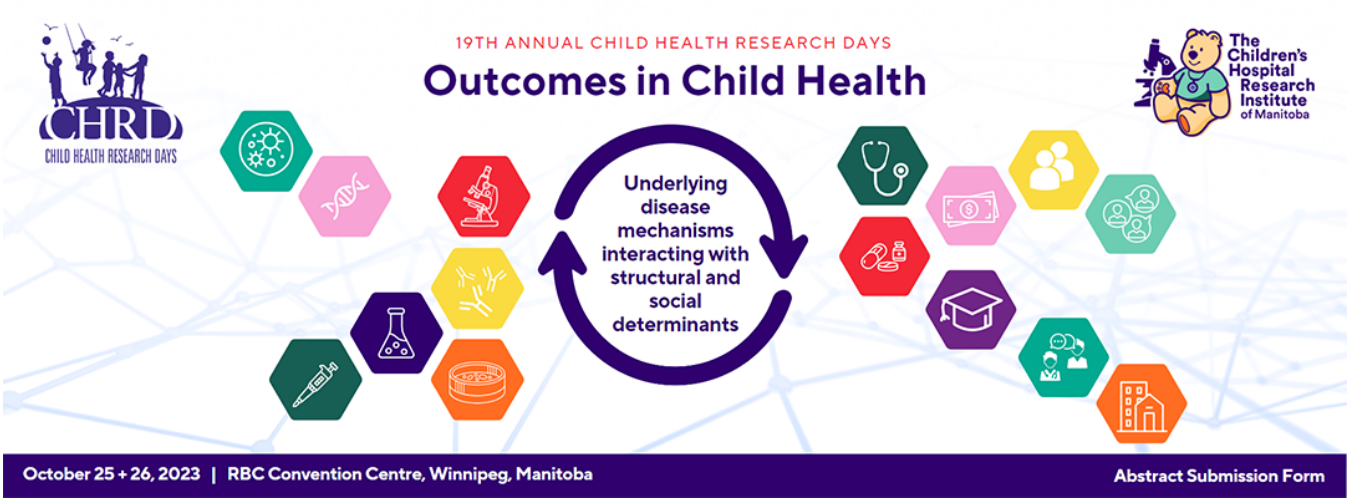

CHRD 2023: Abstract Submission Form

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Presenter Status
Masters Student

Research Category
Basic Science

Role in the project
Design
Perform Experiments
Analyze Data
Write Abstract

Title
Exploring Differences in DNA Methylation Age and Age Acceleration between High and Low CIRS Scores among Patients with Chronic Lymphocytic Leukemia

Background
Modification of methylation patterns provide a record of cellular epigenetic history, from early-life developmental events to neoplastic transformations. Identifying crucial methylation changes by Comparing the epigenetic profiles associated with poorer clinical status and better health outcomes can identify crucial DNA methylation (DNAm) changes for prognostic purposes.

Objective
We examined the differences in DNAm-predicted age between high and low comorbidity scores in both B and non-B subsets of chronic lymphocytic leukemia (CLL) blood samples.

Methods
DNA from 64 B and non-B cells were extracted and measured according to the Illumina EPIC array protocol. Covariates investigated were age, sex, smoking status, IgHV mutation status, and expression of CD38+, p53, and Zap70, and comorbidity scores based on the Cumulative Illness Rating Scale (CIRS). CLL patients with a total CIRS score of 0-5 and 6-14 were dichotomized as low and high, respectively. Different DNAm age measurements were generated using four DNAm age calculators, Horvath, Hannum, PhenoAge, and EpiTOC. The four sets of DNAm-predicted age were regressed onto chronological age while adjusting for covariates. We assessed the strength and direction of CIRS score and epigenetic age

acceleration using Spearman's ρ and two-sample t-tests.

Results
We found that all four clocks did not show significant differences in age acceleration (difference between DNAm age and chronological age) between high and low CIRS groups. Similarly, covariates associated with poor CLL outcomes did not exhibit age-acceleration differences between the two CIRS groups. However, DNAm differences between B and non-B cells were evident in all four calculators and is especially prominent in EpiTOC, which suggest B cells exhibit greater DNAm changes associated with increased mitotic division.

Conclusion
Our results show that DNAm age is not significantly better than chronological age in predicting proxy measures of frailty. Differences in age acceleration between non-B and B cells may indicate distinct mechanistic profiles warranting further exploration.

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