two years immediately after PD diagnosis is high and warrants the initiation of early fall and fracture prevention strategies, in addition to aggressive treatment of PD symptoms by all providers caring for patients with PD.

56

Positive SARS-CoV-2 symptomatology despite persistently negative molecular testing: Insights from a Multicenter Household Transmission Study

Allison Chan[1], James D. Chappell[1], Sarah E. Smith-Jeffcoat[2], Alexandra M. Mellis[2], Melissa A. Rolfes[2], Yuwei Zhu[1], Theresa Scott[1], Melissa S. Stockwell[3], Yvonne Maldonado[4], Huong Nguyen[5], Karen Lutrick[6], Natalie M. Bowman[7], Suchitra Rao[8], Edwin J. Asturias[8], Katherine D. Ellingson[6], Adam S. Lauring[9], H. Keipp Talbot[1], Carlos G. Grijalva[1] and Jonathan Schmitz[1]
[1]Vanderbilt University Medical Center, Nashville, TN; [2]Centers for Disease Control and Prevention, Atlanta, GA; [3]Columbia University, New York, NY; [4]Stanford University, Palo Alto, CA; [5]Marshfield Clinic Research Institute, Marshfield, WI; [6]University of Arizona, Tucson, AZ; [7]University of North Carolina, Chapel Hill, NC; [8]Children's Hospital Colorado, Aurora, CO and [9]University of Michigan, Ann Arbor, MI

OBJECTIVES/GOALS: We describe the prevalence of individuals with household exposure to SARS-CoV-2, who subsequently report symptoms consistent with COVID-19, while having PCR results persistently negative for SARS-CoV-2 (S[+]/P[-]). We assess whether paired serology can assist in identifying the true infection status of such individuals. METHODS/STUDY POPULATION: In a multicenter household transmission study, index patients with SARS-CoV-2 were identified and enrolled together with their household contacts within 1 week of index's illness onset. For 10 consecutive days, enrolled individuals provided daily symptom diaries and nasal specimens for polymerase chain reaction (PCR). Contacts were categorized into 4 groups based on presence of symptoms (S[+/-]) and PCR positivity (P[+/-]). Acute and convalescent blood specimens from these individuals (30 days apart) were subjected to quantitative serologic analysis for SARS-CoV-2 anti-nucleocapsid, spike, and receptor-binding domain antibodies. The antibody change in S[+]/P[-] individuals was assessed by thresholds derived from receiver operating characteristic (ROC) analysis of S[+]/P[+] (infected) versusS[-]/P[-] (uninfected). RESULTS/ANTICIPATED RESULTS: Among 1,433 contacts, 67% had ≥1 SARS-CoV-2 PCR[+] result, while 33% remained PCR[-]. Among the latter, 55% (n = 263) reported symptoms for at least 1 day, most commonly congestion (63%), fatigue (63%), headache (62%), cough (59%), and sore throat (50%). A history of both previous infection and vaccination was present in 37% of S[+]/P[-] individuals, 38% of S[-]/P[-], and 21% of S[+]/P[+] ($P<0.05$). Vaccination alone was present in 37%, 41%, and 52%, respectively. ROC analyses of paired serologic testing of S[+]/P[+] (n = 354) vs. S[-]/P[-] (n = 103) individuals found anti-nucleocapsid data had the highest area under the curve (0.87). Based on the 30-day antibody change, 6.9% of S[+]/P[-] individuals demonstrated an increased convalescent antibody signal, although a similar seroresponse in 7.8% of the S[-]/P[-] group was observed. DISCUSSION/SIGNIFICANCE OF IMPACT: Reporting respiratory symptoms was common among household contacts with persistent PCR[-] results. Paired serology analyses found similar seroresponses between S[+]/P[-] and S[-]/P[-] individuals. The symptomatic-but-PCR-negative phenomenon, while frequent, is unlikely attributable to true SARS-CoV-2 infections that go missed by PCR.

57

Implementation of an analytic resource navigation process at an Academic Medical Center

Lacey Rende[1], Tracy Truong[2], Lexie Zidanyue Yang[3] and Gina-Maria Pomann[2]
[1]Duke University; [2]Biostatistics, Epidemiology, and Research Design (BERD) Methods Core, Duke University and [3]Biostatistician, Biostatistics, Epidemiology, and Research Design (BERD) Methods Core, Duke University

OBJECTIVES/GOALS: In 2018, a novel analytic resource navigation process was developed at Duke University to connect potential collaborators, leverage resources, and foster a community of quantitative researchers and scientists. We provide information about how this process works along with guidance for academic medical centers to develop similar initiatives. METHODS/STUDY POPULATION: Quantitative and qualitative scientists with expertise in data science, biostatistics, epidemiology, and related fields play a critical role in data collection, study design, analysis, interpretation, and implementation. The analytic resource navigation process connects researchers with quantitative scientists and relies on strong institutional knowledge of methodological expertise, understanding of research goals, educating researchers, and ongoing evaluation to understand unmet needs. University staff serve as navigators to help researchers identify the needed expertise, find potential collaborators, and track outcomes. Duke University's tracking system for this navigation process, implemented in 2019, underwent a nearly five-year evaluation (November 2019 – September 2024). RESULTS/ANTICIPATED RESULTS: In the nearly five-year evaluation of the process, 1247 requests from 813 unique researchers were navigated with a success rate of 93.8%. A total of 323 requests (256 unique researchers) were navigated in year 1, 285 requests (239 unique researchers) in year 2, 210 requests (179 unique researchers) in year 3, and 247 requests (192 unique researchers) in year 4. In the current year (partial year 5, 11/1/2023 – 9/18/2024), 182 requests have been navigated (159 unique researchers). Unsuccessful linkages occurred in 35 requests (2.8%) and 42 requests (3.4%) were withdrawn. Among the cases of unsuccessful navigation, 26 failed due to effort (e.g., insufficient effort available to meet the researcher's deadline), 2 failed due to lack of expertise at the institution, and 4 failed due to a lack of sufficient funding. DISCUSSION/SIGNIFICANCE OF IMPACT: The navigation process provides a critical resource for researchers who need to develop collaborations and a method for institutions to understand collaboration needs. Implementation requires training knowledgeable navigators, maintaining updated information about quantitative and qualitative methodologists, and institutional support.

58

Single-cell comparative analysis reveals a similar regulatory subpopulation in white and brown adipocyte precursors

Hoang Bui, Julia Hansen and Andrea Galmozzi
University of Wisconsin-Madison

OBJECTIVES/GOALS: The goal of this study is to resolve the complexity of the adipose precursor cells and identify potential therapeutic targets/mechanism to treat obesity, diabetes, cancer cachexia, and

https://doi.org/10.1017/cts.2024.737

related metabolic conditions in both white and brown adipose tissues. METHODS/STUDY POPULATION: White and brown adipose precursor cells were isolated from neonatal P0 mice and expanded in culture for single-cell RNA sequencing analysis. Unsupervised machine learning was used to unbiasedly cluster and categorize sequenced cells. Differentially expressed genes were used to identify populations via pathway analysis. Populations were then validated with published datasets via integration, reference mapping, and module scoring to ensure our dataset is reflective of known literature. Then, white and brown datasets were combined and unbiasedly clustered. Finally, signaling inferences using CellChat was used to identify significant signals being sent to and received from each cluster based on ligand–receptor pairs. RESULTS/ANTICIPATED RESULTS: ScRNAseq revealed 7 subclusters in both white and brown adipose tissues. Differential expression and trajectory inferences revealed that white and brown precursors develop into two distinct fates: committed adipogenic precursors (CAPs), where these cells will be mature lipid-laden adipocytes; or fibro-adipogenic precursors-like (FAPLs), where these cells preferably stay in a fibroblast-like, antiadipogenic phenotype. Integrating white and brown cells with subsequent reclustering reveals that white and brown FAPLs are highly similar to one another by being clustered together. Cell signaling inferences and pathway analysis reveal that white and brown FAPLs may participate in the regulation of adipogenesis and angiogenesis of the adipose tissue. DISCUSSION/SIGNIFICANCE OF IMPACT: Our results demonstrated that brown and white precursor cells share a common regulatory subpopulation with similar gene expression profiles, highlighting a more interconnected regulatory landscape in adipose tissue than previously understood. These findings reveal novel mechanisms of systemic metabolism and provide new therapeutic targets.

59

Does cytomegalovirus (CMV) infection contribute to social-related health disparities among cancer survivors?

Shuo Wang, Susan A. Everson-Rose, Anne H. Blaes and Anna Prizment
University of Minnesota

OBJECTIVES/GOALS: We aim to explore the associations of race/ethnicity and socioeconomic status (SES): 1) with grip strength, walking speed, and comorbidity index cross-sectionally and 2) with the change in comorbidity index and mortality risk over four years of follow-up in cancer survivors. Both aims will examine the potential mediating role of cytomegalovirus (CMV) infection. METHODS/STUDY POPULATION: This study includes 1,602 cancer survivors (mean age = 72 years, 10% Black, 54% female) from the Health and Retirement Study (HRS), a nationally representative U.S. sample followed for health outcomes until 2020. HRS measured CMV immunoglobulin G (IgG) antibody levels (from blood samples), grip strength, and walking speed in 2016. We will apply linear regression to examine the associations of race/ethnicity and SES with grip strength, walking speed, and comorbidity index cross-sectionally and with the change in comorbidity index over four years of follow-up. We will apply Cox proportional hazard regression to examine the associations of race/ethnicity and SES with mortality over four years of follow-up. In all models, we will investigate the potential mediating role of CMV infection in these associations. RESULTS/ANTICIPATED RESULTS: We expect that CMV infection mediates the associations of race/ethnicity and SES with age-related health outcomes, including muscle weakness (measured by grip strength), decreased functional performance (measured by walking speed), comorbidity index, and mortality in elderly cancer survivors. DISCUSSION/SIGNIFICANCE OF IMPACT: If our hypothesis is confirmed, the findings may inform physicians to closely monitor CMV infection among cancer survivors from socially disadvantaged groups and apply treatment if needed. Several oral medications for CMV exist, and CMV vaccines are currently undergoing testing in clinical trials. This will make the treatment for CMV more accessible.

60

Investigating sociodemographic influence on trauma exposure and neural alterations in young adults*

Abigail Bossa, Claire Marino, Caitlin Sharp, Tanya Garg, Shreya Bavdekar, Mary Halvorsen and Benjamin Suzrez-Jimenez
University of Rochester School of Medicine and Dentistry

OBJECTIVES/GOALS: This study aims to understand the prevalence of trauma in young adults and what sociodemographic factors influence trauma exposure and type of trauma. It also seeks to explore functional connectivity and neural network patterns associated with trauma by analyzing resting state magnetic resonance imaging (MRI) data. METHODS/STUDY POPULATION: Sociodemographic data will be analyzed from participants aged 18–25 years, such as age, gender, race, ethnicity, and highest level of education completed. Trauma exposure will be assessed based on the DSM-5 criteria of trauma through phone screenings and clinical interviews. The data will be categorized based on trauma type and statistical analyses will be conducted to explore potential sociodemographic patterns related to trauma. Additionally, resting-state MRI data will be utilized to identify potential neural correlates of trauma exposure. RESULTS/ANTICIPATED RESULTS: It is anticipated that sociodemographic factors such, race and ethnicity, and highest level of school completed may influence the likelihood of experiencing traumatic events. It is predicted that in the resting-state MRI analysis that there will be altered functional connectivity in trauma exposed young adults in regions such as the amygdala, hippocampus, and prefrontal cortex since those regions are implicated in emotional regulation and stress response. Some changes may also be seen in the default mode network and salience network. DISCUSSION/SIGNIFICANCE OF IMPACT: Trauma exposure can alter neural circuitry, leading to emotional processing difficulties and heightened stress response, with lasting effects on mental health and brain development. Prevention efforts and targeted treatments can be guided by identification of affected brain networks and sociodemographic factors that increase trauma risk.

https://doi.org/10.1017/cts.2024.737