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.

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

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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.

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

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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.


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