Currently, there are no reliable means of identifying women at high risk of preterm labour early or mid-way through pregnancy. However, there is increasing evidence that gene-gene and gene-environmental interactions are associated with, and likely causal for, preterm labour. Determining these biological factors and correlating them to environmental factors will be important for adequate prediction of preterm delivery. Such research will facilitate the development of models to be used early in pregnancy to predict the risk of preterm labour, which will also assist in selecting study populations in the future.

The data from the data repository core will be used to facilitate research on interactions between biology and environment. Genomic and transcriptomic approaches will also be used to find potential markers from blood in the Tissue and Bio Core. Together, Drs. Bocking, Lye and Pennell will help fill a provincial capacity gap, with no investigator from Alberta having applied such approaches to women's reproductive health yet. Likewise, Alberta graduate students will be trained in this area with the help of the Training Core.

Detailed Research Strategies

Project 1: Transcriptomic Prediction of Preterm Birth

Leaders: Dr. Lye
Researchers: Dr. Bocking, Dr. Lyon, Dr. Olson, Dr. Pennell, Dr. Slater, and Dr. Tough

Mononuclear white blood cells in blood can be used to monitor physiologic and biochemical processes in patients. The leukocyte gene expression will be studied in asymptomatic women in order to determine whether a particular signature is predictive of preterm delivery. Microarray technology will be followed by the use of multiplex RT-PCR to confirm such signatures.

Project 2: Gene and Environment Interactions

Leader: Dr. Olson
Researchers: Dr. Lye, Dr. Pennell, Dr. Somerville, Dr. Tough
Collaborators: Dr. Chari, Dr. Hegadoren

The majority of preterm deliveries are still unexplained. There are a variety of environmental factors such as stress, inflammation, socioeconomic, psychosocial and behavioural risk factors that can influence this. These interact with genetic factors, with the single best predictor of preterm birth being a prior preterm birth. Mothers who were born preterm have an increased risk of delivering preterm. Ethnicity is also associated with preterm birth.

Our objective is to identify genetic variants that predispose individuals to preterm birth in a stressful maternal environment, with specific single nucleotide polymorphisms (SNPs) and stress assessment scores helping to predict preterm birth in a multivariate model. Our data will be added to the data repository, with the extensive environmental data helping to complement the genomic wide analysis of PREBIC.