

ARTICLE INFORMATION

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Metabolomic Profile associated with Pre-eclampsia and its severity in Colombian pregnant women: A co-expression network analysis

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ABSTRACT

Introduction: Pre-eclampsia affects maternal and fetal well-being (1). Despite being a problem identified decades ago, its pathophysiology is still not fully understood (2). The inclusion of metabolomics is relevant to better comprehend the disease's pathophysiology (3).

Objective: To establish the metabolomic profile associated with Pre-eclampsia and its severity through a co-expression network analysis.

Methodology: A case-control study derived from the GenPE biobank was carried out. Samples from pregnant women with Pre-eclampsia (cases) and uncomplicated term pregnancies (controls) were randomly selected. The metabolomic study was performed on serum using NMR+ (Nightingale Health Ltd). Other outcomes assessed were the time of onset and HELLP syndrome. Missing metabolite data were imputed and subsequently standardized. A weighted co-expression network (4-5) was constructed using a power of 20, R2 of 0.7, and minModuleSize of 5. Correlation between modules and outcomes was evaluated to identify significant modules.

Findings: The study included 596 women (357 controls and 239 cases). The mean age was 18.6 years (SD 2.8) and 20.7 years (SD 5.2), respectively. Seven modules were identified, but only the red module showed an inverse correlation with Pre-eclampsia (corr: -0.21, p=3x10⁻⁷), HELLP syndrome (corr: -0.12, p=0.004), and onset <34 weeks (corr: -0.2, p=1x10⁻⁶). The metabolites in the red module were XL-HDL-P, XL-HDL-L, XL-HDL-PL, XL-HDL-C, XL-HDL-CE, XL-HDL-FC.

Conclusions: Extra-large HDL molecules in different lipids played a protective role in all three evaluated outcomes. This effect is also observed in cardiovascular diseases in the general population (6).

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