

## **Principal Investigator**

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## **Summary of research**

Diabetes, Hypertension, Pregnancy, Genetics, Foetus, Placenta

## **Application Lay Summary:**

**1a:** The aims of the proposed research are to test whether the passing of a particular set of genes from a mother to her unborn baby are associated with additional risk to that established by the mother's other genes, of that mother developing gestational diabetes or high blood pressure in pregnancy. These genes are 'imprinted' so that only the copy of each gene passed onto the unborn baby from the mother, and not the copy passed on from the father, is active in the foetus.

**1b:** The proposed research will help the diagnosis of gestational diabetes and pregnancy-induced hypertension by providing novel genetic risk factors for these conditions that could be used as part of panels of genes to predict those women most at risk of developing these conditions. By learning more about the aetiology of these conditions it is possible that this proposed research will also open up novel treatment options.

**1c:** For the standard maternal genes conventional genome wide association studies (GWAS) will be performed testing for associations between the available genotypes and both gestational diabetes and a composite variable (that we will

develop) relating to pregnancy-induced hypertension. For the “foetal genotype” part of the study, as foetal genotypes are not available we will analyse data from the two groups of maternal homozygotes as surrogates of foetal genotypes. We will assess variants in or near maternally-expressed imprinted genes (where the copy of the gene inherited from the father is inactivated) for associations with gestational diabetes and pregnancy-induced hypertension.

**1d:** We are only interested in genotype data from women who have had phenotype recorded from at least one of their pregnancies relating to whether or not they developed gestational diabetes or any form of pregnancy-induced hypertension. Therefore based on current variable sizes this will involve a subset of the whole cohort of around 11,000 Biobank participants.