CHRD 2024: Abstract Submission Form

Presenter Name
Anam Ara

Presenter Status
Masters Student

Role in the project
Design
Perform Experiments
Analyze Data
Write Abstract

Research Category
Basic Science

Title
Cell type specific DNA methylation changes in the lung induced by early life cannabis smoke exposure in mice.

Background
In-utero exposure to inhaled pollutants including cigarette smoke has been linked to an increased risk of bronchitis, pneumonia, and asthma in children. Recent work has implicated epigenetics as a promising mechanism linking early life exposure to cigarette smoke with child lung health. Cannabis smoke (CS) contains many of the same products of combustion as tobacco smoke, but while there are many studies of CS on offspring neurodevelopment, its effects on lung function still remains unclear. Therefore, we hypothesize that there are DNA methylation (DNAm) changes that occur across the whole genome as well as in specific candidate genes (Gstm1 and Cyp1a1) directly related to asthma due to CS. We will examine cannabis-induced DNAm changes in the lung in five isolated lung structural cell types (Epithelial, Endothelial, Smooth muscle, Fibroblast and Myofibroblast) and determine whether these changes overlap with the established epigenetic signatures associated with tobacco smoke and asthma.

Objective
DNAm alterations in lung structural cells are linked to early childhood cannabis smoke exposure, and their overlap with tobacco smoke, because to their shared components, can have long-term health consequences such as asthma.

Methods
Female BALB/c mice (8-weeks) were exposed to CS for nine weeks including mating, pregnancy, and weaning using an automated inhalation system. At 8 and 16 weeks of age we performed lung function analysis using Scireq flexiVent on offspring and the collected lung tissue will be analysed for DNAm changes genome-wide using the Illumina Mouse Methylation Array. We will also assess candidate genes by pyrosequencing for Gstm1 (cg40166692) and Cyp1a1 (cg22549041) for any DNAm changes specific to the gene that might lead to asthma.

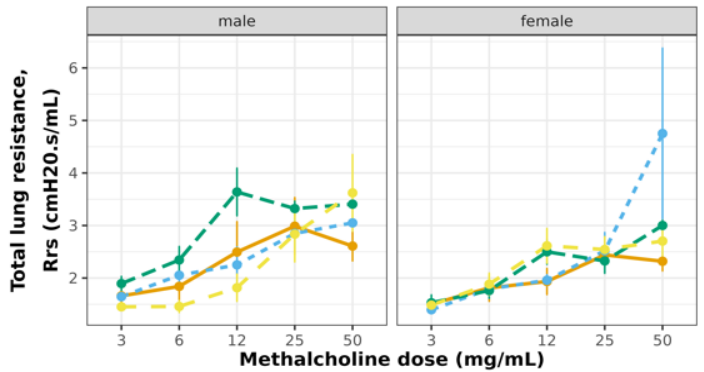
Results
Cannabis smoke exposure resulted in larger pups ($p=0.041$) but no differences in litter size or reproductive success. DNA methylation analysis is in progress. Lung function analysis done on the exposed mice (8week) show variation among the group across different level of methacholine dose (attached figure).

Conclusion
We aim to provide concrete evidence of how exposure to particulate matter of CS in utero affects DNAm, which then can alter physiological pathways and result in diseases such as asthma. Identification of DNA methylation changes between different structural cell type will give more clear picture about the specific cell type affected by CS. Furthermore, as tobacco and cannabis have shown an overlap in health risks, our research will try to identify epigenomic as well as molecular relationships between the two. Our ultimate goal is to identify targets to prevent or reverse epigenetic changes from early life and prenatal environmental exposures, thus reducing poor child health and disease burden.

Do you have a table/figure to upload?
Yes

Authors

Name	Email	Role	Profession
Anam Ara	araa@myumanitoba.ca	Presenting Author	Graduate
Haziqa Kassim	haziqa.kassim@umanitoba.ca	Co Author	
Doris Onuzulu	onuzuluc@myumanitoba.ca	Co Author	Graduate
Sujata Basu	sujata.basu@umanitoba.ca	Co Author	
Meaghan Jones	meaghan.jones@umanitoba.ca	Co Author	Assistant Professor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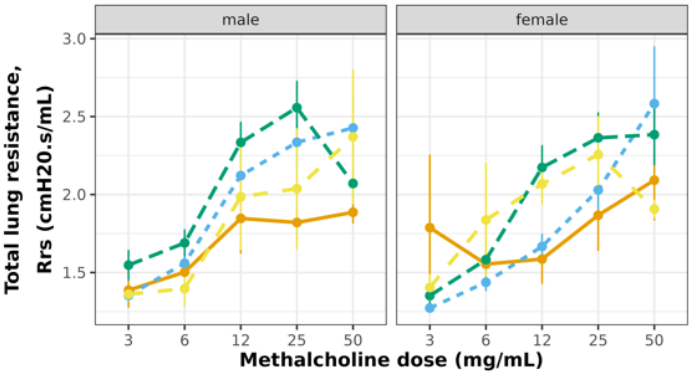
female
Total lung resistance, Rrs (cmH20.s/mL)
Methalcholine dose (mg/mL)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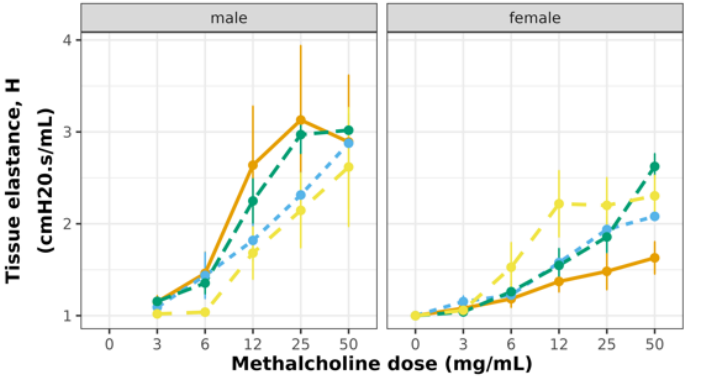
Methalcholine dose (mg/mL)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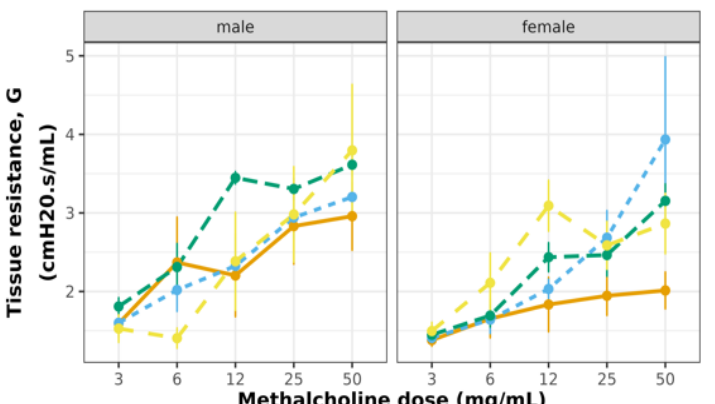
Tissue elastance, H (cmH20.s/mL)
Methalcholine dose (mg/mL)


male
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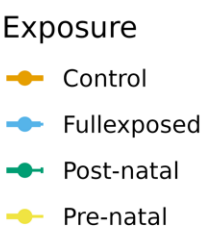
Tissue resistance, G (cmH20.s/mL)
Methalcholine dose (mg/mL)


Exposure
Control
Fullexposed
Post-natal
Pre-natal