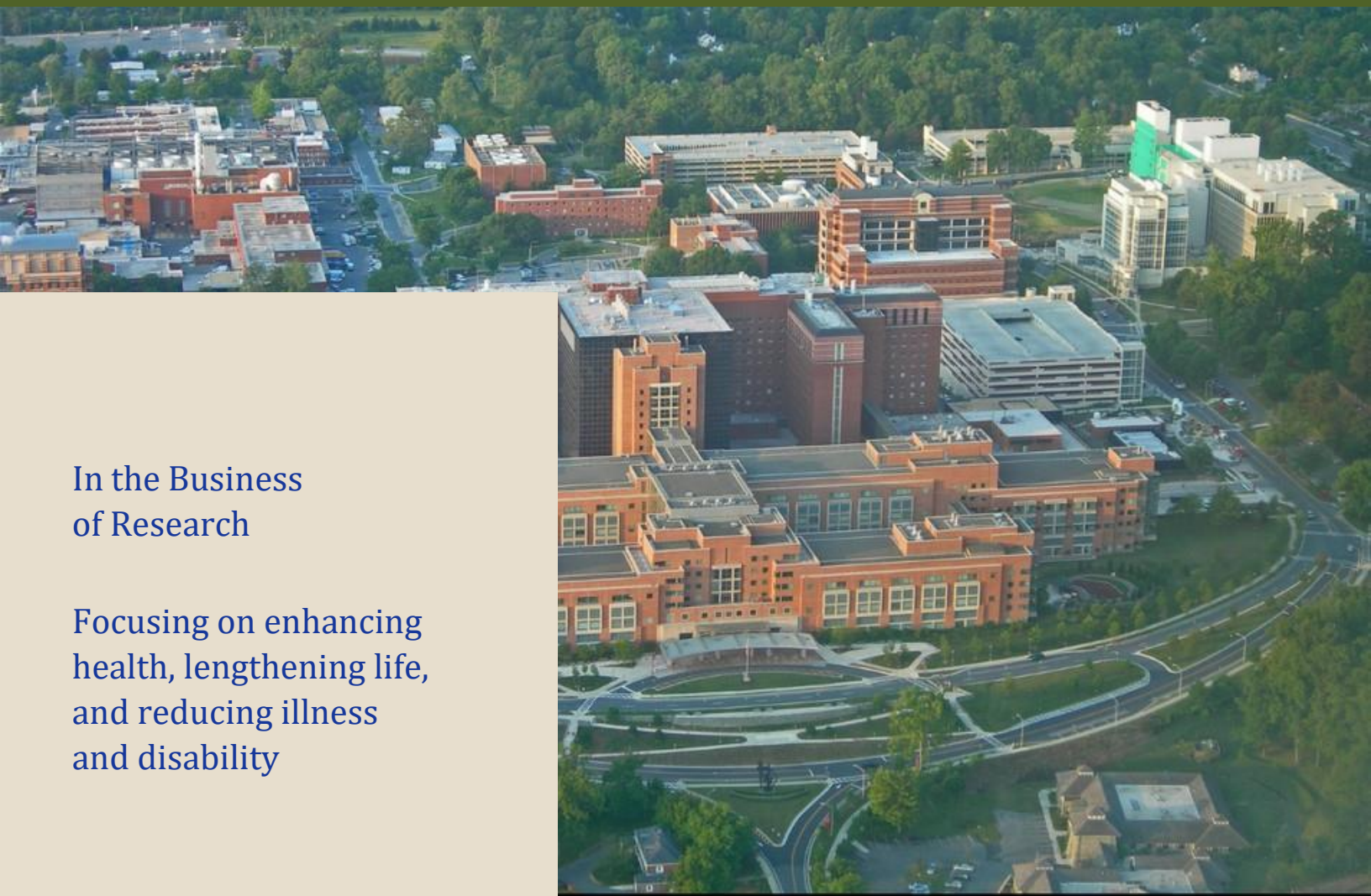
NIH Clinical Center Postbaccalaureate Program

RESEARCH COMPENDIUM

JULY 2026| ISSUE 1

Training The Next Generation



In the Business of Research

Focusing on enhancing health, lengthening life, and reducing illness and disability

MESSAGE FROM THE DIRECTOR

At the NIH Clinical Center, we are proud to welcome each new class of postbaccalaureate fellows into our research community. Year after year, these talented young scientists bring curiosity, enthusiasm, and a genuine commitment to advancing human health. Working alongside our investigators, physicians, nurses, and research staff, they contribute to discoveries that deepen our understanding of disease and improve the lives of patients. Just as importantly, they grow into confident researchers and future leaders in medicine and science.

This compendium is a celebration of their accomplishments and of the extraordinary mentorship that makes those accomplishments possible. Every project represented here reflects the dedication of our postbaccalaureate fellows, the generosity of the mentors who guide them, and the collaborative spirit that defines the NIH Clinical Center. We take great pride in helping prepare the next generation of scientists and clinician-scientists, knowing that the knowledge, skills, and values they develop here will shape the future of biomedical research and patient care. We hope this compendium inspires others, just as these exceptional fellows continue to inspire us.

Tom R. Burklow, MD

Tom R. Burklow, MD
Director, Office of Clinical Research
Training and Medical Education

Program Staff

Jennifer Simmons, MPH
Jennifer Simmons is the Lead Management Analyst in the Office of Clinical Research Training and Medical Education. In this capacity, Jennifer specializes in process improvement and program management, manages the Postbaccalaureate and Summer Internship programs, oversees departmental contracts, information technology systems, and serves as the communications director

Noadia Saint-Louis
Noadia is a Program Assistant in the Office of Clinical Research Training and Medical Education where she provides oversight and support of onboarding trainees and ensures compliance with NIH onboarding requirements. Noad also oversees domestic and foreign travel logistics for office staff.

Justin Haynes
Justin serves as the Data Automation Clerk in the Office of Clinical Research Training and Medical Education. Justin supports training programs through data entry and application system management efforts.

IN THIS ISSUE

Anna Cantilena

Brynn Conrad

Upamanyu Dass-Vattam

Samuel Degenhard

Djaina-Shae Dervil

Sabrina Freidus

Michelle Gras

Neha Gupta

Clare Howard

Arushi Kotru

Collin Le

Peyton Lee

Mattias Lenz

Sawyer Lucas-Griffin

Payton McClarity-Jones

Grace Monette

Prerna Mukherjee

Afreen Mushtaheed

Shubhi Nandi

Morin Nessim

Shreya Papneja

Isha Patel

Anna Roberts

Molly Ruebusch

Mayra Saintilus

Jason Simon

Callista Smith

Leah Stahr

Austin Wang

Ti- Shawn Wellington

Joel Wilkinson

Shirleen Xu

Victoria Yang

Jenny Yarmovsky

Ofek Blivis - *Department of Perioperative Medicine*

HUMAN THALAMIC MEDIODORSAL CART PEPTIDE NEURONS DEFINING ADDICTION AND PAIN

ABSTRACT

Chronic pain is an enduring, aversive state that imposes significant negative emotional and behavioral consequences. This state is the result of integrating diverse nociceptive signals into a unified experience of pain involving multiple cortical regions in addition to the sensory discriminative elements processed in primary somatosensory cortex (S1). The endogenous opioid system modulates pain inputs and reward circuits, however, its relationship to cognitive processes of pain is not clearly defined. Here we focus on the mediodorsal (MD) nucleus, a thalamic hub which is known to have dense reciprocal connections with anterior cingulate (ACC) and prefrontal (PFC) cortices. These networks assign salience, regulate affect, and guide decision making, and through further connections to hippocampus and amygdala, memory and emotional aspects of pain. Using spatial transcriptomics, we identify a large population of MD excitatory neurons that express the Mu- and Kappa- opioid receptors and the neuropeptides CART (cocaine- and amphetamine-regulated transcript) and neurotensin. The glutamatergic CARTPT-expressing neurons are transcriptionally distinct from MD GABAergic neurons. We hypothesize that glutamate-CART peptide signaling from MD neurons drives cortical computations underlying valuation, avoidance, cognitive control and cue selection/reinforcement. These behavioral domains have a strong relationship to substance use disorders and addiction in addition to pain and may form a node of convergence between the two neurobiological constructs. The results provide the first spatially resolved molecular map of an opioid receptor–modulated MD circuit, revealing previously unrecognized peptide-defined excitatory subnetworks with potential roles in affective and motivational dimensions of pain.

Anna Cantilena- *Department of Transfusion*

COMPARISON OF LEUKAPHERESIS PRODUCTS FROM PATIENTS WITH AML AND ALL SUGGESTS INCREASED T-CELL EXHAUSTION AMONG PATIENTS WITH AML

ABSTRACT

CAR T-cell therapy has had limited efficacy in patients with relapsed/refractory (r/r) AML. In a recently completed phase I clinical trial, we observed transient expansion of CD33-targeted CAR T-cells (CD33CART) in 9 of 19 subjects and complete response in only 2 subjects. Potential contributors to inadequate CAR T-cell efficacy include poor T-cell fitness or inhibitory immune cells within the collected leukapheresis products. We compared leukapheresis products from AML and B-ALL patients to identify differences in T-cell or myeloid cell subsets which may be associated with CAR T-cell function. Cryopreserved apheresis products from 14 patients enrolled (12 infused) on the CD33CART trial, 7 B-ALL patients treated on Phase I CAR T-cell trials, and 4 healthy donors (HDs) were compared. Multiparameter flow cytometry analysis included markers of T-cell differentiation, activation, and exhaustion and myeloid/monocytic cell subsets. 5 of 12 apheresis products from infused AML patients demonstrated in vivo CAR T-cell expansion. One subject had CD33CART-induced complete response with incomplete count recovery. All 7 B-ALL patients proceeded to CAR T-cell infusion. 4 achieved CR. Overall, T-cell differentiation and CD4:CD8 ratios did not differ. CD62L expression was higher in AML T-cells, specifically in the T-effector population, in which CD62L loss is associated with enhanced lytic activity (45.5% AML vs 27.6% B-ALL; p=0.016). Expression of the exhaustion marker, CD39, was higher in AML samples (11.8% AML vs 3.9% ALL; p=0.015). CD39, CD69, LAG-3, and TIM3 expressions were higher in AML T-cells compared with HD. T-regulatory cells did not vary between groups. Although leukapheresis products exhibited heterogeneity, only subtle differences in T-cell or monocyte phenotypes were seen in AML- versus B-ALL-samples. Increased T-cell exhaustion was observed in AML samples and merits further study into its potential relation to poor CAR T-cell functionality in r/r AML patients.

PUBLICATIONS

Cantilena, A., Han, K. L., Cai, Y., Yates, B., Jin, P., Shah, N. N., Stroncek, D., & Dreyzin, A. (2026). Impact of blinatumomab and inotuzumab exposure on apheresis composition for CAR T in patients with B-cell acute lymphoblastic leukemia. Cytotherapy, 28(7), 102788. https://doi.org/10.1016/j.jcyt.2026.102788

SURROGATE DECISION-MAKING IN CARCERAL HEALTHCARE

ABSTRACT

The carceral healthcare system is reckoning with a rapidly aging patient population. This is significant because elderly patients are more likely to have medical conditions that render them unable to make their own decisions. Existing laws and ethical guidelines mandate relying on patient-designated and next-of-kin surrogates to make medical decisions for patients who lack decision-making capacity. Yet, providing healthcare to incarcerated patients who lack decisional capacity is especially challenging. As a result, practices vary, and correctional officials, such as wardens or guards, are frequently involved in making medical decisions for incarcerated patients who lack decision-making capacity. The present paper thus considers what qualities make for effective surrogate decision-makers and whether correctional officials tend to possess them. It was concluded that correctional officials frequently lack these qualities before exploring other approaches to surrogate decision-making. Several approaches were identified with greater potential to ensure that incarcerated individuals' treatment is consistent with their preferences and values.

PUBLICATIONS

Chattopadhyay, A., Karel, D., & Wendler, D. (2026). Surrogate Decision-Making in Carceral Healthcare. Journal of general internal medicine, 41(10), 2956–2960. https://doi.org/10.1007/s11606-026-10393-8

Chattopadhyay, A., Asada, Y., Campbell, L. A., Grignon, M., Raju, M., Smith, N. K., & Kim, S. Y. H. (2026). Canadian Medical Assistance in Dying (MAID) and Access to Resources: An Analysis of Media Reports. AJOB empirical bioethics, 17(2), 85–93. https://doi.org/10.1080/23294515.2026.2658449

Pan, S., Chattopadhyay, A., & Taylor, H. A. (2025). A Solution without a Problem. The American journal of bioethics: AJOB, 25(5), 76–77. https://doi.org/10.1080/15265161.2025.2488275

Brynn Conrad - *Department of Radiology and Imaging Sciences*

PET IMAGING OF CNS ASPERGILLOSIS USING FUNGAL-SPECIFIC ANTIBODY FRAGMENT

ABSTRACT

Invasive fungal infections pose a significant threat to immunocompromised patients. Invasive molds, such as Aspergillus spp. and species belonging to the order Mucorales, have high levels of morbidity and mortality due to their angioinvasive nature and the rapid progression of infections. Developing noninvasive diagnostic tools that provide rapid and accurate results are an essential step towards improving patient outcomes. Research efforts focus on creating fungal-specific radiotracers that can detect invasive infections through PET/CT scans.

This project focuses on validating the specificity of antibody fragment (Fab) tracer in identifying mold infections – particularly aspergillosis – that have disseminated into the central nervous system (CNS). Fab targets unique β-glucans found in the cell walls of fungi and is conjugated with an 89-Zr radiolabel. The aim is to exploit disruption in blood-brain barrier integrity brought on by the extensive inflammation of the infection to allow the Fab to penetrate brain tissue. CNS aspergillosis models in immunosuppressed mice were utilized to test the efficacy of our radiotracer through both in vivo and ex vivo protocols. Mouse models were infected through stereotactic surgery and assisting in subsequent PET/CT scans, as well as performing autoradiography and immunofluorescent staining on tissue sections collected from infected mice. The goal is to use these preclinical studies to confirm the functionality and specificity of these diagnostic tracers with the hopes of transitioning to human studies in the future.

Upamanyu Dass-Vattam - *Department of Radiology and Imaging Sciences*

CT-BASED ANALYSIS OF PHEOCHROMOCYTOMA PREDICTS GERMLINE GENOTYPE CLUSTERS

ABSTRACT

In this retrospective study (1999 to 2022), portal-venous phase axial abdominal CT scans from 137 patients with confirmed adrenal PCCs and documented germline or somatic mutations from the NIH Clinical Center were collected. Overall, 274 lesions were manually annotated by expert graders and verified by a senior radiologist (30+ years of experience). Delineations of organs and structures, such as muscle and fat, were obtained using TotalSegmentator and a validated body composition analysis tool. CT imaging biomarkers, including volume and attenuation, were extracted from PCCs and other body regions. Three XGBoost classifiers were developed: (1) binary (Cluster 1 vs. Cluster 2), (2) hereditary subtype (Cluster 1a vs. 1b vs. 2), and (3) granular multi-class (others vs. 1a vs. 1b vs. 2). Performance was evaluated with 10-fold cross-validation using AUC, sensitivity, specificity, and balanced accuracy.

The binary classifier distinguished Cluster 1 from Cluster 2 with an AUC of 0.86 (95% CI: 0.64, 1.00), sensitivity of 0.77 (95% CI: 0.29, 1.00), and specificity of 0.79 (95% CI: 0.45, 1.00). In the hereditary subtype task, Cluster 1b was reliably identified (0.85 (95% CI: 0.57, 1.00) AUC), while Cluster 1a remained challenging (0.48 (95% CI: 0.04, 0.93) sensitivity). Performance declined further in the granular multi-class task, particularly for the "Others" group and Cluster 1a. As contrast-enhanced CT is part of standard diagnostic workup for PCCs, CT-derived imaging biomarkers can distinguish noradrenergic (Cluster 1) from adrenergic (Cluster 2) pheochromocytoma genotypes. This may non-invasively identify patients at higher likelihood of specific genetic alterations and prioritize genetic testing despite costs, insurance barriers, and patient age. Fine-grained subtype discrimination remains limited, particularly for Cluster 1a, underscoring the need for larger, multi-institutional studies and complementary data modalities, such as PET/CT and biochemical profiles.

FOOD INDUSTRY INVOLVEMENT, FAVORABILITY OF FINDINGS, AND RISK OF BIAS IN NUTRITION RESEARCH

ABSTRACT

Objective: To reevaluate the extent of food industry involvement in nutrition research and assess the relationship of industry sponsorship with the favorability of reported findings and risk of bias.

Evidence Review: All research articles published during 2023 in the top five nutrition and dietetics journals were reviewed. Original research articles, reviews, short/brief reports, and short communications were included. Industry involvement and favorability of principal findings were classified by two independent reviewers and conflicts were resolved by another co-author. All randomized controlled trials with industry involvement and an equal number of randomly selected independent trials were assessed for risk of bias using the CLARITY tool by an independent reviewer and an in-house NIH version of ChatGPT-4.0.

Findings: Across the 750 research articles, 19.2% had food industry involvement, and 17.7% reported results classified as favorable to the food industry. Food industry involvement was positively associated with the favorability of reported findings, with direct author affiliation demonstrating the strongest relationship and other involvement the weakest. Of the 62 randomized controlled trials (31 sponsored trials, 31 independent trials), a higher proportion of sponsored trials exhibited a high risk of bias in allocation concealment and other bias, and more independent trials contained high risk of bias in blinding of participants and healthcare staff.

Conclusions and Relevance: Although most articles did not contain industry involvement, the presence of industry involvement in nutrition research was relatively common. Sponsored research demonstrated a risk of bias in certain areas of study design and in the favorability of findings to the food industry. Researchers and clinicians should carefully consider food industry involvement when synthesizing nutrition research, and journal editorial processes should emphasize transparency to mitigate potential bias.

PUBLICATIONS

Degenhard, S. M., Farmer, N., Yang, L., Barb, J. J., Maki, K. A., & Wallen, G. R. (2025). Specific Nutrients Mediate the Association of Food Insecurity and Sleep Regularity Index (SRI) in U.S. Adults: NHANES 2011-2014. Nutrients, 17(2), 340. https://doi.org/10.3390/nu17020340

NEUROIMAGING MEASURES TO UNDERSTAND NEURAL AND PSYCHOLOGICAL CORRELATES IN COOKING: A SCOPING REVIEW PROTOCOL

ABSTRACT

Background: Neuroimaging and cooking are two contrasting items that are vital for day-to-day operations, either on a micro-level between a doctor and patient to multi-layer operations. Nevertheless, the aspect of using neuroimaging to measure cooking and food-related tasks seems to be an area of science that is relatively novel. Therefore, a scoping synthesis of primary sources investigating the usage of neuroimaging techniques in cooking is needed to obtain a broader understanding to evaluate the current available literature on the incorporation in neuroimaging in cooking. Through this scoping review, a comprehensive overview of the existing literature, highlighting knowledge gaps will be examined to determine what is the current state of neuroimaging on cooking-related behaviors.

Methods: This scoping review follows the methodological framework first developed by Arksey and O'Malley, further revised by Levac et al., and updated by Joanna Briggs Institute (JBI) methodology for scoping reviews. The following five step framework for scoping reviews was used: (1) identifying the research question, (2) identifying relevant studies (developing the search strategy), (3) study selection, (4) charting the data (data extraction), and (5) collating, summarizing and reporting the results. The scoping review will be conducted using the Preferred Reporting Items for Systematic reviews and Meta-analysis (PRISMA) extension for Scoping Reviews (PRISMA-ScR). The reviewed included primary literature, usage of neuroimaging on cooking, and populations aged 18 years or order. Two reviewers will independently perform data extraction of included articles and conflicts will be resolved by consensus with a third reviewer checking for accuracy and conflicts.

Results (In progress): The initial search yielded 2,421 citations. Title and abstract screening is currently underway. A PRISMA flow diagram will be used to report the selection process.

Sabrina Freidus - *Department of Bioethics*

SHOULD EUTHANASIA AND ASSISTED SUICIDE BE PROVIDED BY HEALTH CARE PROFESSIONALS? A SYSTEMATIC REVIEW OF REASONS

ABSTRACT

Euthanasia and/or assisted suicide (EAS) has been legalized in a small number of countries, yet it remains highly controversial and contested. One continuing area of contention concerns the role of health care professionals in EAS—for example, whether it is a form of treatment, is consistent with professional ethics, etc . Even when a majority of physicians support the legality of EAS, only a minority would be willing to provide it themselves. This study aims to systematically identify and categorize arguments for and against health care professionals' involvement in EAS. Doing so is important for understanding the nature of the practice and its potential impact on health care professions and society.

Using a modified systematic review of reasons, a systematic review of the literature for arguments for and against health professionals' involvement in EAS was conducted . PubMed/MEDLINE, Web of Science, and PhilPapers were searched for peer-reviewed publications in English that argue for or against healthcare practitioner involvement in EAS . Two reviewers independently screened the publications and extracted data from each eligible publication. A third reviewer assisted with resolving conflicts.

The anticipated results will address: how might providing EAS change, if at all, the professional identity of physicians? How might providing EAS change, if at all, the relationship between physicians and patients? Based on the current stage of our findings, we speculate that this review will also address how health care professional involvement may stem from differences in underlying models of medicine, i.e., how strongly a model emphasizes patient autonomy and/or the alleviation of suffering versus physician's role a healer. By systematically mapping the types of arguments made in favor of or against health care professional involvement in EAS, this review will contribute to ongoing debates about whether EAS should be practiced within the healthcare system.

Michelle Gras - *Department of Laboratory Medicine*

DIFFERENTIAL BONE MARROW METHYLATION PATTERNS IN GATA2 DEFICIENCY

ABSTRACT

Germline heterozygous LOF mutations in GATA2 lead to immunodeficiency, chronic lymphedema, and high propensity to develop myeloid neoplasms. Epigenetic changes associated with myeloid malignancy in GATA2 deficiency are largely unexplored. Here, we present findings of methylation studies in bone marrow (BM) from patients with GATA2 deficiency versus healthy control (HC) marrows.

BM aspirates from 9 patients with GATA2 deficiency and 8 HC were evaluated. Median age of GATA2 patients was 23 (range 15-79). Four had MDS, 2 had CMML, and the remaining had immunodeficiency with a bone marrow failure-like phenotype. Cytogenetic abnormalities were present in 4/9 and included -7 and 8+. 3/7 with NGS studies had mutations in ASXL1, DNMT3A, U2AF1, and SETBP1.

For methylation studies DNA from mononuclear cells was isolated and analyzed using a methylation microarray. Data analysis was conducted in RStudio. There were significant differences in the methylation signatures in the GATA2 group versus the HC group. Differential methylation was found in genes related to DNA damage repair, methylation, and apoptosis. Similarly, genes involved in hematopoiesis including RUNX1 and ETV6 as well as those involved in myeloid malignancy were significantly differentially methylated. Pathway analysis via Gene Ontology revealed a substantial change in methylation between the two groups in pathways involved in leukocyte migration, lymphocyte differentiation, chemokine production, and T-cell differentiation.

In summary significant differences in methylation patterns were seen in BM cells from GATA2 deficiency in comparison to HCs. The findings suggest that epigenetic changes may play a role in the pathogenesis of myeloid malignancy in GATA2 deficiency, warranting further studies.

PROTEOMIC PROFILING IDENTIFIES AUTOANTIBODY-SPECIFIC SIGNATURES AND PREDICTS LUNG FUNCTION AND MORTALITY RISK IN MYOSITIS-ASSOCIATED INTERSTITIAL LUNG DISEASE

ABSTRACT

Idiopathic inflammatory myopathies (IIM) may be complicated by interstitial lung disease (ILD) in up to 40-70% of patients. ILD is characterized by acute and chronic inflammation in the pulmonary interstitium and is strongly associated with myositis-specific autoantibodies (MSA). Various MSA are markers of IIM; some are pathogenic. The clinical challenge is how MSA can be used to both diagnose and inform treatment for these patients. This study integrated highly quantitative Luciferase Immunoprecipitation System (LIPS) autoantibody measurements with targeted proteomic profiling to further understand IIM-ILD pathogenesis. Sera from 191 patients with autoantibodies associated with ILD risk were, 26 patients with autoantibodies not associated with ILD, and 33 controls were analyzed. Proximity extension assays were used to measure 184 biomarkers. Correlation, pathway, and unsupervised clustering analyses were conducted to identify biological disease endotypes and signaling. Across MSA groups, elevated levels of interferon-related chemokines (CXCL9, CXCL10, CXCL11), pro-fibrotic mediators (LAP-TGF- β1), and inflammatory markers (MCP-3, CASP8) were observed in patients with increased autoantibody titers. Pathway analysis indicated enrichment of IL6/JAK/STAT3 and interferon-γ signaling. Unsupervised clustering defined four distinct proteomic endotypes. One endotype exhibited increased epithelial injury and inflammatory stress markers, higher autoantibody levels, reduced lung function, and worse survival. Exploratory modeling found SERPINA9, a protease inhibitor, to predict lung function decline. PLIN1, a modulator of lipid metabolism, was associated with improvement. These findings reveal both shared and distinct proteomic signatures across MSA-defined subgroups. Integration of targeted proteomic and quantitative autoantibody profiling has the potential to improve risk stratification and insight into IIM disease mechanisms.

PUBLICATIONS

Burbelo, P. D., Pinal-Fernandez, I., Casal-Dominguez, M., Tian, X., Gao, S., Gupta, N., Robbins, E. W., Chiorini, J. A., Mecoli, C. A., Christopher-Stine, L., Casciola-Rosen, L., Mammen, A. L., Danoff, S. K., Suffredini, A. F., & Huapaya, J. A. (2026). Improved Detection of Myositis-Specific Autoantibodies Using Luciferase Immunoprecipitation Systems Assay: Comparison With Line Blot and Conventional Immunoprecipitation. Arthritis & rheumatology (Hoboken, N.J.), 10.1002/art.70103. Advance online publication. https://doi.org/10.1002/art.70103

Clare Howard - *Department of Transfusion Medicine*

ASSESSING ACCURACY AND RELIABILITY OF RESEARCH AND DIAGNOSTIC TESTS IN TRANSLATIONAL RESEARCH

ABSTRACT

Clinical testing assays are considered the gold standard for diagnosis and preliminary disease screening but require an extensive validation process to obtain FDA approval. Unequal access to these tests presents a problem for resource limited labs due to their expensive costs and specialized equipment requirements. Research use only (RUO) tests are a more affordable and flexible alternative, but it is unclear if these tests are a reliable substitute. Rheumatoid Factor (RF) is an autoantibody that has been associated with autoimmune diseases. It can be tested for with both clinical assays and commercially available RUO kits. To evaluate the performance of RF RUO kits, I compared the results from two RF RUO ELISAs to clinical results from a patient cohort (n=33) that had been previously analyzed by clinical testing. This sample set included n=17 true positives and n=16 true negatives, with varied collection dates and result ranges. The performance of each RUO test was evaluated by calculating the sensitivity, the ability to identify true positives, and specificity, the ability to identify true negatives. These results were compared to recommended clinical test sensitivity and specificity values, which should be greater than 90%. Kit #1 had a sensitivity of 47.1% and a specificity of 87.5%. The kit correctly identified many true negative samples but misidentified over half the true positive samples as negative for RF. Kit #2 had a sensitivity of 82.4% and specificity of 18.8%. While the sensitivity was improved, the specificity was very low. This kit misidentified a significant number of true negative samples as positive for RF. When quantitative values of RUO kits were compared to known clinical results there was a low correlation (Kit #1, $R2 = 0.2424$, P value = 0.0447; Kit #2, $R2 = 0.3691$, P value = 0.0097). Overall, we found RF RUO kits to be highly variable and believe they should be used with caution for clinical preliminary disease screening.

Zhanpeng Kuang - *Biostatistics and Epidemiology Service*

IDENTIFYING DRINKING PATTERNS IN ALCOHOL USE DISORDER USING TIMELINE FOLLOW-BACK DATA

ABSTRACT

The Timeline Follow-back (TLFB) method collects self-reported daily alcohol use over a specified period, providing continuous and individualized data on drinking behavior. Advancing methods for analyzing TLFB data can improve our understanding of drinking patterns and enhance the prediction of related outcomes. The current study applied heatmap clustering methods to 84-day TLFB data to identify drinking patterns in both treatment-seeking (TS, n = 837) and non-treatment-seeking (NTS, n = 1258) groups. Data were aligned to the most common last day within each treatment group (Tuesday for TS; Friday for NTS), and were standardized by column (drinking day). Euclidean distances were calculated and Ward's clustering algorithm was implemented. Mean profile plots were generated. Clinical and demographic factors were analyzed via Chi-squared and Kruskal-Wallis tests. For both treatment groups, four clusters were created. The mean profile plots for all the clusters revealed a cyclical pattern in mean number of drinks over time, with an increase on Fridays and Saturdays. As the mean number of drinks increased between clusters in the TS group, there was a corresponding increase in AUD Identification Test (AUDIT) scores, anxiety scores, ALT and AST levels. Patients in clusters with larger mean number of drinks were more likely to be male, smoke, and use other substances. Similar trends were observed in the NTS group; moreover, those patients were more likely to be older and diagnosed with psychiatric disorders. These results suggest the importance of categorizing patients by drinking trajectory into distinct clusters to help develop more personalized treatment plans.

Arushi Kotru - *Rehabilitation Medicine Department*

ASSOCIATIONS BETWEEN POSTURAL LIMITS OF STABILITY AND GAIT IN TRAUMATIC BRAIN INJURY

ABSTRACT

The objective of this study was to examine relationships between balance and gait in individuals with traumatic brain injury (TBI) and their association with self reported symptoms. 60 patients (36 males, 24 females) were seen up to 1 year post TBI. Their TBI diagnosis was determined using the Department of Veterans Affairs and Department of Defense TBI Severity Rating Scale.

Gait was assessed using the GAITRite® electronic walkway for three averaged 20-m trials at comfortable pace. Balance assessed using the Limits of Stability (LOS) test on the NeuroCom SMART Balance Master System, requiring participants to shift their center of gravity toward targets while maintaining upright posture and stationary feet. Self-reported dizziness, loss of balance, and poor coordination measured with the Neurobehavioral Symptom Inventory (NBSI). Pearson or Spearman correlations used as appropriate.

Greater double support time was associated with reduced forward maximum excursion (r_s=-0.34, p=.0066) and trended with reduced forward endpoint excursion (r_s=-0.23, p=.0715). Higher left single support time was associated with greater lateral endpoint and maximum excursions (r_s=0.25, p=.0487; r_s=0.25, p=.0513). Gait speed trended with forward endpoint excursion (r_p=0.25, p=.0554). Reduced forward LOS endpoint excursions were present in 18 participants, reduced left maximum excursions in 44, and abnormally slow gait speed in 6.

Associations between forward LOS and double support time suggest compensatory strategies to maintain stability when postural control is impaired. Relationships between left single support and lateral balance indicate side-specific postural control differences. Despite clinically elevated mean NBSI scores, symptom burden varied substantially, and individuals with minimal symptoms still demonstrated measurable gait-balance impairments. Findings support incorporating performance-based gait and balance assessments in TBI and warrant further longitudinal investigation.

Collin Le - *Department of Radiology and Imaging Sciences*

PET IMAGING WITH 18F-FLUOROCELLOBIOSE TO ASSESS TREATMENT RESPONSE IN AN ASPERGILLUS INFECTION MODEL

ABSTRACT

Invasive aspergillosis (IA) is a leading cause of mortality in immunocompromised patients. Prompt antifungal treatment improves patient outcomes, but clinicians lack reliable tools to measure therapeutic response. Our lab previously developed a PET radiotracer, [18F]-fluorocellobiose (FCB), which non-invasively detects live, metabolically active A. fumigatus infections. In this study, we evaluated the ability of [18F]-FCB PET imaging to assess treatment response in A. fumigatus-infected mice treated with first-line Voriconazole (VCZ) versus a suboptimal drug, Liposomal Amphotericin B (LAmB).

Mice were immunosuppressed with cyclophosphamide and infected intramuscularly with A. fumigatus conidia. VCZ treatment was administered daily, while the suboptimal LAmB treatment was given intermittently. [18F]-FCB PET/CT imaging was performed at baseline and weeks 1–3. PET images were quantified to obtain Standard Uptake Values, and infected thighs were evaluated using Grocott's Methenamine Silver (GMS) staining at study completion.

[18F]-FCB uptake was observed in infected thighs in both groups at baseline. Over the treatment course, the VCZ group exhibited a steady decline in tracer uptake, whereas the LAmB group showed no significant change. Terminal GMS staining confirmed near-complete resolution of infection in VCZ-treated mice, with only minimal residual hyphae, while the LAmB group displayed persistent branching hyphae, corresponding to the sustained [18F]-FCB uptake.

In conclusion, it was determined that PET imaging with [18F]-FCB can noninvasively monitor antifungal efficacy and distinguish effective from suboptimal treatment in A. fumigatus infection. This data supports expanding [18F]-FCB's use to evaluate treatment response of A. fumigatus (and potentially other cellulolytic molds) to different novel antifungals or antifungal combinations in animal models. The ultimate goal is to translate [18F]-FCB for the evaluation of treatment response in infected patients.

Peyton Lee - *Department of Pediatrics*

EXPLORING FACTORS INFLUENCING PERCEPTION OF SELF-MANAGEMENT AND HEALTH-RELATED QUALITY OF LIFE IN CONGENITAL ADRENAL HYPERPLASIA (CAH) AS MEASURED BY CAHQL

ABSTRACT

Congenital adrenal hyperplasia (CAH) is an inherited disorder that impacts the adrenal glands, often due to 21-hydroxylase deficiency (21OHD). This leads to impaired cortisol and/or aldosterone output, excess androgens, and risk of adrenal crisis. Therefore, disease self-management is critical in preventing adverse outcomes and involves daily glucocorticoid (GC) medication, properly stress dosing when ill, and identifying social support. Various sociodemographic factors may influence patients' perception of their ability to self-manage and overall health-related quality of life (HRQoL). To elucidate these relationships, results were interpreted from administration of CAHQL, the first CAH-specific patient-reported outcome (PRO) questionnaire, recently created at the NIH. In its development, the CAHQL tool was administered to 69 adults with 21OHD CAH and contained 7 Likert-scale questions regarding patient perception of self-management. The final survey covered 7 domains: General Health, Adrenal Insufficiency, GC Excess, Physical Functioning, Mental Health and Cognition, Social Functioning, and Sexual Functioning. It was found that a majority of patients mostly or strongly agreed feeling comfortable managing CAH, yet over half worried about adrenal crises. Self-management was similar regardless of phenotype, age, biochemical markers of disease control, insurance type, income bracket, education or work status. Increased confidence in receiving help from others in an adrenal crisis was associated with male sex, more household members, and being married. Those with increased worry about stress dosing and adrenal crises had more stress doses or hospitalizations in the past 6 months. Overall, better HRQoL was associated with higher self-management confidence. These results surface the importance of evaluating HRQoL burden of CAH, and behavioral and psychosocial factors influencing care. Future aims included finding correlations among biochemical and lifestyle factors impacting CAH HRQoL.

PUBLICATIONS

Flokas, M. E., Kulkarni, S., Lee, P., Yang, L., Sukin, C., Kollender, S., & Merke, D. P. (2026). Perceptions of CAH self-management and stress dosing in relation to health-related quality of life as measured by CAHQL. Frontiers in endocrinology, 17, 1810137. https://doi.org/10.3389/fendo.2026.1810137

Mattias Lenz - *Department of Transfusion Medicine*

INVESTIGATING THE BCR REPERTOIRE IN PERIPHERAL B CELLS AND TISSUE FROM HEPATITIS ASSOCIATED BNHL PATIENTS

ABSTRACT

Chronic infection with Hepatitis B Virus (HBV) or Hepatitis C Virus (HCV) is associated with the development of B-cell non-Hodgkin's lymphoma (BNHL). Despite this association, the mechanism by which chronic infection may lead to lymphoma is not fully understood. Additionally, limited research has been done on the effect HBV coinfection with Hepatitis D (HDV) may have on lymphoma development. One hypothesis is that lymphomagenesis may occur through an indirect mechanism in which hepatitis viruses chronically stimulate viral-specific B cells. Previous studies support this mechanism, with B cells expressing viral-associated B cell receptors (BCR) having been found in viral-associated lymphoma, and our lab has previously reported expansion of peripheral B cells in HCV-BNHL patients expressing BCRs associated with lymphoproliferative disorders and viral infections. To further investigate an indirect mechanism of lymphomagenesis, we performed RNA-sequencing (RNA-seq) on peripheral B cells and BCR-sequencing (BCR-seq) on matched lymphoma tissue from patients with and without viral infection. To validate RNA-seq as a method for BCR expansion detection, RNA-seq and BCR-seq were performed on a cohort of n=15 peripheral B cell samples. RNA-seq was comparable to BCR-seq, detecting n=10/11 BCR expansions. RNA-seq data was then analyzed from a cohort of peripheral B cells obtained from patients with HBV-BNHL, HBV/HDV-BNHL, HCV-BNHL, and BNHL alone. Expansion was observed in 100% (n=1/1) of HBV-BNHL, 33% (n=1/3) of HBV/HDV-BNHL and 75% (n=6/8) of HCV-BNHL patients, and was absent in patients with BNHL alone (n=0/6). Although clonal expansion in circulating B cells was absent in some hepatitis-associated BNHL, our data support chronic stimulation as a mechanism for lymphomagenesis in some patients, especially in HCV-BNHL. BCR-seq of matched lymphoma tissue from this cohort is currently underway in order to determine if the peripheral BCR repertoire is mirrored in lymphoma tissue.

PUBLICATIONS

Miller, M. J., Price, C., Shields, T. C., Zarpak, R., Lee, P., Osterwind, Z., Lenz, M., Argueta Guevara, M., Fowler, S., Livinski, A. A., & De Giorgi, V. (2026). Alpha-gal sensitization and allergic transfusion reactions: a scoping review protocol. Systematic reviews, 15(1), 109. https://doi.org/10.1186/s13643-026-03134-9

Miller, M. J., Zarpak, R., Lee, P., Osterwind, Z., Lenz, M., Guevara, M. A., Fowler, S., Price, C., Shields, T. C., Livinski, A. A., Conry-Cantilena, K., Stroncek, D. F., West-Mitchell, K., & De Giorgi, V. (2026). Alpha-gal sensitization and allergic blood transfusion reactions: a scoping review. Journal of translational medicine, 24(1), 325. https://doi.org/10.1186/s12967-025-07614-9

AWARDS

2025 NIH Clinical Center CEO Award, Science Category (Team) - Awarded for the scientific impact of validating an in-situ hybridization methodology in specific immune cells with technical rigor.

Langston Locke - *Department of Radiology and Imaging Sciences*

UTILITY OF PORTAL VEIN TAPERING AND ABDOMINAL IMAGING BIOMARKERS FOR STAGING LIVER FIBROSIS AT CT

ABSTRACT

Liver fibrosis is the gradual degradation of liver tissue into fibrous scar tissue. Asymptomatic mild to moderate fibrosis may lead to late diagnoses, and advancement into cirrhosis. Portal vein tapering (PVT) is the gradual narrowing of the portal vein, often indicative of pathology due to fibrotic pressure on liver vasculature. We aim to develop a tool capable of automatically measuring PVT to develop a tool capable of staging liver fibrosis from CT images.

Four CT datasets were utilized for training a 3d-nnUNet segmentation model comprised of 504 total CT images: (1) 443 volumes from the public Medical Segmentation Decathlon dataset, and three datasets collected at the NIH featuring patients with(2) splenomegaly, (3) ascites, and (4) undergone hepatic artery embolization (HAE). These images were annotated by fellows and verified by a MD, with labels denoting the portal vein, its branches, and the splenic vein. Spleen and liver annotations were obtained using a previously developed segmentation tool.

Two datasets were used for model training and validation: (1) 207 patients who were imaged at the NIH measured with ISHAK scale of liver fibrosis, and (2) 480 patients from the University of Wisconsin-Madison measured with METAVIR. To evaluate the model segmentation, 50 patients were randomly selected from each validation dataset, and the same fellows annotated the volumes with the same labels. Dice Similarity Coefficient and 95th percentile Hausdorff Distance were calculated on the results of the segmentation model. Next, XGBoost models were trained on the NIH dataset with a 70/30 train-test split and tested on the University of Wisconsin-Madison dataset. XGBoost models were trained on PVT measurements only, clincal results only, and a combination of both. One version of the model was trained to predict advanced fibrosis, and another to predict cirrhosis, resulting in a total of six models. Sensitivity, specificity, and ROC-AUC were calculated.

PUBLICATIONS

Liu J., Locke, L., Mukherjee, P., Mathai, T.S., Zhuang, Y., Khoury, B., Eckhardt, L., Kozycki, .T., and Summers, R.M. (2025). Benchmarking MRISegmenter++ for Splenomegaly: A Comprehensive Comparative Study. In Applications of Medical Artificial Intelligence: 4th International Workshop, AMAI 2025, Held in Conjunction with MICCAI 2025, Daejeon, South Korea, September 23, 2025, Proceedings. Springer-Verlag, Berlin, Heidelberg, 329–338. https://doi.org/10.1007/978-3-032-09569-5_33

Sawyer Lucas-Griffin - *Department of Bioethics*

"YOU'RE KIND OF THAT PERSON'S WORLD": DISABILITY SERVICE PROVIDER TURNOVER IMPACT ON ADULTS WITH INTELLECTUAL AND DEVELOPMENTAL DISABILITIES

ABSTRACT

Disability service providers (DSPs), also known as direct support professionals, disability aides, support staff, care workers, or waiver providers, serve a vital role in the intellectual and developmental disability (IDD) community. Funded by Medicaid or paid privately, DSPs support people with IDD in various settings—homes, schools, institutions, and workplaces—to develop independent living skills related to health and safety, household tasks, success at work, and self-advocacy (Friedman, 2021). However, limited DSPs and high turnover rates have resulted in a "workforce crisis." While much has been written about DSP turnover, reasons for its high rates, and ways to address the workforce shortage, there is very little research about how DSP turnover actually affects people with IDD. We investigate this question via semi-structured interviews with adults with IDD and primary caregivers of adults and teenagers with IDD that elucidate the practical, interpersonal, and ethical nuances of the DSP landscape.

PUBLICATIONS

Lucas-Griffin, S., Wasserman, D., & Wendler, D. (2026). Intellectual Disability and Supported Decision-Making in Clinical Research: Anticipating Ethical Challenges. The Journal of law, medicine & ethics : a journal of the American Society of Law, Medicine & Ethics, 54(S2), 20–26. https://doi.org/10.1017/jme.2025.10199

Lucas-Griffin, S., & Raju, M. K. (2026). True Respite? Analyzing the Challenges and Opportunities of Autistic Adolescent Respite Care Investment. The American journal of bioethics : AJOB, 26(5), 82–84. https://doi.org/10.1080/15265161.2026.2645621

Payton McClarity-Jones - *Department of Radiology and Imaging Sciences*

THE EFFECTS OF IMMUNE SYSTEM DYSREGULATION ON FDG PET IN CNS INFECTIONS

ABSTRACT

While MRI remains foundational for structural assessment in the central nervous system, its utility is limited in the setting of immune dysregulation or recovery, where inflammatory responses can mimic or attenuate the radiologic signals of active infection. Fluorine-18 fluorodeoxyglucose PET (FDG PET) may address this by providing complementary metabolic information to help distinguish active infection from inflammation. My primary project examines this role across four disease contexts: immune reconstitution inflammatory syndrome (IRIS) in human immunodeficiency virus (HIV) and progressive multifocal leukoencephalopathy (PML), paradoxical reactions (PR) in tuberculous meningitis (TBM), post-infectious inflammatory response syndrome (PIIRS) in cryptococcal meningitis (CM), and cerebral aspergillosis in immunocompromised hosts.

Using a retrospective longitudinal design, I quantify FDG uptake within infectious lesions over time with MIM software and correlate findings with MR imaging, clinical presentation, immune status, laboratory data, and treatment response. This work aims to establish imaging guidelines that improve differentiation between active infection and inflammation while informing therapeutic decisions.

In a secondary project focused on TBM-PRs, I assist in quantifying abnormal FDG uptake associated with TB and organ-specific metabolic activity to determine whether systemic patterns correlate with disease progression and inflammation. With these findings, I hope to identify predictive imaging markers for paradoxical reactions and improve early recognition of immune-mediated complications during treatment.

Together, these projects represent an ongoing effort to characterize the metabolic signatures of immune-mediated CNS complications, with the long-term goal of developing standardized FDG PET criteria to guide diagnosis and management in altered immune states.

Grace Monette - *Rehabilitation Medicine Department*

PHYSICAL EXERCISE: A REHABILITATION ASSESSMENT AND STRATEGY FOR CLINICAL POPULATIONS

ABSTRACT

Utilizing physical exercise as an assessment and intervention strategy to understand the physiology of various diseases are neccessary to inform better rehabilitation practices across diverse patient populations. This project has centered on a trial involving exercise intervention in patients with Long COVID. Additionally, I have had the opportunity to conduct research involving individuals with systemic lupus erythematosus, RYR1-related diseases, Gulf War Illness, and Takayasu's arteritis (TA). Although these populations differ widely, our protocols often rely on similar methods of data collection. A range of assessments have been administered including, cardiopulmonary exercise testing, near-infrared spectroscopy, patient-reported outcomes, arterial occlusion testing, ultrasound, and 6-minute walk tests. These assessments are used in tandem to understand whether patients may be limited in certain areas, and how exercise may promote improvements. For instance, among individuals with Long COVID, participation in exercise training promotes better function and self-reports of symptom alleviation. Adults with TA report via survey that they care capable of exercise, that it seems to attenuate disease-associated pain, and that exercise intervention may benefit these patients. Those with RYR-1 related myopathies exhibit unexpected heart rate responses to exercise, and individuals within a cohort may exhibit limitations that are either central cardiovascular or peripheral muscle dependent.

AWARDS

First Place - NIH Clinical Center Three-Minute Talk Competition

Prerna Mukherjee - *Department of Radiology and Imaging Sciences*

SCREENING FOR CHITIN-SPECIFIC NANOBODIES TO DEVELOP FUNGAL-SPECIFIC IMAGING TRACERS

ABSTRACT

Positron Emission Tomography (PET) detects invasive fungal infections (IFIs), mainly impacting immunocompromised patients, as there is a critical need for rapid and noninvasive imaging diagnostics to improve prognosis. Current imaging techniques such as MRI and CT scans are often nonspecific and can have overlapping diagnoses. We utilize PET tracers to target fungal structural components and specifically detect IFIs. Chitin is a major fungal cell wall component present in a wide range of fungal species, making it a promising pan-fungal diagnostic tool. Our project is focused on developing chitin-specific nanobodies to identify IFIs noninvasively, using phage display. This year, we generated a nanobody library from chitin-immunized llamas, completed phage display panning to amplify chitin-binding nanobodies, and selected high chitin-binders using the ELISA method. The phage was transformed into E. coli TG1 cells, and we screened individual colonies for their chitin-binding potential using ELISA. We identified positive clones with chitin affinity by selecting clones that had absorbance values above 0.3. After selecting positive clones for sequencing, we identified conserved regions (CDRs) unique to nanobodies and chose two candidates (named C3 and B1) for further purification. We performed nickel affinity chromatography to purify the nanobodies and further assessed their chitin-binding potential, using ELISA and chitin pulldown assays. Through in-vitro characterization, we found that C3 and B1 are promising chitin-binding candidates, as they showed binding to chitin beads and native chitin present in the Aspergillus strain. Our future work includes assessing the nanobodies' pan-fungal nature with in vitro fungal models using different fungal species (such as Aspergillus and Mucorales), radiolabeling the nanobodies, performing in vivo work with infectious mouse models, and eventually completing clinical translation to diagnose fungal infection in humans.

SELECTIVE MUSCLE INVOLVEMENT QUANTIFICATION IN LATE-ONSET TAY SACHS AND SANDHOFF DISEASE USING NEUROMUSCULAR ULTRASOUND IMAGING

ABSTRACT

Despite functional mobility losses being the primary complaint in late-onset Tay-Sachs and Sandhoff disease (LOTS-SD), a quantitative understanding of neuromuscular degeneration is lacking. Our aim is to quantitatively characterize muscle degeneration using ultrasound measures of muscle thickness, echogenicity, and stiffness. Additionally, we investigate if elbow and knee extensors are preferentially affected in LOTS-SD. Twenty patients diagnosed with LOTS-SD and 20 matched controls (age, sex, BMI) participated. Muscle thickness, echogenicity, and stiffness were quantified and compared across cohorts in the triceps, biceps, rectus femoris (RF) and semimembranosus (SM). For each measurement, the extensor-to-flexor and lower-to-upper-limb muscle ratios (triceps-to-biceps, RF-to-SM, and RF-to-triceps) were also compared. Patients with LOTS-SD demonstrated triceps, RF, and SM atrophy (24–47%), increased RF and triceps echogenicity (21–36%), and increased RF stiffness (10%). The triceps-to-biceps and RF-to-SM thickness ratios were decreased (−42%, −25%) and increased for echogenicity (32%, 35%). Notably, for the RF-to-triceps ratio, only the stiffness ratio was elevated (18%) in patients. Neuromuscular ultrasound confirmed patterns of preferential elbow/knee extensors degeneration in LOTS-SD. While lower (RF) and upper limb (triceps) atrophy appeared proportionate, elevated RF stiffness indicates potentially varied degeneration pathways for these two muscles.

PUBLICATIONS

Mushtaheed, A., Lind, P. M., Assefa, Y. M., Druckenbrod, M., Toro, C., Tifft, C. J., Alter, K. E., & Sheehan, F. T. (2026). Selective muscle involvement quantification in late-onset Tay Sachs and Sandhoff disease using neuromuscular ultrasound imaging. Clinical neurophysiology: official journal of the International Federation of Clinical Neurophysiology, 187, 2111739. https://doi.org/10.1016/j.clinph.2026.2111739

Ly, A., Mushtaheed, A., Soliman, M.E., Karp B. and Cho, H.J. (2025). A narrative review: clinical trials in therapeutic interventions for dystonia (2020 - 2025). Dystonia 4:14547. doi: 10.3389/dyst.2025.14547

Stowers, J. A., Day, D. S., Jow, S., Heins, S., Forrest, E., Assefa, Y. M., Lind, P. M., Mushtaheed, A., Sheehan, F. T., & Alter, K. E. (2025). The Relationship Between Stiff Knee Gait Runner's Dystonia and Musculoskeletal Knee Pathology: A Case Series. Toxins, 17(3), 121. https://doi.org/10.3390/toxins17030121

UNDERSTANDING HOLISTIC INTERVENTIONS FOR PEOPLE WITH ALCOHOL USE DISORDER: A SCOPING REVIEW.

ABSTRACT

Purpose: Alcohol Use Disorder (AUD) affects millions worldwide and contributes to chronic disease and premature mortality. As AUD impacts physical, emotional, and social health, there is growing interest in complementary and integrative interventions used alongside or beyond conventional biomedical treatment. This scoping review synthesized the literature on complementary and integrative interventions for AUD and evaluated their reported effectiveness.

Methods: A scoping review was conducted using the Arksey and O'Malley framework and PRISMA-ScR guidelines. PubMed/MEDLINE, Embase, CINAHL, Web of Science, and Scopus were searched and screened in Covidence. Qualitative and quantitative studies of behavioral, psychosocial, and other integrative interventions for AUD were included. Extracted data included study design, sample size, intervention type, diagnosis, and outcomes.

Results: Of 4,486 records identified, 4,388 underwent title and abstract screening. Of 593 full-text articles assessed, 316 studies were included. AUD was reported in 188 studies (59.5%). Over half included a pharmacologic component alongside an integrative approach (n=164, 51.9%). The most common non-pharmacologic approaches were Alcoholics Anonymous-based programs (n=138, 43.7%), psychotherapy (n=53, 16.7%), and mindfulness programs (n=31, 9.8%). Most interventions showed mixed findings (n=145, 45.9%) or no effect (n=76, 24.0%), while about one-third reported positive effects.

Conclusion: Complementary and integrative interventions for AUD show heterogeneous effectiveness, with some approaches demonstrating potential benefit. Evidence remains inconsistent, and long-term outcomes are limited. More rigorous and standardized research is needed to identify integrative strategies that support sustained recovery.

PUBLICATIONS

Barb, J. J., Hughes, A. N., Nanda, S., Tuason, R. T. S., Wallen, G. R., & Maki, K. A. (2025). Longitudinal assessment of oral and gut microbiome overlap in patients with Alcohol Use Disorder undergoing inpatient treatment. Frontiers in cellular and infection microbiology, 15, 1681781. https://doi.org/10.3389/fcimb.2025.1681781

Barb, J. J., King, L. C., Nanda, S., Barnett, D., Darcey, V. L., Yang, S., Turner, S., Ahmed, A., Maki, K. A., Vizioli, C., Butera, G., Farokhnia, M., Wallen, G. R., & Leggio, L. (2026). Dietary intake, quality, and assessment tools in individuals with problematic alcohol use: a scoping review and meta-analysis. Translational psychiatry, 16(1), 51. https://doi.org/10.1038/s41398-026-03842-9

Nanda, S., Roberts, A., Butera, G., Barnett, D., Wallen, G. R., & Barb, J. J. (2025). Assessing Holistic Health Interventions and Approaches for Individuals with Alcohol Use Disorder (AUD): Protocol for a Scoping Review. medRxiv : the preprint server for health sciences, 2025.06.04.25328277. https://doi.org/10.1101/2025.06.04.25328277

AWARDS

People's Favorite: CCND Nursing Week Poster Day 2025

Morin Nessim - *Translational Biobehavioral and Health Promotion Branch*

CHARACTERIZATION OF RYR1 VARIANTS IN CONGENITAL MYOPATHY ZEBRAFISH MODELS

ABSTRACT

Variants in the ryanodine receptor 1 gene (RyR1) are a major cause of congenital myopathies. However, many RyR1 variants are classified as variants of unknown significance (VUS) limiting clinical implications. Zebrafish are a good model for neuromuscular disease studies as they have optically transparent larvae and have fast and slow twitch muscle fibers that are spatially segregated. The primary objective of this project is to functionally characterize clinically relevant RyR1 variants utilizing zebrafish and to determine its effects on muscle performance and calcium transport. Using base editing and prime editing, we generated a pathogenic variant, I4898T, and two variants of unknown significance, C2233R and P4642L. To characterize the variants, we performed a touch behavioral assay and calcium imaging to test if muscle function is impaired. The I4898T variant demonstrated significant impairment in both touch-evoked response assay and calcium imaging analysis. The C2233R variant similarly demonstrated impaired performance in the touch-evoked response assay, with calcium imaging analysis currently underway. We are also actively characterizing the P4642L variant to further define its functional impact. These findings demonstrate that zebrafish models can detect functional consequences of RyR1 VUS through behavioral and calcium imaging assays. This platform provides a translational tool to aid in the classification of RyR1 variants and improve understanding of genotype–phenotype relationships in congenital myopathies.

BIOLOGICAL MECHANISMS UNDERLYING METABOLIC, MICROBIAL AND IMMUNOLOGICAL ALTERATIONS ASSOCIATED WITH ULTRA-PROCESSED FOOD ADDITIVES: A REVIEW OF THE LITERATURE

ABSTRACT

Ultra-processed food (UPF) consumption is associated with increased chronic disease risk, though underlying biological mechanisms remain unclear. We synthesized mechanistic evidence from eleven preclinical and translational studies examining how UPF additives influence gut microbial composition, metabolic function, and inflammation. Studies were identified through targeted literature searches and selected based on relevance to microbial and metabolic outcomes. Full texts were systematically reviewed to extract data on UPF additives, microbial composition, diversity metrics, metabolites, and inflammatory biomarkers. Extracted features were tabulated and summarized using JMP to identify consistent patterns across studies. Additive exposure was associated with changes in alpha diversity, defined as the richness and evenness of microbial species within a sample. Emulsifiers showed the most consistent effects, including reduced gut microbiome alpha diversity compared with controls. Additives also shifted the relative abundance of key bacterial taxa, indicating disruption of microbial community structure. These compositional changes were accompanied by functional alterations in microbial metabolism, with emulsifier exposure consistently linked to reduced short-chain fatty acid production. Seven studies reported downstream effects on host immune responses, including impaired intestinal barrier integrity, microbial encroachment into the gastrointestinal mucus layer, and induction of low-grade intestinal inflammation. The findings suggest additives may drive pro-inflammatory responses via the microbiome. The results support a mechanistic model in which UPF additives alter the gut microbiome, leading to shifts in microbial composition and subsequent functional and metabolic changes. This synthesis also informs ongoing multi-omic analyses from a recently completed inpatient UPF feeding trial examining metabolic and microbial determinants of dietary-associated disease risk.

PUBLICATIONS

Maki, K. A., Yang, L., Farmer, N., Papneja, S., Wallen, G. R., & Barb, J. J. (2025). Sleep regularity and duration are associated with depression severity in a nationally representative United States sample. Neurobiology of sleep and circadian rhythms, 19, 100133. https://doi.org/10.1016/j.nbscr.2025.100133

Maki, K. A., Xu, S., Wallen, G. R., Gerrard, C., Sung, C., Papneja, S., Tuason, R. T. S., Ramchandani, V. A., Diazgranados, N., & Barb, J. J. (2025). Associations between oral health behaviours, oral health, salivary biomarkers and clinical phenotype in individuals with alcohol use disorder: protocol for a longitudinal observational study. BMJ open, 15(12), e101197. https://doi.org/10.1136/bmjopen-2025-101197

Maki, K. A., Barb, J. J., Xu, S., Papneja, S., Alkhatib, J., Butera, G., & Wallen, G. R. (2026). From alpha diversity to zeitgebers: Functional implications and potential mechanisms linking the gut microbiome to sleep and circadian disruption (Part II). Neuroscience and biobehavioral reviews, 184, 106609. https://doi.org/10.1016/j.neubiorev.2026.106609

Isha Patel - *Critical Care Medicine Department*

ENDOTHELIAL SENESCENCE IN COVID-19 VASCULOPATHY USING A PULMONARY ARTERY-ON-A-CHIP MODEL

ABSTRACT

Background: COVID-19 complications include ARDS, shock, and thrombotic angiopathy. Endothelial injury contributes to disease pathogenesis and likely increases risk of cardiovascular disease among survivors. Human pulmonary artery endothelial cell (PAEC) senescence, an inflammatory, prothrombotic phenotype, was investigated in vitro after challenge with SARS-CoV-2 recombinant proteins. However, more physiologically relevant in-vitro models with multiple cell types are needed to clarify mechanisms of endothelial dysfunction and cell-cell interactions.

Methods: 2D cultured-PAECs were exposed to SARS-CoV-2 S1 spike protein (100 ng/mL, 24h) and evaluated for γH2AX expression, a marker of DNA damage and senescence. Next, to establish a physiologically relevant in vitro pulmonary artery model, we manufactured a polydimethylsiloxane (PDMS)-based microfluidic chip. Chips were loaded with PAECs, smooth muscle cells (PASMCs), and fibroblasts (NHLF), cultured, and characterized by cell specific markers using flow cytometry. SARS-CoV-2 Nucleocapsid protein (NP, 100 ng/mL, 72h) was added through the endothelial channel of the chip and Ki-67 expression, a proliferation marker decreased in senescence, was examined using flow cytometry.

Results: SARS-CoV-2 S1 protein increased γH2AX expression in the 2D PAEC culture. Sequential loading of chips was validated using Celltracker-dyed PAECs, PASMCs, and NHLF to confirm formation of interfaces between multiple cell types. Each cell type was characterized in the chip through flow cytometry. NP decreased Ki-67 expression compared to media control in all cell types in the chip.

Conclusions: SARS-CoV-2 S1 spike protein induced DNA damage in PAECs, indicating a senescent-like phenotype. NP decreased proliferation in the chip suggesting that cells are entering a senescent state after NP exposure. Viral replication, cell-cell signaling, and gene expression will be investigated in the chip before and after introducing viral proteins.

Amber Rayford - *Critical Care Medicine Department*

PHARMACOKINETIC CHARACTERIZATION OF RIBAVIRIN IN LASV-INFECTED RHESUS MACAQUES USING A VALIDATED LC-MS WORKFLOW

ABSTRACT

Lassa virus (LASV) is a single-stranded negative-sense RNA virus in the family Arenaviridae. Ribavirin remains the standard-of-care treatment for Lassa fever despite limited and conflicting clinical and preclinical data. Prior animal studies have been limited by variable dosing, timing, and routes of administration without clear correlation to current clinical practice. To address this, translational non-human primate (NHP) studies were performed to evaluate ribavirin treatment using dosing designed to approximate human ribavirin exposure.

A validated liquid chromatography–mass spectrometry workflow was used to quantify ribavirin concentrations in irradiated plasma samples. Sample preparation included perchloric acid protein precipitation, incorporation of isotopically labeled 13C5-ribavirin internal standard, and evaluation of sample handling variables relevant to high-containment workflows. Pharmacokinetic analyses demonstrated rapid plasma clearance of ribavirin ($t_{1/2}$=~0.5 hr) despite achievement of target peak concentrations >100 ng/µL, supporting prior reports suggesting limited sustained plasma exposure during treatment. A 150 mg/kg loading dose most closely replicated clinically observed time above EC50. Shipment and irradiation required for high-containment sample handling did not significantly affect measured ribavirin concentrations.

Longitudinal analyses in LASV-infected NHPs demonstrated achievement of peak ribavirin concentrations above EC50 and EC90 comparable to human clinical data, although trough concentrations remained consistently lower. Increasing cumulative ribavirin exposure was strongly associated with progressive hemoglobin decline consistent with clinically significant hemolytic anemia. Collectively, these findings demonstrate that clinically relevant ribavirin exposure can be modeled in NHPs while highlighting the limited sustained plasma exposure and dose-limiting toxicity associated with treatment.

Anna Roberts - *Translational Biobehavioral and Health Promotion Branch*

STRESS EXPOSURE AND SLEEP DEPRIVATION IN A PRECLINICAL MODEL: GUT MICROBIOME AND METABOLITE PATHWAYS LINKED TO COGNITIVE OUTCOMES

ABSTRACT

Introduction: Military service members exposed to combat-related stressors frequently experience sleep deprivation (SD), associated with impaired cognition and potential neurobiological and gut–brain mechanisms. While stress alters microbiome composition, functional pathways remain unclear. This multi-omics study is part of the DARPA-funded SOMNUS initiative in collaboration with Washington State University–Spokane and Walter Reed Army Institute of Research, focused on identifying gut–brain microbial and metabolite pathways underlying cognition in a preclinical model with low and high stress burdens. Methods: Adult Sprague Dawley rats were randomized to control or 12-hour SD via low-stress gentle handling (GHSD) or high-stress rotary bar (RBSD) (n=12/group; N=36). Jejunoileal samples were collected post-SD and underwent shotgun metagenomic sequencing (Illumina NovaSeq). Taxonomic and functional profiling used bioBakery; neuroactive and metabolic potential were quantified with gut–brain (GBM) and gut–metabolite (GMM) modules (Omixer-RPM). Group differences were analyzed using generalized linear models with multiple comparisons correction. Results: GBM/GMM analyses showed stress-dependent functional differences. Twelve GBM pathways significantly (p-adj ≤0.05) differed from controls in both SD models, including inositol synthesis (GHSD: β=4.3; RBSD: β=4.03), DOPAC synthesis (GHSD: β=-2.08; RBSD: β=-2.5), glutamate synthesis I (GHSD: β=3.2; RBSD: β=3.0), ClpB (GHSD: β=2.8; RBSD: β=2.6), and tryptophan synthesis (GHSD: β=2.9; RBSD: β=2.5). Isovaleric acid synthesis II (β=2.3) was unique to GHSD; dopamine degradation (β=-1.45) to RBSD. GMM analysis identified three pathways altered only in GHSD: aspartate degradation II (β=3.9), arabinoxylan degradation (β=4.4), and lactate consumption I (β=-3.9). Conclusions: GHSD and RBSD induce gut microbial functional shifts relevant to gut–brain signaling. Ongoing work tests associations with host pathophysiology (e.g., intestinal permeability) and neurocognitive outcomes.

PUBLICATIONS

Barb, J. J., Yang, L., Martinez-Steele, E., Ahmed, A., Medina, P. V., Valencia, E. M., Roberts, A. E., Farmer, N., & Wallen, G. R. (2025). Consumption of ultra-processed foods by foreign-born adults rise with increased levels of acculturation in the United States. Frontiers in public health, 13, 1570832. https://doi.org/10.3389/fpubh.2025.1570832

Nanda, S., Roberts, A., Butera, G., Barnett, D., Wallen, G. R., & Barb, J. J. (2025). Assessing Holistic Health Interventions and Approaches for Individuals with Alcohol Use Disorder (AUD): Protocol for a Scoping Review. medRxiv : the preprint server for health sciences, 2025.06.04.25328277. https://doi.org/10.1101/2025.06.04.25328277

Wallen, G. R., Hughes, A. N., Roberts, A. E., Tuason, R. T. S., Ahmed, A., Maki, K. A., & Barb, J. J. (2026). Examining circadian rhythm dysregulation using actigraphy among treatment-seeking individuals with alcohol use disorder. Frontiers in neuroscience, 20, 1803129. https://doi.org/10.3389/fnins.2026.1803129

AWARDS

Outstanding Abstract Award for 2026 Nurses Week Poster Day 2026
Outstanding Poster Award for NIH PostBac Poster Day 2025

Molly Ruebusch - *Department of Pediatrics*

GENOTYPE-PHENOTYPE CORRELATIONS IN PEDIATRIC CUSHING'S SYNDROME

ABSTRACT

Pediatric Cushing's syndrome (CS) is a rare but severe disorder characterized by prolonged exposure to supraphysiological glucocorticoid (GC) levels during critical periods of growth and metabolic development. Despite well-established biochemical diagnostic criteria, considerable heterogeneity exists in adiposity, metabolic outcomes, and neurocognitive function that is not fully explained by cortisol burden or disease etiology alone. The glucocorticoid receptor and other components of cortisol metabolism pathways play key roles in mediating tissue-specific GC sensitivity, and common functional single nucleotide polymorphisms (SNPs) in these genes have been associated with variable glucocorticoid responsiveness. In children with endogenous CS, such genetic variants may influence tissue-level responses to cortisol and contribute to clinically significant phenotypic variability. We aim to investigate whether inherited variation in glucocorticoid signaling pathways modifies susceptibility to cortisol-induced metabolic complications, including type 2 diabetes mellitus (T2DM), altered BMI, insulin resistance, and changes in body composition. Additionally, we will characterize the frequency of selected functional polymorphisms in glucocorticoid pathway genes and evaluate their association with phenotypic stratification in a pediatric CS cohort.

Mayra Saintilus - *Translational Biobehavioral and Health Promotion Branch*

CHARACTERIZATION OF RYR1 IN HEK293 CELLS

ABSTRACT

Mutations in the Ryanodine Receptor 1 (RyR1) channel cause severe neuromuscular disorders, including Malignant Hyperthermia and Central Core Disease. The rapid expansion of clinical genetic testing has identified numerous RyR1 Variants of Unknown Significance (VUS), necessitating robust in vitro platforms for functional validation. Characterizing these variants is technically challenging due to the massive size of the RyR1 open reading frame (~15kb); standard site-directed mutagenesis on the full-length ~20kb expression plasmid is highly inefficient and prone to secondary errors. Furthermore, random integration of these large constructs into host cells yields variable expression levels, confounding functional comparisons.

To overcome these limitations, we developed a modular, high-fidelity cloning and expression pipeline. The wild-type RyR1 gene was divided into three manageable ~5kb cassettes within pBSL shuttle vectors. Using this system, we performed targeted mutagenesis on the isolated C-terminal cassette to rapidly engineer the novel VUS P4641L (homologous to human P4642L). Following sequence verification, the mutated cassette was directionally subcloned into the pcDNA5/FRT backbone to assemble the full-length mutant expression vector. This construct will be integrated into host HEK293 cells via the Flp-In recombination system, ensuring single-copy, site-specific integration. By establishing these isogenic cell lines, we guarantee uniform RyR1 protein expression. Subsequent single-cell calcium imaging will compare the P4641L variant against wild-type and pathogenic controls, providing definitive functional evidence to resolve its clinical classification.

Jason Simon - *Department of Laboratory Medicine*

THE CLEAN-MED DIET STUDY

ABSTRACT

During my time as a post baccalaureate fellow at the Clinical Center, I have contributed to the Clean-MED Diet Study, a clinical research trial assessing the effects of a minimally processed, Mediterranean-like diet on the gut microbiome and overall health. Volunteer enrollment began in September 2022 and closed in February 2026. During the volunteer enrollment phase, my responsibilities included interacting with the clinical team, processing blood, urine, and stool samples for future analysis, entering food logs into the Nutrition Data System for Research database (NDSR), entering surveys into the REDCap database, assembling sample collection kits and mailing them to participants. Over this time, I ensured that all necessary samples and data were collected during the weekly or monthly patient visits, and I input hundreds of food logs into the NDSR database.

Since the close of enrollment for the Clean-MED study, I have been helping with data organization and analysis. I have reviewed hundreds of food logs for compliance with study rules and identification of ultra-processed foods using photos submitted by volunteers. I have also scored physical activity questionnaires from volunteers in our short-term cohort. I have also presented at the Clinical Center Three-Minute Talk Competition on a unique method for classifying ultra-processed foods for research, and Post Bac Poster Day using preliminary data on the short-term effects of the diet on cardiovascular markers and the gut microbiome. In June 2026, I will be presenting a poster and rapid-fire talk at the American Society for Microbiology (ASM) Conference in Washington D.C.

This study is highly dynamic, and I regularly interact with team members both inside and outside of my department who are associate investigators with expertise in various areas of the research. We aim to complete the first high-impact publication, which will focus on data from the short-term cohort, for submission in February 2027.

Callista Smith - *Rehabilitation Medicine Department*

ESTABLISHING MINIMAL CLINICALLY IMPORTANT DIFFERENCE OF THE MOTOR FUNCTION MEASURE IN CHILDREN WITH GIANT AXONAL NEUROPATHY

ABSTRACT

Purpose: Calculate minimal score change on the Motor Function Measure (MFM-32) reflecting meaningful quality-of-life change for people with Giant Axonal Neuropathy (GAN). GAN: rare genetic neurodegenerative disease, starts early childhood, progressive peripheral neuropathy, CNS involvement, motor function loss, early adult mortality. MFM-32 is a motor assessment validated for neuromuscular disease. No GAN-specific minimal clinically important difference (MCID) exists to connect objective score change to a patient's perception of relevant functional change.
Subjects: 23 (age: 6-21y; M=8)

Methods: Retrospective review of GAN natural history study (NCT:01568658). Inclusion required ≥2 MFM-32 visits and parent proxy question completed. At follow-up visits, parents reported perceived change in participant's strength since their last MFM-32. Score changes grouped by perceived stability or progression. Linear mixed effects models accounted for repeated measures-6 participants had 3 visits. MCID calculated as mean score change within participants in the progression group and difference in mean change in progression and stability groups.
Results: Mean change in MFM-32 score in the progression group was -8.98 (SE=1.29) and -0.83 (SE=2.83) in the stability group. MCID is estimated as 8.98 within group and 8.15 between groups. No participant reported improved strength.

Conclusion: MFM-32 score change ≥8.98 or 8.15 points may translate to perceived changes in quality of life. Small samples and progressive decline complicate MCID calculation in rare neurodegenerative diseases; however, MCID links score changes to life impact.

Relevance: MCID is a valuable tool to link outcome measures to changes in daily function meaningful to a patient. Finding MCID establishes objective goals. For diseases like GAN, it's crucial to demonstrate MCID is attainable even with few patients/no improvement group, as it helps focus interventions on benefits meaningful to a patient.

Leah Stahr - *Critical Care Medicine Department*

DEVELOPMENT OF A DDPCR MULTIPLEX PANEL FOR NEUROINVASIVE ARBOVIRAL TARGET DETECTION

ABSTRACT

Arboviruses are viral pathogens transmitted through the bites of an arthropod vector. Many arboviruses endemic to the United States overlap in clinical presentations, with severe cases leading to neuroinvasive disease. Changes to vector behavior due to climate- and anthropogenic-related factors are increasing infection risks, emphasizing the need for fast and reliable diagnostics for arboviral disease. Common methods of diagnosis such as serologic tests suffer from antibody cross-reactivity leading to false-positive results and molecular diagnostics including RT-PCR are often not available. Droplet digital PCR (ddPCR) provides high sensitivity for low-abundance targets and can be multiplexed to detect multiple pathogens. We propose that a ddPCR multiplex panel can provide a sensitive diagnostic test for neuroinvasive arboviral infections. Our design includes a primer-probe multiplex set against the six most common US-endemic neuroinvasive arboviruses: West Nile Virus (WNV), St. Louis Encephalitis Virus (SLEV), Powassan Virus (POWV), La Crosse Virus (LACV), Jamestown Canyon Virus (JCV), and Eastern Equine Encephalitis Virus (EEEV). For design, conserved regions on the following viral gene targets were selected: NS2A, E, NS5, G2, G1, and NSP2. Preliminary validation results for JCV, LACV, and WNV primer-probe sets show target amplification for JCV and LACV, with an optimal annealing temperature around 57-58°C, and inadequate amplification for WNV, indicating potential problems with binding specificity. Next steps include testing positive arboviral controls in combination with different target primer-probes to further test specificity, while confirming an optimal annealing temperature for the rest of the panel once appropriate positive controls are acquired. Individual primer-probe redesign will also be completed if a primer-probe fails to display specific and sensitive binding.

Austin Wang - *Rehabilitation Medicine Department*

DESIGN OF 3D-PRINTED GENERALIZED ORTHOTIC SHELLS FOR UBIQUITOUS EXOSKELETON USE IN CHILDREN

ABSTRACT

Cerebral palsy (CP) is the most prevalent childhood physical disability, with crouch gait as a common symptom. Excessive knee flexion in crouch gait makes walking more difficult, which results in 50% of children with CP losing the ability to walk completely as adults. Exoskeletons are a possible therapy but have only been clinically validated on treadmills and in level overground walking. There is a need to translate exoskeletons to ubiquitous environments; to pursue this, a new protocol was designed to investigate exoskeleton controller performance in novel mobility tasks like stair and ramp navigation. However, current clinical exoskeletons use custom-made orthotic shells, which are time-consuming and expensive, and do not allow placement of wearable sensors on the legs, which are needed to conduct biomechanical analysis to evaluate and validate controllers.

A 3D-scan of an adult male leg was obtained from the NIH 3D Database and imported into Autodesk Meshmixer for design prototyping. Prototypes were then 3D-printed. CDC reference data and measurements from a previous study (IRB001180) were used as parameters to create generalizable shells in SOLIDWORKS.

3D-Printing enabled rapid prototyping of orthotic shells to converge on a suitable design for proper sensor access and comfort, which was then parameterized with three clinical anthropometric measurements: mid-thigh circumference, maximum calf circumference, and upper leg length.

Current selection of target parameters is not optimal as calf anatomical variations are not captured. Moreover, other parameters such as print infill density and print material change shell properties, affecting fit and comfort. However, the process to generalize shells is robust; process validation in the target patient population may yield more optimal parameter selections. The long-term goal of this system is to have multiple cuff sizes such that the entire study population is accommodated without personalized orthotic shells.

Ti-Shawn Wellington - *Critical Care Medicine Department*

LONGITUDINAL ABUNDANCE OF PLASMA PROTEINS FROM A NONHUMAN PRIMATE MODEL OF EBOLA VIRUS DISEASE

ABSTRACT

Ebola virus disease (EVD) patients typically present during critical illness when antiviral therapies show reduced efficacy. To investigate the host immune response and ultimately test immune-targeted therapies during severe EVD, we previously developed a nonhuman primate model with a therapeutic window during severe illness. Three rhesus macaques infected with 1 PFU EBOV developed disease onset on day 6, critical illness on day 7, and met euthanasia criteria on day 10. We measured relative (NPX) and absolute abundance (pg/mL) of 89 proteins longitudinally using Olink Target 48 cytokine and immune surveillance proximity extension panel assays on irradiated plasma (due to biosafety). Longitudinal changes were evaluated using linear mixed-effects models (LMM) with false discovery rate (FDR) correction. We determined that irradiation did not impact the validity of the assay. Principal component analysis revealed that the proteins on days 7 and 10 clustered separately from earlier timepoints, indicating distinct disease phases. On days 3-5 (pre-clinical illness), 10 proteins including IL6, CXCL8, IL7, and HGF decreased compared to baseline. By day 7 (critical illness onset), 21 analytes increased when heart rate and body temperature elevated. By day 10 (when animals met endpoint criteria), 73 of 89 proteins showed increased abundance, with only EGF consistently decreasing. These findings reveal distinct immune profile phases during EVD progression. Next, we will explore cellular and molecular mechanisms underlying dynamic early and late plasma proteome changes to guide therapeutic intervention.

Joel Wilkinson - *Department of Transfusion Medicine*

PERSPECTIVES RELATED TO INDIVIDUAL DONOR ASSESSMENT FOR BLOOD DONORS

ABSTRACT

In May 2023, the Food and Drug Administration (FDA) removed the requirement to defer men who have sex with men (MSM) and women who had sex with MSM (WMSM) from donating blood in the United States. The revised guidance, Individual Donor Assessment (IDA), recommends that screening questions be applied universally, regardless of donor sex, and adds new questions about sexual partners and anal sex. Since perceptions of blood donor eligibility policies may affect overall willingness to donate blood, we sought to evaluate public perspectives on the shift in policy. Between June 2024 and January 2025, we recruited participants in the Washington, D.C. metropolitan area to complete a 20-question, self-administered online survey including questions about blood donation history, attitudes towards the previous MSM deferral policy and the elements of the new IDA policy. Of 512 completed responses, most respondents were Caucasian (70.16%), female (55.8%) and had previously donated blood (88.76%). Most participants (80.7%) believed that gay and bisexual men were excluded from donating blood, which negatively affected donation practices for 36 respondents. Overall, 449 (87.7%) of participants supported the change to IDA primarily for the reduced stigmatization of gay and bisexual men (327, 63.87%). Only 51 (10.0%) respondents opposed IDA, with some concern about invasive or sexually shaming questions (37, 7.22%). Respondents expressed an overall positive perception of the shift to IDA as a means of safely maximizing the donor pool. Public perception of this policy change may favorably affect the sustainability of the blood supply.

PUBLICATIONS

Wilkinson J., Pogue S., West-Mitchell K. (2024). Blood Donor Attitudes Regarding the Changes to Individual Donor Assessment. 2024 Poster Information. Transfusion, 64: 9A-334A. P-PH-2. https://doi.org/10.1111/trf.18002

AWARDS

2024 NIH Postbac Poster Day Winner

METHODOLOGICAL CONSIDERATIONS IN SALIVA-BASED BIOMARKER RESEARCH: ADDRESSING PATIENT-SPECIFIC VARIABILITY IN TRANSLATIONAL RESEARCH PROTOCOLS

ABSTRACT

Saliva plays a central role in maintaining oral homeostasis by supporting tooth integrity, providing lubrication, and functioning as an antimicrobial wash. It also serves as a transport medium, carrying byproducts and signaling metabolites across oral niches and through the gastrointestinal tract. Because of its biological relevance and ease of collection, saliva is increasingly used as a noninvasive biospecimen for measuring cortisol, cytokines, and metabolites. However, the validity and reliability of saliva as an indicator of local and systemic biomarkers remain under investigation across diverse populations and research applications. Specific patient populations (e.g., individuals with alcohol use disorder) are particularly vulnerable to oral health problems, periodontal disease, and high rates of nicotine use. In addition to behavioral factors (e.g., food, drink, toothbrushing, and mouthwash), patient-specific variables can introduce contaminants such as nicotine and blood into saliva, potentially compromising the accurate measurement of analytes of interest. Protocols that account for possible contaminants are essential to ensure rigorous and reproducible biomarker research. Assessing factors such as pH, flow rate, and visible discoloration helps reduce limitations in analysis and improves interpretation in studies that include heterogeneous populations and health behaviors. Yet, the literature provides limited guidance on standardized methods for saliva collection, processing, and measurement of patient-specific confounders alongside analytes of interest. This protocol addresses these gaps by presenting detailed methodologies for saliva collection and processing, assessment of quantitative and qualitative salivary properties, and quantification of patient-specific modifiers. These approaches support reproducible diagnostics and have applications in populations with high rates of smoking, periodontal disease, and alcohol use.

PUBLICATIONS

Xu, S., Mumuni, A. N., Tuason, R. T. S., & Maki, K. A. (2025). Methodological Considerations in Saliva-Based Biomarker Research: Addressing Patient-Specific Variability in Translational Research Protocols. Current protocols, 5(10), e70235. https://doi.org/10.1002/cpz1.70235

Maki, K. A., Xu, S., Wallen, G. R., Gerrard, C., Sung, C., Papneja, S., Tuason, R. T. S., Ramchandani, V. A., Diazgranados, N., & Barb, J. J. (2025). Associations between oral health behaviours, oral health, salivary biomarkers and clinical phenotype in individuals with alcohol use disorder: protocol for a longitudinal observational study. BMJ open, 15(12), e101197. https://doi.org/10.1136/bmjopen-2025-101197

Maki, K. A., Barb, J. J., Xu, S., Papneja, S., Alkhatib, J., Butera, G., & Wallen, G. R. (2026). From alpha diversity to zeitgebers: Functional implications and potential mechanisms linking the gut microbiome to sleep and circadian disruption (Part II). Neuroscience and biobehavioral reviews, 184, 106609. https://doi.org/10.1016/j.neubiorev.2026.106609

Victoria Yang - *Department of Perioperative Medicine*

RED BLOOD CELL DEFORMABILITY IN MICE WITH SICKLE CELL DISEASE AND CO-INHERITANCE OF PK DEFICIENCY

ABSTRACT

Growing evidence indicates that PKLR, the gene that encodes pyruvate kinase (PK), is a genetic modifier of the sickle cell phenotype. Co-inheritance of specific PKLR variants is associated with increased pain-related hospitalization rates and can trigger sickle cell disease (SCD) phenotypes in asymptomatic carriers. PK deficiency disrupts RBC glycolysis, leading to ATP deficits and accumulation of 2,3-diphosphoglycerate, which exacerbates sickling in SCD. Using CRISPR-Cas9, we generated null mutations in Pklr [Pklr(13ntdel/13ntdel) or Pklr(246ntdel/246ntdel)] specific for the RBC isoform (PKR) in Townes mice that were homozygous (SS) or heterozygous (AS) for the human sickle globin gene, or homozygous for human hemoglobin A (AA, controls), to investigate the effect of PKR deficiency on the sickle phenotype in mice. We have shown that PKR-deficient AA and AS mice developed severe anemia, reticulocytosis, and substantial spleen and liver iron deposits. Unlike what is observed in humans, PKR-deficiency in AS and SS mice surprisingly decreased sickling, but it was also associated with increased extramedullary hematopoiesis and mitochondrial retention in mature RBCs. These results demonstrate the differential effect of Pklr mutations on the phenotype of both AS and SS mouse models, offering new insights into the complex role of PKR deficiency in SCD pathology. WE are now examining the effect of PK deficiency on deformability of RBC in these animals

Jenny Yarmovsky- *Translational Biobehavioral and Health Promotion Branch*

STRESS EXPOSURE AND SLEEP DEPRIVATION IN A PRECLINICAL MODEL: GUT MICROBIOME AND METABOLITE PATHWAYS LINKED TO COGNITIVE OUTCOMES

ABSTRACT

The gut microbiome is a key contributor to human health and a central component of the gut–brain axis, a bidirectional communication network between the gastrointestinal tract and the central nervous system. Dysbiosis has been associated with metabolic, inflammatory, and neuropsychiatric disorders, highlighting its role in host regulation. Shotgun metagenomic sequencing enables high-resolution profiling of microbial communities at both taxonomic and functional levels, making robust bioinformatics pipelines essential for accurately characterizing microbiome composition. When developing such workflows, several factors must be considered, including methodological approach (e.g., taxonomic vs. functional; read-based vs. assembly-based), computational requirements, and expected outputs. Workflow selection should align with study objectives, desired resolution, and user expertise. The aim of this project is to establish reproducible and robust bioinformatics pipelines that can be applied to both preclinical and clinical research with the outcome of creating a reliable microbiome profiling interpretation of the gut–brain axis.

Three-Minute Talk Competition

THE POSTBAC WINNERS

The Office of Clinical Research Training and Medical Education sponsored the inaugural Three-Minute Talk Competition for Clinical Center trainees on Aprill 22, 2026. This competition provided the Clinical Center community the opportunity to learn more about the research being conducted by trainees. CC TMT finalists/winners are entered into the NIH IRP TMT Competition held in June.

Grace Monette – 1st Place
Title: Heart or Muscle: What Limits Aerobic Capacity in RYR1 Myopathies?
Department: Rehabilitation Medicine Department

Samuel Degenhard – 2nd Place
Title: Using the PERMA Model of Well-being as a Conceptual Framework to Understand the Potential Role of Cooking in Psychiatric Treatment
Department: Translational Biobehavioral and Health Promotion Branch

TMT POSTBAC PARTICIPANTS

Brynn Conrad
Title: Radiolabeled Fragment Antibodies as PET Tracers for Invasive Mucormycosis
Department: Radiology and Imaging Sciences Department

Djaina-Shae Dervil
Title: A Scoping Review of Neuroimaging and Cooking
Department: Translational Biobehavioral and Health Promotion Branch

Clare Howard
Title: Assessing Accuracy and Reliability of Research and Diagnostic Tests in Translational Research
Department: Department of Transfusion Medicine

Arushi Kotru
Title: Assessing Postural Limits of Stability and Gait in Traumatic Brain Injury
Department: Rehabilitation Medicine Department

Mattias Lenz
Title: Using BCR Repertoire Analysis to Uncover Mechanisms of HCV-Associated B Cell Lymphoma
Department: Department of Transfusion Medicine

Shubi Nanda
Title: Exploring Diet Quality and Ultra-Processed Food (UPF) Intake Among Adults with Colorectal Cancer and their Spouses
Department: Translational Biobehavioral and Health Promotion Branch

Morin Nessim
Title: Characterization of RYR1 Variants in Congenital Myopathy Zebrafish Models
Department: Translational Biobehavioral and Health Promotion Branch

Mayra Saintilus
Title: Characterization of RYR1 Variants in HEK293 Cells
Department: Translational Biobehavioral and Health Promotion Branch

Jason Simon
Title: Ultra-Processed Foods Classified by Ingredient Label
Department: Department of Laboratory Medicine

Isabelle Yaremenko
Title: CD36 Regulates Adenoviral Transduction In Vitro and In Vivo
Department: Department of Laboratory Medicine

Jenny Yarmovsky
Title: Staying the course: Outpatient treatment predictors for Alcohol Use Disorder
Department: Translational Biobehavioral and Health Promotion Branch