Single Cell Biomarker exploration in Cord blood to predict Allergy susceptibility and development

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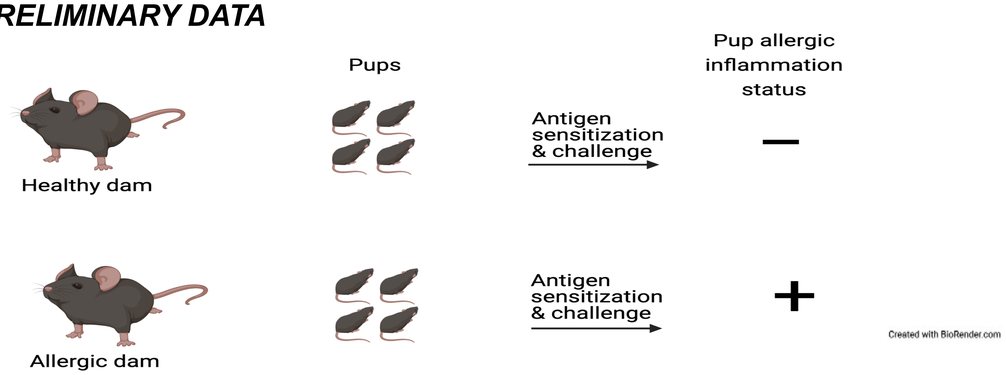
BACKGROUND

- In Canada as of 2017 allergy was noted as one of the four main chronic health conditions among residents[1]. Roughly 8.4million people were reported to have been diagnosed that year alone[1]. This high incidence of allergic disease is not only a problem in Canada. The US CDC reported about a 50% increase in food allergies between 1997 to 2011[2].

- The prevalence of allergic diseases including food allergies and asthma are increasing world-wide and substantial evidence suggests that this is driven, at least in part, by changes in the Western lifestyle and early life environmental factors(lifestyle, improved hygiene, antibiotics etc.)[3] . Allergic and atopic disease are characterized by a robust immune response which involves a variety of immune cells resulting in the the typical symptoms; excessive mucus production, rashes/hives, coughing, wheezing, itchiness etc.

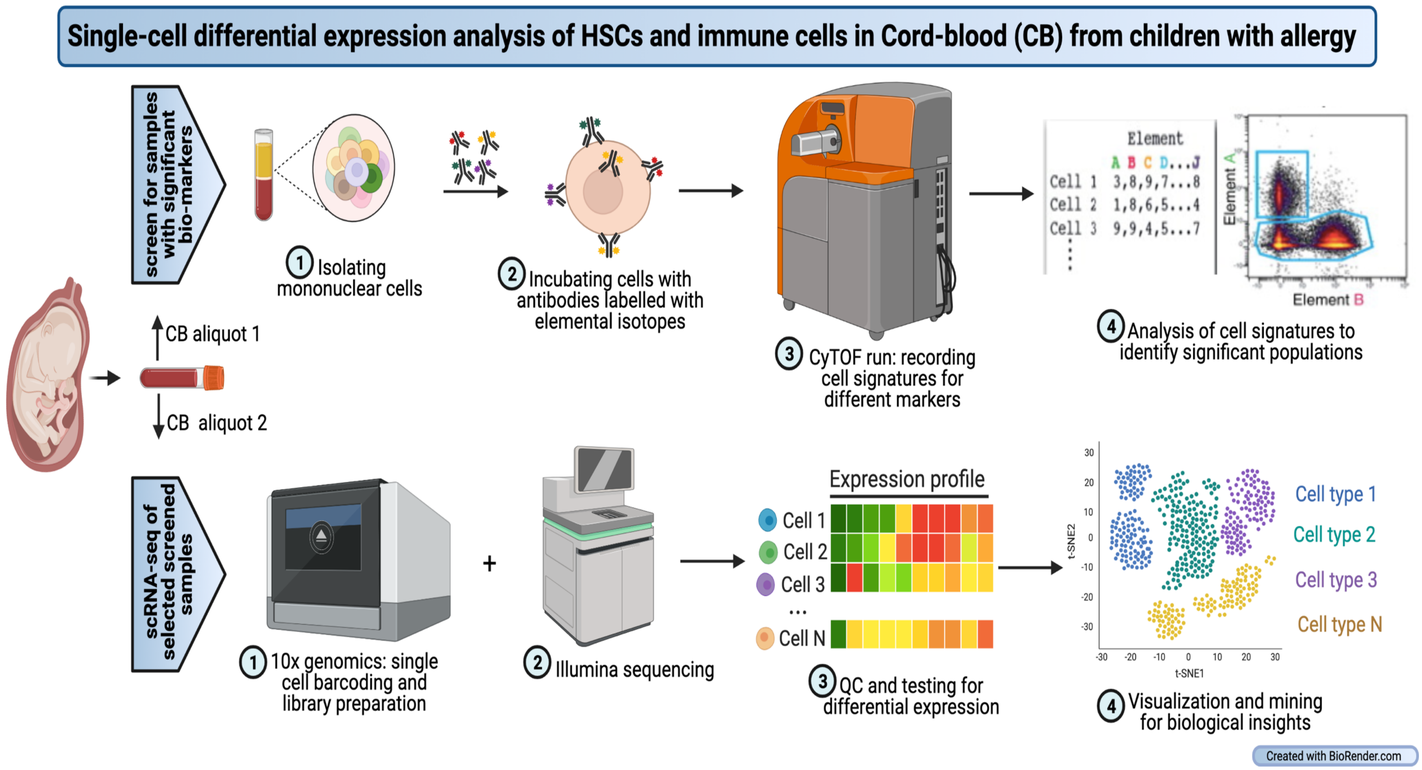
- Quite a lot is known about some common allergens in the environment including the mechanisms through which they initiate an immune response, and many effective treatments exit for allergy and asthma sufferers of whom children in infancy still have the greatest burden of disease. However very little is known about the origin of allergy and how to prevent allergic disease. This study hopes to address this issue

PRELIMINARY DATA



- Prenatal exposure of pregnant mice to Acinetobacter lwoffi, a common farm bacterium, is sufficient to dampen allergic responses in adult offspring[4]
- Models for studying the microbiome and its effect on Th2 skewing in our lab involve exposure to microbiome / antibiotics during pregnancy and neonatal
- A mouse model of allergic airway inflammation showed that pre- and perinatal exposure to low dose antibiotics leads to a profound increase in susceptibility of adult animals to allergic disease[5]

STUDY DESIGN



AIMS

- Identifying gene signatures from cells and using this information to compile a list of signatures associated with allergy and atopy.

- Overlaying RNA-seq and mass cytometry data to construct a full cell and gene signature.

- Investigating the association between these gene signatures from the cord blood samples and patient's development of allergy and atopy.

EXPECTED OUTCOMES

- Illuminate existing patterns of gene expression that may be used to infer new-born's potential to develop allergy.

- Provides us with a better diagnostic tools for allergic disease and possible pathways for future therapeutics which may dampen or eliminate the over sensitization of the immune system.

- Improve understanding of the different factors influence HPC development

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