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Project Title

A comprehensive approach to quantifying chronic inflammation in older adults

Project Summary

Inflammation is a critical defence mechanism that is observed across numerous species. Not only does it signal when there is significant danger or damage to the host, it activates and sustains many of the cellular and molecular processes that ultimately act to return the organism back to its homeostatic state. Under optimal circumstances, inflammation comes and goes when needed; however, with age, these processes become dysregulated, resulting in a chronic, low-grade inflammatory state that can be disruptive to many of the fundamental biological systems needed for day-to-day life, thereby promoting poor health outcomes over time. Although regarded as a "hallmark of aging", the causes of chronic inflammation in older adults remains a mystery, partly due to our inability to properly measure it. We have shown that not only does chronic inflammation alter patterns of methylation occurring to DNA across our genome, these changes can be quantified into an exciting epigenetic measure of chronic inflammation. Although the epigenetic inflammation score (EIS) is significantly associated with sociodemographics, risky lifestyle behaviours and poor health outcomes, it does not fully reflect the complex nature of chronic inflammation. In the following proposal, our research team aims to take advantage of the richness of the Canadian Longitudinal Study on Aging (CLSA) database and develop an epigenetic signature that reflects multiple forms of chronic inflammation - protein, cellular, and metabolic. This signature will reveal new insights into the biological impact of chronic inflammation in older adults, and be used to generate a refined, comprehensive EIS. We will then validate the comprehensive EIS against sociodemographic, lifestyle and health-related traits in CLSA participants, and test for associations with longitudinal outcomes including mortality, cognitive decline, and the trajectory of frailty.

Keywords

biomarkers, cognitive decline, DNA methylation, epigenetics, frailty, inflammation, risk score