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# H4K16ac mediated transposable over expression leads to inflammation in Preeclampsia

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## Abstract

Preeclampsia (PE) is a pregnancy-associated hypertension disorder which affects 5–10% of pregnant women each year worldwide. Here, we aimed to investigate the epigenetic mechanisms contributing to preeclampsia by genome-wide profiling of histone acetylations and transcriptome in healthy and preeclamptic placenta. We found a specific increase in acetylation level at histone H4 lysine 16 (H4K16ac) across transposable elements in preeclamptic placenta compared to control. H4K16ac hyperacetylation in pre-eclampsia is associated with increased transcript levels of endogenous retrovirus (ERV/LTR) and long interspersed nuclear element 1 (L1, LINE1) subfamilies of TEs in PE placenta from independent pregnancy cohorts. Further, analysis of the additional cohorts along with this study, we discover upregulation of the LTR and L1 subfamilies as well as type I interferon (IFN) responsive genes upregulated in Preeclampsia. These findings were consistent with the validation using RT-qPCR for the L1 ORF and 5' UTR as well as IFN-genes, indicating the contribution of H4K16ac-mediated upregulation TE contributing to inflammation in PE.

**Keywords:** H4K16ac, Preeclampsia, Transposable elements, Inflammation

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