Methodology for isolation of miRNA from serum of women investigated for Preeclampsia

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Preeclampsia remains a leading cause of maternal and foetal mortality with a poorly understood pathophysiology. It can lead to a range of clinical presentations, but proteinuria and hypertension are key components of the diagnosis. These signs arise due to disordered placental implantation due to poor trophoblastic invasion and resulting in placental oxidative stress due to hypoxia. Oxidative stress triggers the release of syncytiotrophoblast microvesicles (STMBs), of which placenta-derived exosomes may be a key component. The high specificity of exosomes to their cell of origin makes them ideal candidates as diagnostic biomarkers. We are particularly interested in the miRNAs (micro RNAs) contained within these exosomes as they may give us an insight into the genomic regulation within the pre-eclamptic placenta which leads to the disease state. The development of workflows for miRNA quantitation may enable us to identify novel biomarkers.

We have successfully isolated RNA from 23 samples; however, the concentration of the total RNA was too low for downstream molecular analysis. We did gain an insight into how to optimise and develop the workflow, so that with each attempt, the yield was increased. Our greatest concentrations were obtained by combining serum samples from multiple patients, demonstrating that we needed a higher volume to optimise the yield. Future studies should aim to obtain samples specifically for use in this research so that we could process a larger volume of serum.

The next steps will be to optimise the concentration of RNA for use in downstream applications including NGS (Next-Generation Sequencing). We have also noted that there is a positive correlation between the overall concentration of total RNA and a high sFlt-1/PlGF ratio, in the future it will be interesting to identify any miRNA candidates which contribute to this finding.

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