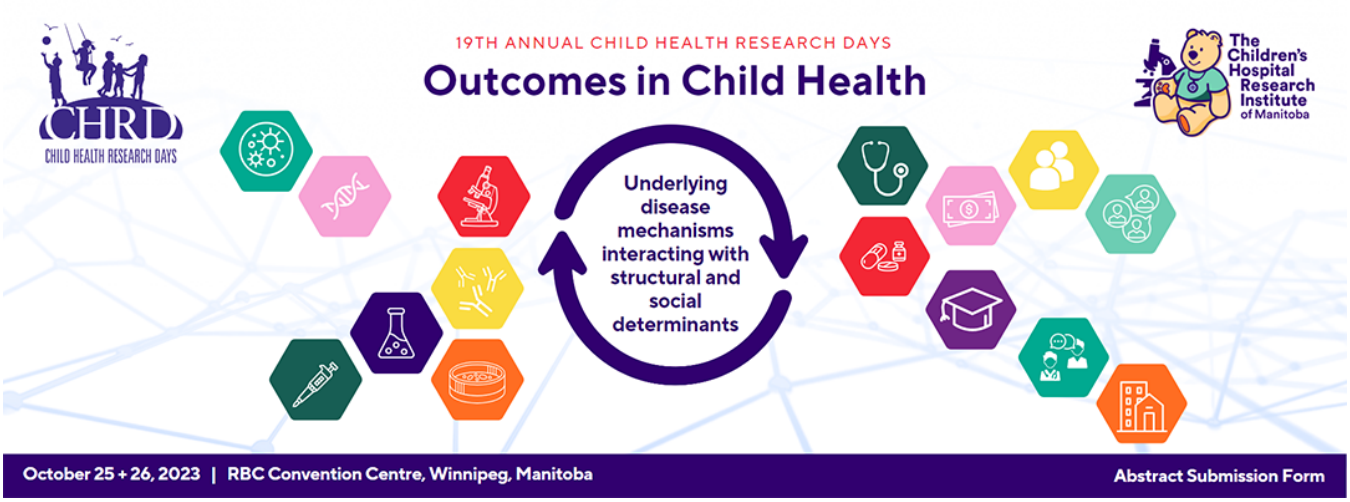

CHRD 2023: Abstract Submission Form

Submitter Name
Haziqa Kassim

Presenter Name
Haziqa Kassim

Presenter Status
Non-Trainee

Research Category
Basic Science

Role in the project
Perform Experiments
Analyze Data
Write Abstract

Title
Combined exposure of cigarette smoke and hyperglycaemia alters DNA methylation patterns in human airway smooth muscle cells.

Background
Studies suggest that early-life exposure to smoking or hyperglycaemia alters DNA methylation (DNAm) patterns and potentially increase asthma risk. However, the effect of a combinative exposure to both during early-life asthma development is not well studied. This study identifies changes in DNAm patterns within human airway smooth muscle (hASM) cells exposed to cigarette smoke extract (CSE) in low and high glucose concentrations, which simulates hyperglycaemic conditions.

Objective
We hypothesize that hyperglycaemia modifies cellular response to CSE in hASM cells by in part by altering DNAm patterns.

Methods
Primary hASM cells from four non-asthmatic individuals were grown in media containing low glucose (5.5mM), high glucose (25mM), low glucose with 5% CSE or high glucose (HG) with 5% CSE for 12 days. DNAm was quantified using the Infinium MethylationEPIC array to obtain intensity data for pre-processing, batch correction and data analysis in RStudio. Linear regression with surrogate variables was used to model DNAm values for each CpG, any cytosine base in the DNA sequence that is followed by a guanine base.

Results

We identified 40 significant CpGs for the co-exposure condition, 48 significant CpGs for the CSE only condition and 83 significant CpGs for the HG only condition. Out of the significant CpGs in the co-exposure condition, 34 CpGs were unique to this group alone. Mapping CpG sites to protein coding genes, we identified genes that have been linked to asthma development and pathology in the combined exposure.

Conclusion
We found distinct DNAm patterns in hASM cells co-exposed to hyperglycemia and CSE compared to either exposure alone. These differences in methylation patterns allows us to identify CpGs or groups of CpGs regulating gene expression and look for causative genes in human samples. This would further our understanding of mechanisms by which the combination of environmental factors may contribute to increasing asthma risk.

Authors

Name	Email	Role	Profession
Haziqa Kassim	haziqa.kassim@umanitoba.ca	Presenting Author	Other
Christopher Pascoe	cpascoe@chrim.ca	Co Author	Assistant Professor
Meaghan J. Jones	meaghan.jones@umanitoba.ca	Co Author	Assistant Professor