schiff and mucin-2 (muc-2) was measured in the colon. F4/80, an inflammatory marker for macrophages, was higher in all ORX animals. E-cad, essential for cellular adhesion, and lysozyme, an antimicrobial protein, were downregulated in all ORX groups. ORX:EB animals had significantly increased number of goblet cells compared to all other groups ($p \leq 0.05$). Muc-2, a glycoprotein providing a protective barrier between the gut and pathogens, was less evenly distributed in colon tissue in all ORX animals compared to CTL and Intact:EB+F mice. These data suggest that ORX with or without EB appears to induce morphological changes in the gut as follows: ORX:EB > ORX:oil > Intact:EB+F > Intact:oil. Future studies will include western blot analysis of the colon to determine the density of estrogen alpha and beta receptors following E-GAHT. Supported in part by Rutgers University Faculty Funds and NIH R25ES020721.

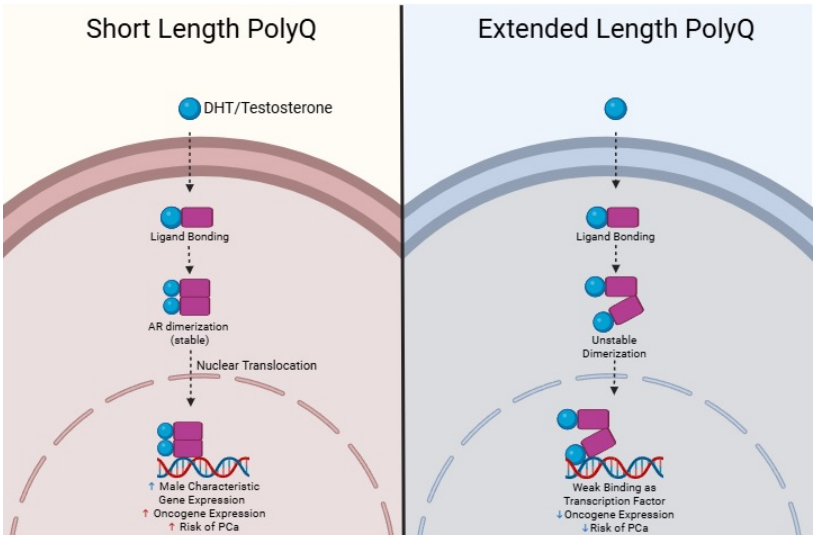


Role of Poly-Glutamine Repeats on Androgen Receptor Signaling in Prostate Cancer

Sean Chen, Steven Zheng, Jialin Fan, Amer Alasadi

Androgen Receptor (AR) is a transcription factor and primary oncogenic driver in prostate cancer. Poly-glutamine (Poly-Q) repeats in AR are highly variable in different populations. Poly-Q length has been associated with the aggressiveness of prostate cancer. This study aims to determine how Poly-Q length influences AR signaling in prostate cancer cells. We have constructed plasmids carrying AR with different Poly-Q lengths: 12Q, 24Q (Wild-Type), and 48Q. The initial goal is to assess their expression in prostate cancer cell lines. 0.25ug of AR plasmids with different Poly-Q variants, and a vector control, were each transfected into the prostate cancer cell line PC3. Cells were allowed to proliferate for 2 days before treatment with 5nM DHT, the active form of testosterone, or a mock control for 2 hours. AR Expression was analyzed by Western blot, and its activity was quantified through dual-reporter luciferase assay driven by an AR promoter. It was found that between DHT and non-DHT treatment, Wild-Type AR showed a significant increase in expression of 10%. The 12Q and 48Q variants do not exhibit any significant difference; however, the 48Q variant is significantly lower in expression by 37% compared to the Wild-Type in the DHT treatment group. 12Q variants exhibit numerically higher expression in DHT than in non-DHT treatment groups, but this difference is insignificant. Because the Wild-Type AR polyQ length is similar to 12Q, this result is promising. Future optimization must be done to confirm this trend in PC3 and related cancer cell lines in vitro. Supported by NIH R25ES020721.

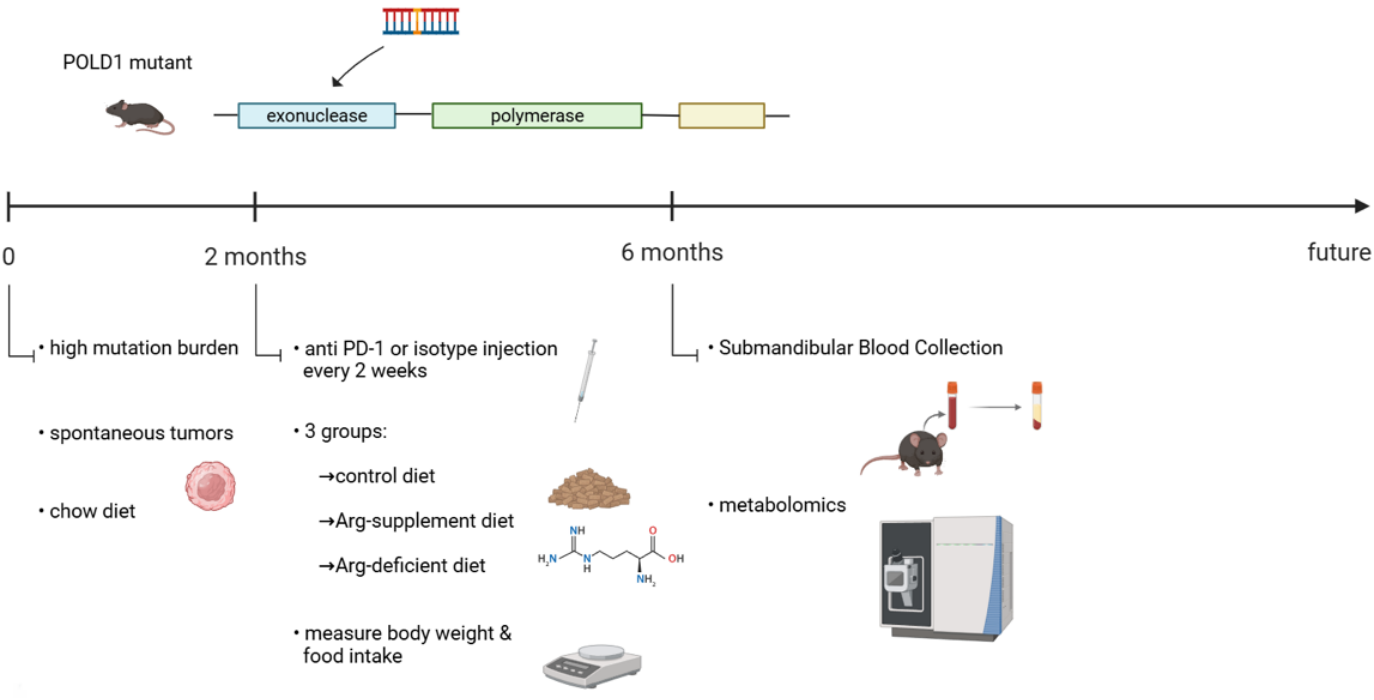




Dietary Arginine Impact on Cancer Progression and Immune Checkpoint Blockade in Mutator Cancer Models

Fan Li, Edisa Pirani, Eileen White
Rutgers, the State University of New Jersey

Alterations in amino acid metabolism significantly influence cancer development and therapeutic resistance by modulating tumor cell growth and immune responses within the tumor microenvironment (TME). Among these amino acids, arginine (Arg) has emerged as a key metabolic regulator, due to its dual role in supporting tumor growth and modulating antitumor immunity. Previous findings from our laboratory revealed that systemic arginine availability, regulated by hepatic arginase 1 (ARG1) in an autophagy-dependent manner via Atg7, directly impacts tumor growth, identifying arginine as a potential metabolic vulnerability in cancer. This study aims to investigate how manipulating dietary arginine availability affects tumor growth and the response to immune checkpoint blockade (ICB) therapy. To this end, we utilized a genetically engineered mouse model (GEMM) developed in our laboratory, bearing mutations in the Pold1 exonuclease domain (Pold1D400A/D400A) on a C57BL/6 background, which mimics the high tumor mutational burden (TMB) observed in hypermutated human cancers. Mice were randomized into three dietary groups: arginine-deficient, arginine-supplemented, and control diet. Each group received intraperitoneal injections of either anti-PD-1 antibody or isotype control every two weeks. Food intake, body weight, and targeted blood metabolomics were assessed to monitor systemic effects of dietary interventions. As expected, modulation of dietary arginine intake significantly altered circulating metabolites in the arginine metabolic pathway, confirming systemic perturbation of arginine metabolism. These included both increases and decreases in metabolites such as ornithine, citrulline, and creatine across dietary groups. Further studies are needed to clarify whether these metabolic alterations directly influence tumor growth or therapeutic outcomes.

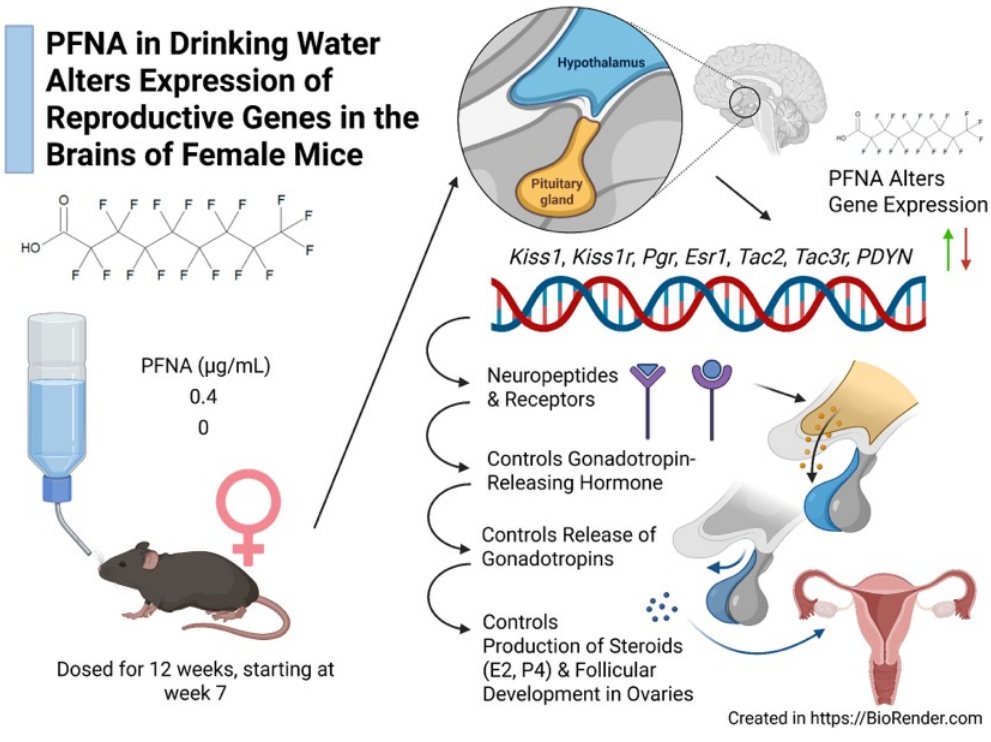


PFNA in Drinking Water Alters Expression of Reproductive Genes in the Brains of Female Mice

Brock Shahinian[2,3], Ali Yasrebi[1], Caylee Brown[2], Jiyang Zhang[2],
Shuo Xiao[2], Troy A. Roepke[1]

[1]Rutgers, Department of Animal Sciences; [2]Rutgers, Department of Pharmacology and Toxicology;
[3]New Jersey Institute of Technology, Department of Chemistry and Environmental Science

PFAS are a class of chemicals that are a common drinking water contaminant and endocrine disruptor, harming human reproductive health. While well-studied types of PFAS have been revealed to harm human health and have since been phased out of production, understudied PFAS compounds, like PFNA, continue to be found above harmful levels in drinking water, with little known impacts on human health. The genes *Kiss1*, *Kiss1r*, *Pgr*, *Esr1*/ERa, *Tac2/*NkB, *Tac3r,* and *PDYN* act from the arcuate nucleus of the hypothalamus, part of the HPG axis, controlling fundamental reproductive processes like the onset of puberty, the estrus cycle, and pregnancy. It is hypothesized that PFNA will disrupt signaling pathways in the brain, leading to differing levels of expression of these essential genes. This study elucidates the reproductive health impacts of PFNA exposure on women by using a model of female mice exposed to PFNA through drinking water and testing the expression of these reproductive genes in the mouse hypothalamus post exposure. Gene expression is measured through micro-dissecting the arcuate hypothalamus, extracting RNA, assessing RNA quality, and performing quantitative PCR on target genes. We expect the expression of these neuropeptide and receptor genes to differ between the control and exposure groups, allowing us to predict downstream effects of PFNA on reproductive health and through which mechanisms PFNA disrupts the HPG axis, further uncovering the impacts of this drinking water pollutant on women's reproductive health. Supported by NIH R25ES020721, NIEHS CEED P30ES005022, the RISE Program, the Ernest Mario School of Pharmacy, and the Society of Toxicology.

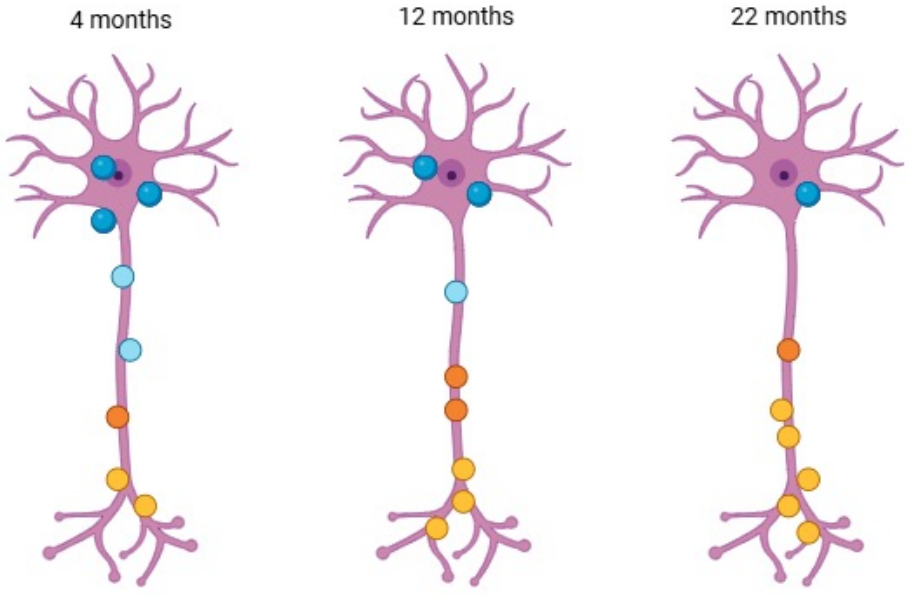


A Study of the Impact of Aging on Autophagic Vacuole Maturity in the Synapse

Fathima Syed, Hilary Grosso Jasutkar
Rutgers University, Institute for Neurological Therapeutics, Robert Wood Johnson Medical School

Macroautophagy, herein referred to as autophagy, is the process by which cells break down old or damaged cytosolic proteins and organelles and plays an important role in the homeostasis and normal function of the synapse. Autophagy in neurons begins with the formation of an immature phagophore in the synapse, which travels via retrograde transport to the soma, simultaneously progressing into a mature autophagic vacuole (AV). This process is implicated in having an important role in neuronal processes such as synaptic plasticity and neurotransmitter release. The importance of autophagy increases as a person ages, while disrupted autophagy has been associated with Alzheimer's disease. The purpose of this study is to examine how the retrograde transport of autophagic vacuoles changes with age. Immunofluorescent imaging was used to assess the density and maturity of AVs in the axons of mice at different ages. Brain sections will be labeled with different markers for the corresponding stages of AV maturity and a marker to visualize the axon. Brain sections from mice expressing GFP-tagged LC3, a protein found on all AVs, were labeled with an axonal marker and markers of AV maturity and then visualized using a Leica microscope. We hypothesize that there is decreased retrograde transport, and therefore maturation, of AVs as the mice age. We therefore expect that more immature AVs will accumulate at the distal axon and that there will be an overall lower number of AVs at the soma in older mice. Supported by NJ ACTS NIH R25TR004777 CREST Program.

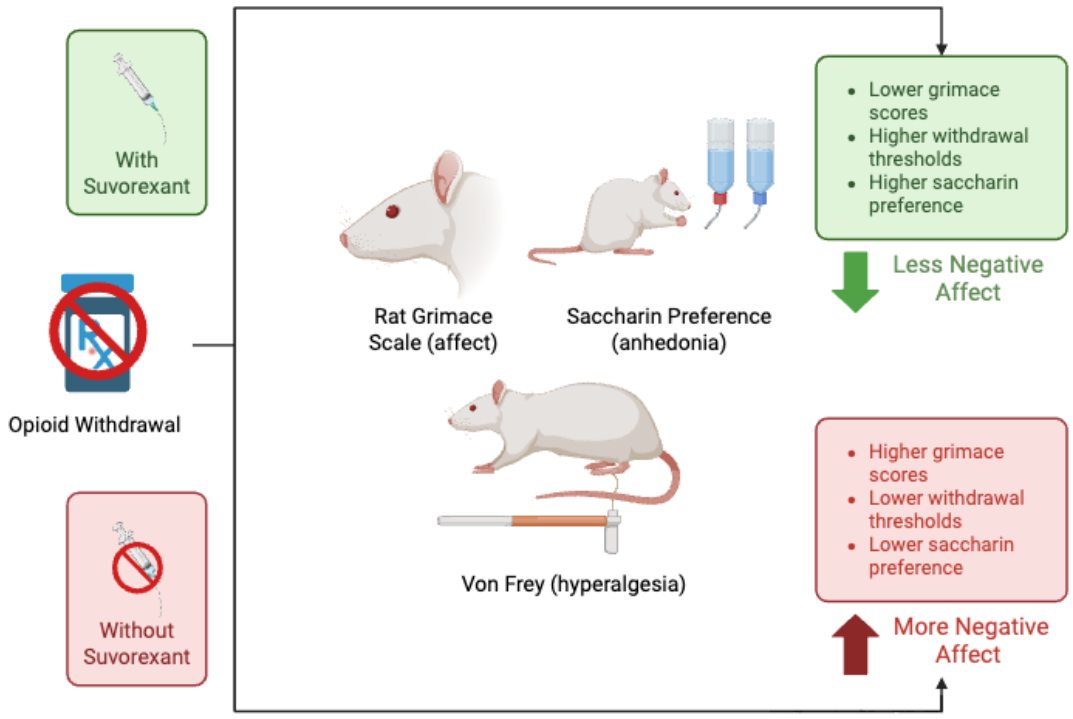
Antibody	AV Maturity	Symbol
Atg16L1	Phagophores	
Syntaxin 17	Autophagosomes fusing with endosomes	
Rab7	Amphisomes	
LAMP2	Autolysosomes	



Using Rat Grimace Scale to Evaluate Effect of Orexin on Opioid Withdrawal-Induced Negative Affect

Kelly Huang, Alicia Zumbusch, and Gary Aston-Jones
Rutgers, The State University of New Jersey, Piscataway, NJ

Suvorexant, an orexin antagonist, has shown potential in mitigating addictive behaviors. For example, suvorexant decreases general negative affect severity associated with opioid withdrawal while maintaining analgesia. The Rat Grimace Scale (RGS) is a well-validated technique for evaluating pain-specific affect by examining facial features. The purpose of this study was to replicate data showing that orexin antagonism decreases opioid-induced negative affect and to determine if withdrawal-related negative affect is captured by the RGS. To do so, 11 female rats were assigned to either a suvorexant (30 mg/kg) or control group and tested for mechanical allodynia and video recorded for pain-induced facial grimacing. We used the RGS to analyze facial grimacing and automated von Frey to evaluate paw withdrawal thresholds before pain induction and for 2 days after intraplantar injection of Complete Freund's Adjuvant into one of the hindpaws (i.e., main effect of pain). After the pre-pain and pain-only days, rats received daily injections (i.p.) of oxycodone (3 mg/kg) and either suvorexant or vehicle. On day 8 we performed the saccharin preference test (SPT) to assess anhedonia-like behavior. Rats in the suvorexant group had lower RGS scores compared to control rats on days 2 and 7, had higher saccharin preference and significantly higher withdrawal thresholds on the ipsilateral and contralateral paws for all days following drug administration. Because suvorexant resulted in decreased withdrawal-induced negative affect (SPT and RGS) and increased withdrawal thresholds on both the ipsi and contralateral paw, it may be that suvorexant is a useful complementary treatment for non-induced pain and related-affect such as that experienced during opioid withdrawal. Supported by NJ ACTS NIH R25TR004777 CREST Program.



The Autism- and Schizophrenia-Associated 3q29 CNV Deletion Elicits a Transient Increase in Proliferation in Embryonic Mouse Cortical Development

Lindsey Buchanan[1,2], Luna Wang[1,3], Xiaofeng Zhou[1], Rebecca Pollak[4], Jen Mulle[4], Emanuel DiCicco-Bloom[1,5]

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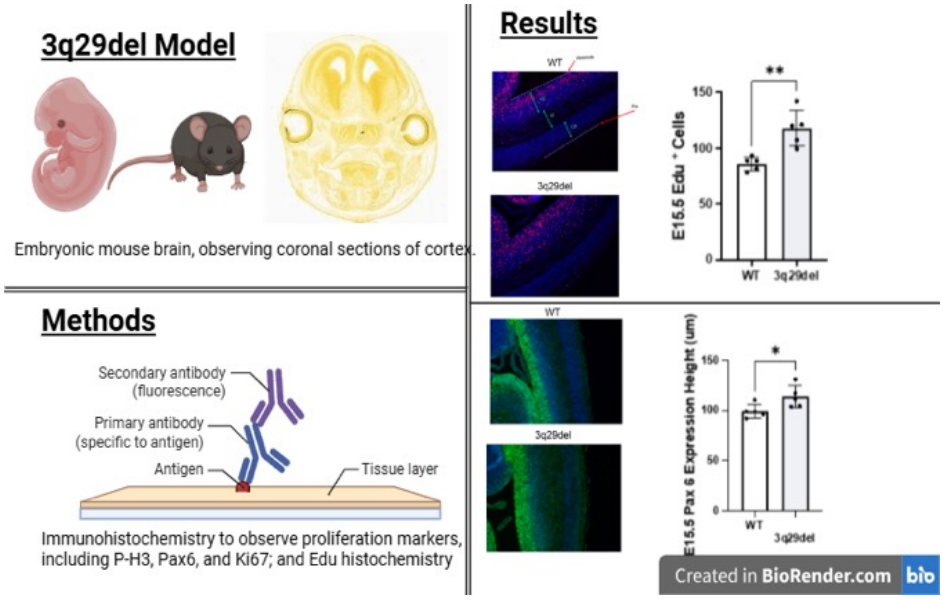
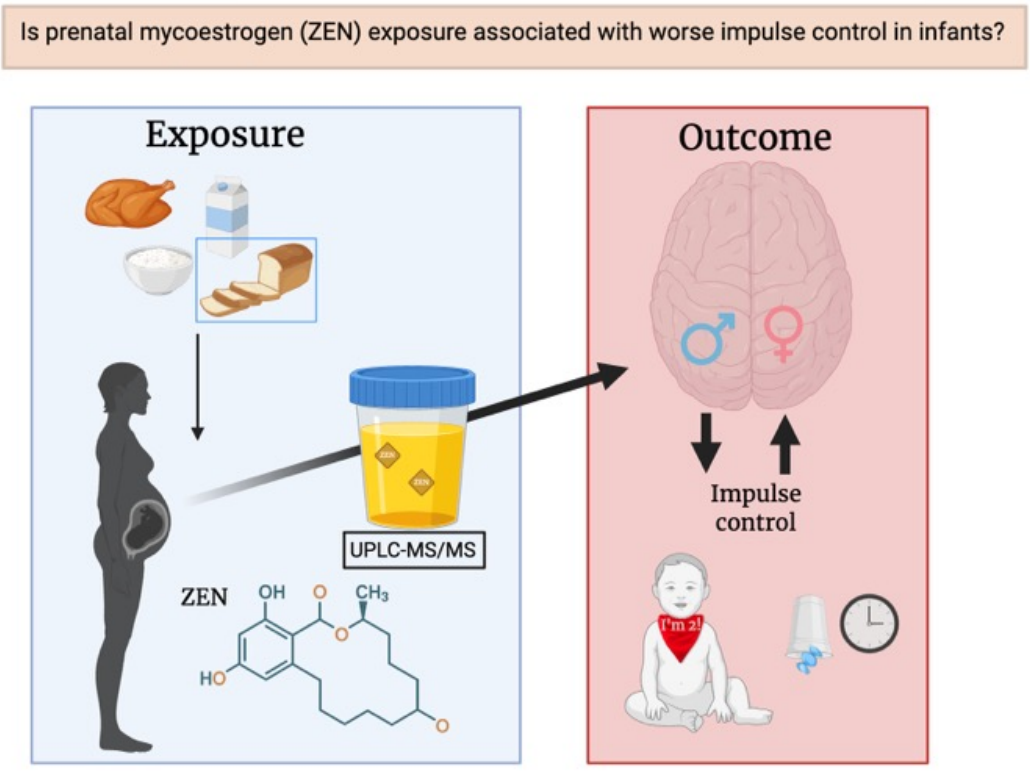
Neurodevelopmental disorders impact an individual's behaviors, emotions, and learning, and are the consequence of both genetic and environmental factors. Abnormal development in the prefrontal cortex contributes to disorders such as autism spectrum disorder (ASD), intellectual disability, and schizophrenia (SZ). A heterozygous deletion of the 3q29 copy number variant (CNV) induces intellectual disability and increases risk for ASD and SZ, and in the mouse model, produces reduced forebrain weight soon after birth, indicating that abnormalities begin in the embryonic period. We characterized the course of embryonic cortical neurogenesis, the process of generating neurons from precursors, and we hypothesize that the 3q29 CNV deletion disrupts cortical neurogenesis. We found that the 3q29 deletion elicits increased proliferation at embryonic days (E) 14.5 and E15.5 selectively, with no differences before or after, as revealed by immunohistochemistry for proliferation markers including Edu (cells in S phase), P-H3 (M phase), Pax6 (ventricular zone, VZ), and Ki67 (stem cells, VZ and sub-VZ). At E15.5, the deletion increases cells entering S phase by 37% (p=0.0008), mitotic cells by 25% (p=0.03), and proliferative precursors in the VZ and SVZ, reflected by heights of 15% (p=0.045) and 19% (p=0.039), respectively. In future studies we will examine roles of apoptosis and characterize consequences for cortical layer formation. Changes in cortical neuron numbers, distribution, and types may underlie neurodevelopmental disorder phenotypes (ASD, SZ) and severity. These insights may improve the accuracy and efficiency of diagnosis and treatment of these conditions. Supported by the Rutgers School of Graduate Studies and NIH R25ES020721.



Prenatal Mycoestrogen Exposure and Impulse Control in the UPSIDE Pregnancy Cohort

Daniel Heltberg, Alyssa Juenke and Dr. Emily Barret
Rutgers, The State University of New Jersey

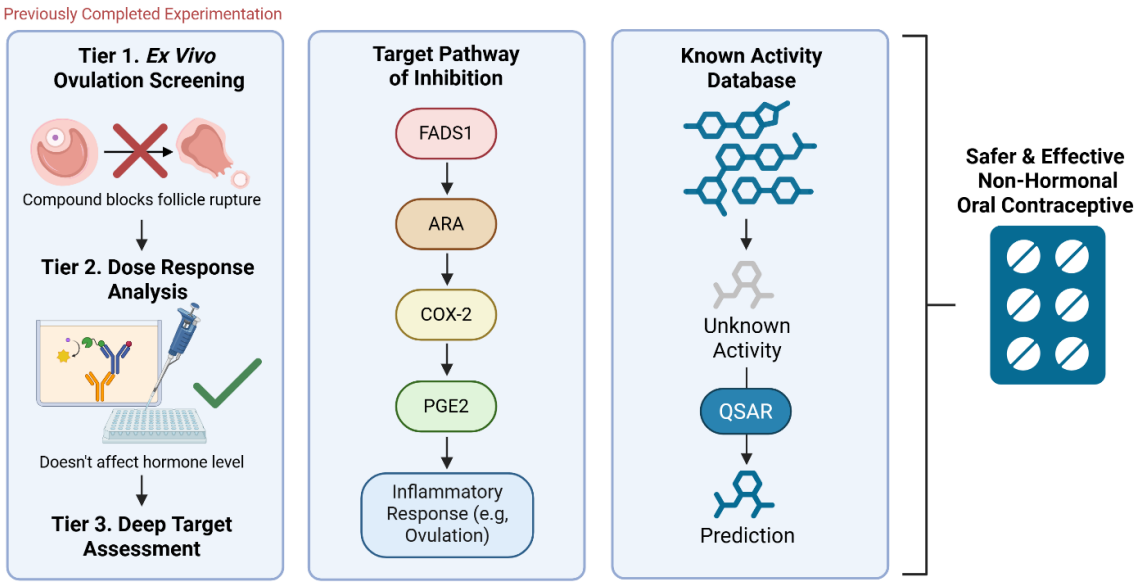
There is concern about the prevalence of mycotoxins like zearalenone (ZEN) found on cereal crops globally. ZEN and its metabolites mimic 17β-estradiol, classifying them as mycoestrogens and indicating their potential for endocrine disruption. Consumption of ZEN is linked to negative effects on fetal development, possibly due to hormonal dysregulation during pregnancy. Though evidence has linked other environmental estrogens to attenuated neurodevelopment, the effect of ZEN exposure on executive functioning is unknown. Using data from the Understanding Pregnancy Signals and Infant Development (UPSIDE) cohort (Rochester, NY; n=113), we examine the relationship between prenatal mycoestrogen exposure and impulse control measures in infants at 2 years of age. ZEN and its metabolites were measured in urine at each trimester via UPLC-MS/MS. Snack delay tests were administered by trained study staff at clinics to gauge impulse control in the infants. Unadjusted and adjusted mixed effect logistic regression models were fitted to assess the association between exposures at each trimester and impulse control scores. Concentrations of ZEN above the limit of detection was measured in 93% of maternal urine samples and appear to have a sex-specific distribution during pregnancy. We hypothesize a sex-specific association whereby prenatal exposure in girls is more negatively associated with impulse control than in boys. Analyses are underway. This study's results can be applied to inform future risk assessment investigation into the neurodevelopmental hazard of prenatal mycoestrogen exposure. Supported by NIH R25ES020721, the RISE Program, the Ernest Mario School of Pharmacy, and the Society of Toxicology.



Developing Novel Non-Hormonal Female Contraceptives; Targeting the FADS1-COX2-PGE2 Pathway

Madisyn Moore[1,3], Jiyang Zhang[2], Shuo Xiao[2]
[1]Research Intensive Summer Experience, Summer Undergraduate Research Fellowship, Rutgers University, [2]Department of Pharmacology and Toxicology, Environmental and Occupational Health Sciences Institute, Rutgers University, [3]Department of Biological Science, Rowan University

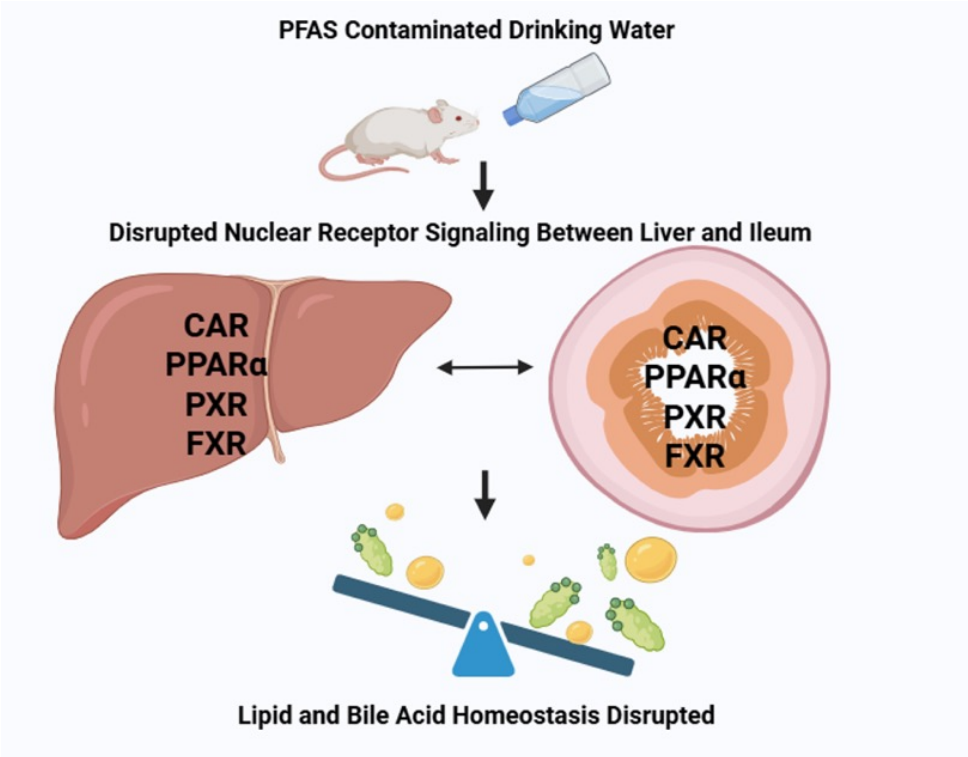
Many oral birth control pills for blocking ovulation contain primarily progestin, a synthetic sex steroid hormone of progesterone. However, current oral contraceptives containing hormones can cause serious side effects such as depression, hormone-related cancers, and stroke. Unfortunately, there is a lack of effective screening platforms which has impeded the development of novel non-hormonal female contraceptives. With there currently being no non-hormonal birth control pill available on the market, we wanted to elucidate the FADS1-COX2-PGE2 pathway, a crucial signaling underpinning ovulation, and identify key knowledge gaps to develop a model to optimize our leads for better efficacy. A complex 3-tiered drug screening system was utilized to locate optimal druggable candidates. Literature reviews were conducted utilizing PubMed as the primary database and [20] primary research articles were selected to locate key knowledge gaps in this target pathway. Understanding these pathways will allow us to better evaluate the non-hormonal contraceptive promises of our compounds. With our compounds being shown to inhibit the FADS1-COX2-PGE2 pathway, we aim to establish a model to identify potential contraceptive analogs. Quantitative structure activity (QSAR) analysis in drug discovery describes how changes in a molecule's chemical structure affect its biological activity, which facilitates the design of effective and safer compounds for more advanced drug development activities. QSAR models will be developed to locate core chemical structures of analogs and ensure the safety of these lead compounds. These findings will aid in establishing a platform for identifying and validating contraceptive candidates, furthering research regarding women's reproductive health. Supported by the Gates Foundation INV-003385, NIH/NIEHS R01ES032144, and NIH R25ES020721, the RISE Program, the Ernest Mario School of Pharmacy, and the Society of Toxicology.



Per- and Polyfluoroalkyl Substances in Enterohepatic Bile Acid Homeostasis

Taylor Troncoso, Veronia Basaly, Shi Hong, Bo Kong, Grace L. Guo
Rutgers, The State University of New Jersey

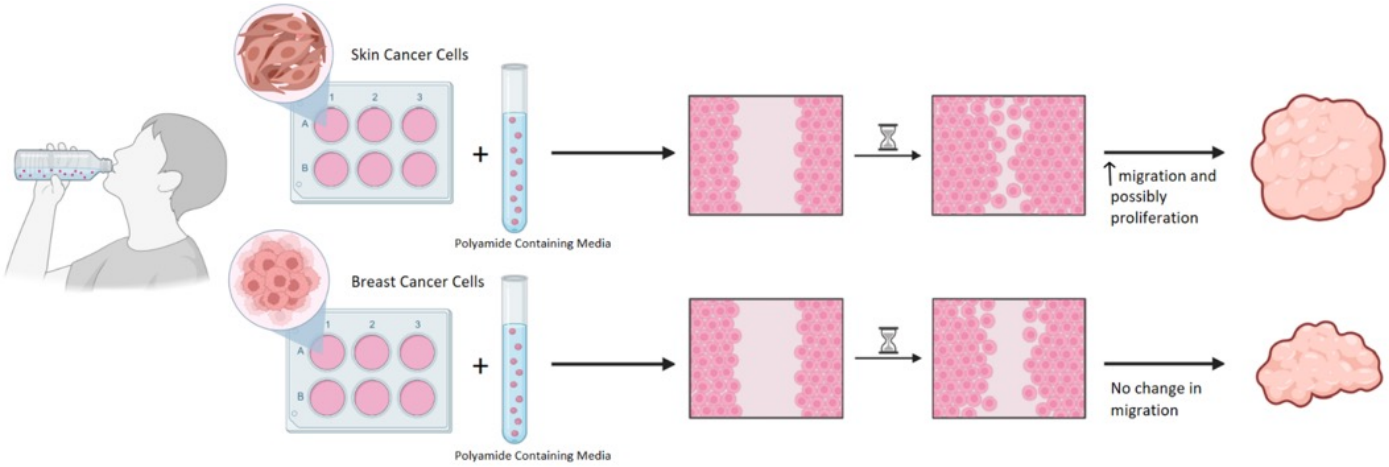
Per- and polyfluoroalkyl substances (PFAS), or "forever chemicals," are environmental pollutants with high resistance to degradation. An estimated 98% of the U.S. population has detectable levels of PFAS in their bodies (Coulson, 2024). Nuclear receptors, such as Farnesoid X Receptor (FXR), Peroxisome Proliferator-Activated Receptor α (PPARα), Constitutively Active Receptor (CAR), and Pregnane X Receptor (PXR), are ligand-activated transcription factors that play a crucial role in regulating lipid and bile acid synthesis, transport, and detoxification. The purpose of this study was to investigate the effects of PFAS on the activation of CAR, PPARα, FXR-FGF15/19 axis, and PXR in mice and their regulation of gene expression in lipid and bile acid homeostasis. Eight-week-old CD-1 female mice received 0, 0.4, 1.2, and 4 μg/mL of Perfluorononanoic acid (PFNA) via drinking water for 8 weeks. Gene expression at mRNA levels was quantified using RT-qPCR. Ileal Fgf15 shows dose response inhibition; however, both classic and alternative bile acid synthesis pathways show no significant change. Cyp2b10 and Cyp3a11 were dose-dependently induced, indicating activation of CAR and PXR-mediated detox pathways. Cyp4a10, a PPARα target gene involved in fatty acid oxidation, showed up to 16-fold induction. Cd36 and Fabp1, PPARα target genes associated with lipid transport and metabolism, showed upward regulation, indicating PFAS-induced PPARα activation and increased intracellular lipid load. These changes imply PFAS exposure disrupts bile acid detoxification and hepatic lipid metabolism. This study provides insight into how forever chemicals disrupt lipid and bile acid homeostasis and can contribute to the pathogenesis of liver diseases. Supported by NJ ACTS NIH R25TR004777 CREST Program.

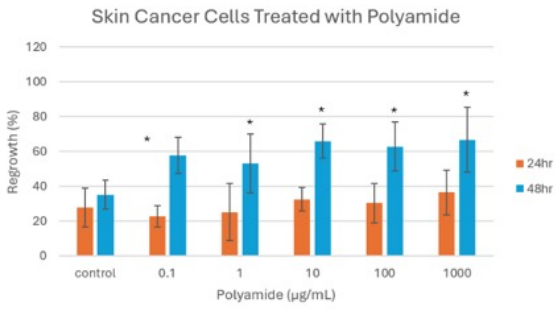


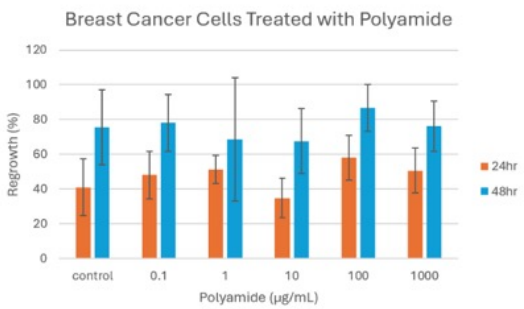
In Vitro Study of Polyamide on Cancer Cell Migration and Proliferation

Felise Coulon, Lori White, Kyle Murphy
Rutgers, The State University of New Jersey

Microplastics are a worldwide pollutant and are important for investigative research to better understand health impacts due to microplastic exposure. Studies show how microplastics can have harmful effects on our bodies, cells, and environment; specifically, that microplastics can cause an inflammatory response in our cells and increase proliferation. However, previous work in our lab suggests that the microplastic polyamide (PA) inhibits migration and possibly proliferation of MCF-7 breast cancer cells. We chose to incorporate A2058 melanoma cells into our study to get a better understanding if migration inhibition due to PA can be seen across multiple cancer cell lines. Our hypothesis is that PA will inhibit migration and proliferation of MCF-7 breast cancer cells and A2058 melanoma cells. Through scratch assays, our data showed that for A2058 cells, percent regrowth at 48 hours increased with the presence of PA compared to MCF-7 cells where there was relatively no effect/change compared to control. Increased migration rate of A2058s in the presence of PA but no change in MCF-7s migration rate is interesting and requires further investigation especially since it contradicts previous data from our lab. Utilizing RT-qPCR and confocal microscopy in the future could help us to understand the mechanism as to how and why PA is increasing migration in one cancer cell line but has no effect on the other. Supported by NIH R25ES020721.





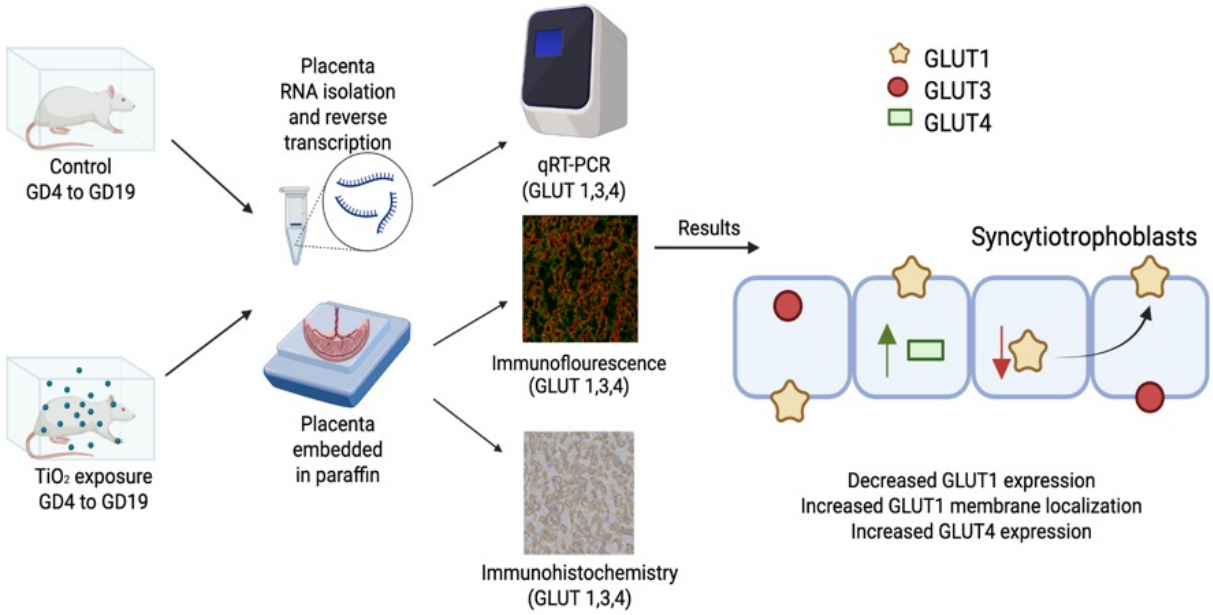


Impact of Gestational Inhalation of Nanoparticles on Glucose Transporters in Rat Placenta

Sara Hoffmann[1], Talia Seymore[2,3], Pedro Louro[4], Carol Gardner[2,3], Michael Goedken[3,4], Debra Laskin[2,3], Phoebe Stapleton[2,3]

[1]Bucknell University, Lewisburg, PA; [2]Department of Pharmacology and Toxicology, [3]Environmental and Occupational Health Sciences Institute, [4]Research Pathology Services, Rutgers University, Piscataway, NJ

Particulate matter exposure can induce adverse health effects during pregnancy including fetal growth restriction. Glucose, a primary nutrient required for fetal growth, is transferred from maternal blood to the fetus via the placenta. Placental glucose transport relies on three glucose transporters (GLUT): GLUT1, GLUT3, and GLUT4. GLUT1 is the primary glucose transporter. We hypothesize that glucose transport in the placenta will be compromised following maternal inhalation of titanium dioxide nanoparticles (nano-TiO2) during pregnancy, impacting fetal glucose access and growth. Dams were exposed to nano-TiO2 as a surrogate for particulate matter in a whole-body inhalation chamber from gestational day (GD) 4 to GD19 and compared to naïve controls. Dams were fasted 16 hours before sacrifice on GD20. Placental tissue was isolated and sex of the corresponding fetus was determined. GLUT expression and localization were evaluated using qRT-PCR, immunohistochemistry (IHC), and immunofluorescence confocal microscopy. There was a significant decrease in GLUT3 mRNA expression of exposed placentas compared to control. IHC identified a significant decrease in GLUT1 protein (p=0.035) and significant increase in GLUT4 protein (p=0.001) of exposed placentas, with females driving this observation. Conversely, membrane localization of GLUT1 increased (p=0.056) while there was no difference for GLUT3 and GLUT4. Gestational nanoparticle inhalation decreases GLUT1 protein expression, but increases membrane localization. Interestingly, there is an upregulation of GLUT4, which may act as a compensatory mechanism to maintain fetal glucose. Overall, these studies demonstrate perturbations to placental glucose transport after maternal nano-TiO2 inhalation. Supported by NIH R25ES020721 and the American Society for Pharmacology and Experimental Therapeutics.

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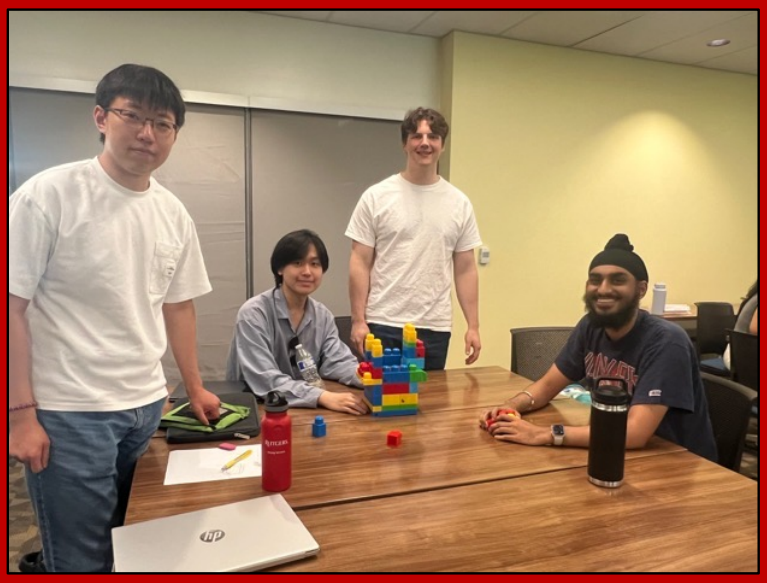


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