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Proteomic Analysis Identifies Complement Factor H as a Novel Biomarker for Preeclampsia

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Abstract

BACKGROUND: Preeclampsia is the leading cause of maternal and fetal morbidity and mortality. Despite decades of research, the pathophysiology of preeclampsia is still not fully understood. Clinically useful biomarkers for predicting this condition are warranted. The objective of this research is to identify novel biomarkers for preeclampsia involved in its etiology, pathophysiology, and prediction.

METHODS: Blood serum was obtained from pregnant women with preeclampsia and matched with healthy controls. Samples were subjected to nano liquid chromatography - tandem mass spectrometry analysis. Protein analysis was conducted using Mascot search engines. A p-value and a false discovery rate (FDR) of less than 0.05 were used to indicate statistical significance.

RESULTS: Sixteen preeclampsia and sixteen healthy controls were selected. No significant differences were identified in main demographics and baseline obstetric data. From 1,821 identified proteins in preeclampsia, 85 (4.2%) were significantly upregulated (abundance ratio>1.5, $p<0.05$), and 69 (3.7%) were significantly downregulated. Complement activation was the functional pathway more significantly associated with preeclampsia. Complement factor H was the protein with the most significant abundance.

DISCUSSION/CONCLUSION: Complement activation pathway was significantly dysregulated in antepartum preeclampsia. Complement factor H appears to be a potential novel biomarker significantly upregulated in preeclampsia. Further research in these specific protein subfamilies is warranted.