Health Sciences

UNIVERSITY OF Southampton

Plasma proteomic profiling one year postpartum of women with Pre-eclampsia shows dysregulated cardiometabolic profile.

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Introduction

- Pre-eclampsia(PE) is a relatively common pregnancy complication, affecting 2-8% of all pregnancies, and a leading cause of perinatal and maternal death. The condition is defined by the new onset of hypertension (over 140/90 mmHg, measured on two occasions at least four to six hours apart) that ensues after the 20th week of gestation. Pre-eclampsia that occurred during the first pregnancy was considered to have no long-term adverse cardiovascular effects [1].

- Emerging epidemiological data suggest that pre-eclampsia is associated with long-term complications, including a two to four fold increased risk of cardiovascular disease. Specifically, women with pre-eclampsia are at-risk for chronic hypertension, fatal and non-fatal coronary heart disease, venous thromboembolism and stroke [2-3].

- Plasma proteomics refers to the untargeted analysis of the global circulating proteome. Shotgun proteomics is becoming a very important tool in clinical research, as it can provide valuable insight into the pathophysiology of disease but also identify novel disease markers and therapeutic targets [4-5].

Aim

The aim of the present study was to examine the global plasma proteomic profile one year postpartum of women with PE during pregnancy, in order to identify which processes are dysregulated.

Method

A case-control study of a total of 10 women was consented to take part in the study. Non-depleted plasma collected one year postpartum from women with PE (n=5) and age-matched, BMI-matched women with normal pregnancy (n=5) was analysed using quantitative proteomics.

Results

The plasma proteomic study resulted in the identification of 1,421unique proteins (peptide FDR $p<0.05$). Principal component analysis of all identified proteins showed that women with pre-eclampsia during pregnancy had a distinct plasma proteomic profile one-year post-delivery compared to the control group (**Figure 1**). One-hundred and seventy two proteins were differentially expressed in the PE vs. control. Gene ontology analysis using DAVID showed that terms related to ***Inflammatory / Immune response***, ***Blood coagulation*** **and** ***Metabolism*** were significantly enriched. A volcano plot of the analysed proteome [mean iTRAQ log_2ratio (PE/control) plotted against the minus log_{10}p-value of the one-sample T-Test] is presented in (**Figure 2**).

Conclusion

Our results suggest the increased CD14 levels one year postpartum in women with pre-eclampsia compared to controls could reflect their increased inflammatory status and increased risk of developing insulin resistance and type 2 diabetes mellitus. Also, adiponectin has found down-regulated in women with pre-eclampsia could also reflect an increased risk of developing insulin resistance. The present plasma proteomics profiling one year postpartum of women with PE vs. controls provides insight into the dysregulated cardiometabolic profile in this population group, thus highlighting the need for long-term health monitoring

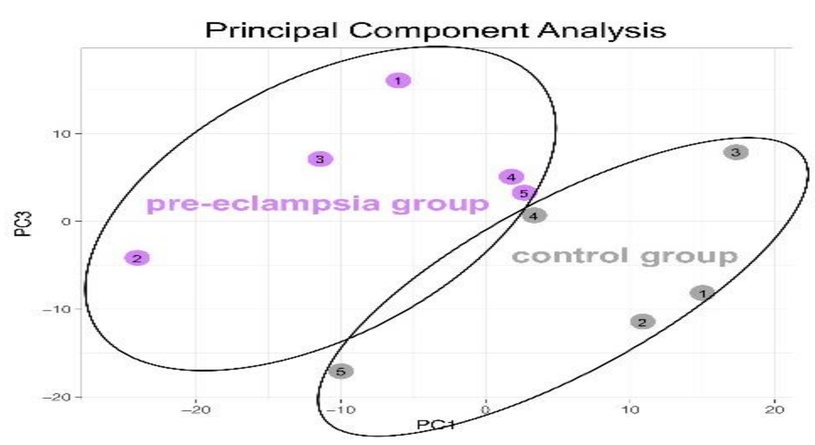

Figure 1: Principal component analysis of all analysed plasma proteins.

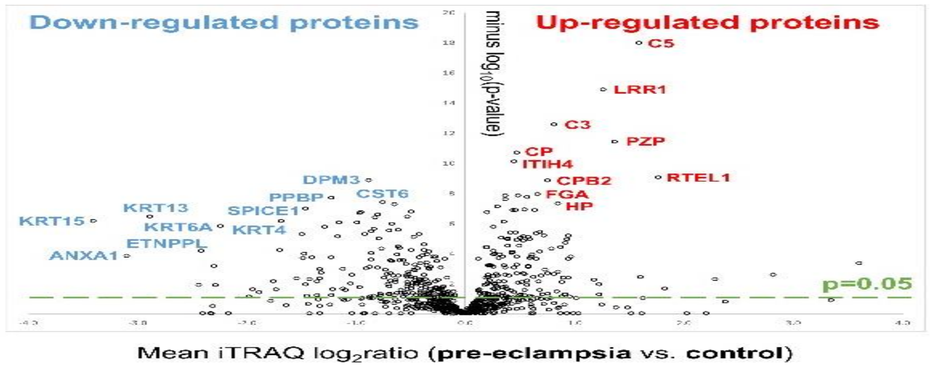

Figure 2: Volcano plot of analysed proteins.

References

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