MATERNAL MICROBIOME LEGACY PROJECT

PARTICIPANT NEWSLETTER #1
JANUARY 2022



A message from the Legacy Team

Welcome to the first Legacy Newsletter! Through these newsletters, we will be sharing our latest study results with you, our participants, now that we're closed to enrolment and in the analysis phase. In this edition, we highlight our first paper which was published in Oct 2021!

To our participants, thank you for participating in Legacy! We are most grateful to all of you who took the time and effort to participate in our research during the busy time of caring for a newborn. This research would not have been possible without you!

About Legacy

Some research has proposed that delivery type (vaginal or C-section) influences how the infant gut microbiome develops. One theory is a potential transfer of maternal vaginal bacteria may be prevented by a caesarean delivery. However, a clear link between delivery type and the infant's bacterial community has not been established. Legacy is using bacterial gene-sequencing methods to determine how the maternal microbiomes (vaginal, breast milk, and areola skin) and delivery type contribute to the development of the infant gut microbiome in the first 3 months of life.

Why is this research important?

The practice of "vaginal seeding" has emerged, where a newborn delivered via caesarean section is swabbed with the mother's vaginal secretions to transfer the mother's vaginal bacteria to the infant, However the benefits of "vaginal seeding" have not been evaluated and the safety of this practice has not been proven. The goal of Legacy is to determine if the maternal bacterial community is actually transferred to the infant during delivery and in early infancy.











Learn about our first paper published Oct 2021!

Read the full paper here

Goal:

To see if meconium (the earliest stool of a newborn) harbours a microbiome that originates from *in utero* exposure or environmental contamination.

Samples collected:

141 meconium samples underwent DNA extraction and their microbiome was profiled

Findings:

To analyze a sample that is low in bacteria, like meconium, you need to have really good controls in the lab to determine whether the bacteria you're seeing is from the meconium or from the environment. We found that meconium does not have a bacterial community that can be distinguished from environmental sources during sample processing.

What this means:

This provides strong evidence that the gut microbiome is not established prior to birth.

What's Next?

We are now looking at how the vaginal microbiome and type of delivery influences the gut microbiome.

Meet the Team

The Legacy investigator team includes Drs. Deborah Money, Janet Hill, Chelsea Elwood, Arianne Albert, Sheona Mitchell-Foster, Kirsten Grabowska, K.S. Joseph, Julie van Schalkwyk, Soren Gantt, Jennifer Hutcheon, Matthew Links, Amee Manges, , Tim Dumonceaux, Zoë Hodgson, and Janet Lyons.

Scott Dos Santos is a PhD student in the University of Saskatchewan Dept. Veterinary Microbiology since Jan 2018. He is studying the vaginal microbiome and mode of delivery in relation to the infant gut microbiome development.

Zahra Pakzad is a PhD student in the UBC Dept. of Microbiology and Immunology since Jan 2021. You may recognize Zahra as the team member who visited many of you as part of your home visits! She is studying breast milk microbiome and probiotics in relation the the infant gut.

About the UBC Reproductive Infectious Diseases Program

LEGACY is a study of the UBC RID program. Our team leads and trainees are committed to ethical, inclusive, and evidence-based research and care in OBGYN and reproductive infectious diseases. Our research areas include COVID-19 in pregnancy, HIV, HPV, hepatitis, perinatal infections, the microbiome, and antimicrobial stewardship.

ridprogram.med.ubc.ca

Stay tuned for more results from the Maternal Microbiome Legacy Project!!

Please contact us with any questions or feedback at zahra.pakzad@cw.bc.ca.



@maternallegacy









