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Atherosclerosis is a chronic inflammatory disorder that is responsible for approximately 71% of incidents of cardiovascular disease. A mathematical model of atherosclerosis has been developed, capturing the cell types and proteins involved in atheroma formation and describing the dynamics of disease progression. This is the first model of this type to be developed using open systems biology standards. We have predicted tertiary protein structures for all the proteins involved in this atherosclerosis model and all of their recorded mutations, using phase 3 sequence data obtained from the 1000 Genomes Project. By comparing the electrostatic potentials of these tertiary structures, we predict how the dynamics of atherosclerosis stratifies across population subgroups.

**P14. A feasibility study investigating whether methylation of the oxytocin receptor (OXTR) can serve as a potential biomarker for response to oxytocin administration in women during and after labour.**

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The aim of this pilot study was to test the feasibility of carrying out a large scale study using this design to investigate whether methylation of the oxytocin receptor (OXTR) can serve as a potential biomarker for response to oxytocin administration in women during and after labour.

**Background:** Oxytocin is a nine-amino acid peptide with hormonal and neurotransmitter functions during labour and lactation. We hypothesised that a difference in methylation levels of the oxytocin receptor (OXTR) gene may impact the woman’s ability to become established in labour and her response to oxytocin administration.

**Method:** Blood samples were taken pre-birth and postnatally from 21 women and subjected to DNA methylation analysis of the OXTR gene by pyrosequencing. Methylation status of CpG sites -924 and -934 upstream from the initiation transcription site (ITS) of the OXTR gene was determined. Expression of the OXTR gene before and after birth was measured using qPCR. Global methylation levels were examined using Luminometric Methylation Assay (LUMA).

**Results:** We found both hypo and hypermethylation of OXTR promoter at CpG sites -924 and -934 in individual samples, however we observed no profound changes in overall OXTR methylation levels within the patient cohort at these CpG sites. We found a strong correlation between OXTR promoter methylation levels found in whole blood and those found in matched PMBC samples. Global methylation analysis using Luminometric Methylation Assay (LUMA) revealed no significant differences between whole blood and PMBC.

**Conclusions:** A larger sample is required to determine whether OXTR methylation status is predictive of response to oxytocin administration. Whole blood sampling is a suitable alternative for OXTR methylation analysis in a larger cohort of women undergoing labour.

**P15. Investigating microRNAs as Serum Markers of Elevated Blood Pressure.**

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**Background:** Cardiovascular disease (CVD) is the leading cause globally of morbidity and mortality. microRNAs (miRNAs) are small, non-coding RNAs which have a fundamental role in the pathology of various diseases including CVD. Circulating serum levels of miRNAs have been proposed as potentially valuable markers of heart failure, stroke, myocardial infarction and arterial hypertension, but the specific miRNAs involved and their function remains unclear. Therefore, this pilot study aims to profile miRNA expression in premature CVD patients to identify which miRNAs correlate best with hypertension.

**Methods:** The Multiplex Circulating miRNA Assay with Firefly™ Particle Technologies was used to profile 68 miRNAs on a cardiology focus panel in serum samples from 170 premature CVD patients recruited from Altnagelvin Area Hospital and screened for the C677T polymorphism in methylenetetrahydrofolate reductase, a risk factor for hypertension. Samples were collected at baseline and following intervention with riboflavin, a co-factor for MTHFR, which significantly lowers blood pressure specifically in adults with this polymorphism. Statistical analysis was used to correlate miRNA expression with blood pressure, MTHFR genotype and other relevant clinical data.

**Results:** The assay successfully measured miRNA expression in the sample set. miRNAs which expressed differentially between MTHFR genotype groups were highlighted and the functional significance of these miRNAs was assessed using bioinformatics to identify target genes involved in CVD.

**Conclusions:** The data provides further evidence that using specific miRNAs as serum markers could aid early prediction of CVD and may lead to better diagnostic modalities and therapeutic regimes.

**P16. Investigating the association between genetic and epigenetic variability in the 5-HTT and BDNF genes and depression in young adults.**

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Gene-environment interactions, particularly in genes related to regulation of serotonin and neuronal function, have been implicated in the aetiology of depression. Allelic variations in the 5’ flanking transcriptional region of the serotonin transporter gene (5-HTTLPR) and higher levels of promoter DNA methylation are associated with depression. Brain derived neurotrophic factor (BDNF) plays an important role in neuronal differentiation and survival, and is also involved in regulation of serotonin. A single nucleotide polymorphism in the BDNF gene, leading to a valine to methionine substitution at codon 66 (Val66Met), and increased methylation of the BDNF promoter have also been associated with depression. The goal of this study is to determine whether length of the 5-HTTLPR, prevalence of the Val66Met polymorphism of the BDNF gene and DNA methylation in both 5-HTT and BDNF...