An Analysis of the Regulatory Role of Small Nuclear and Nucleolar RNA Expression Pathways in the Pathogenesis of Preeclampsia

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This research studied the gene expression profiles of small nuclear RNA (snRNA) and small nucleolar RNA (snoRNA) in Preeclampsia (PE), compared to term and idiopathic (iPTB) patients. The purpose of this study was to establish the expression profiles of sn/snoRNAs in order to identify which pathways contribute to PE and how. Through the use of a deidentified database of the expression values in transcripts per kilobase million (TPM), differentially expressed sn/snoRNAs were identified, based on TPM values, fold changes, and p-values. These genes were uploaded to Ingenuity Pathway Analysis (IPA) to construct the pathways in PE. 485 sn/snoRNAs were commonly expressed in PE vs. both iPTB and control-term. In PE vs. control-term, 47% of the genes were upregulated while 53% were downregulated. However, in PE vs. iPTB, the majority of sn/snoRNAs were upregulated (92% vs. 8%). Multiple canonical pathways were affected in PE, including systemic lupus erythematosus (SLE) signaling and retinoic acid receptor (RAR) activation. This data had a 12.2% overlap with the SLE signaling pathway. With both of these disorders being related to hypertension, the overlapping genes are likely involved in PE hypertension. Furthermore, SMARCB1 was identified as a potential biomarker for PE. The gene was also a regulator in the SLE signaling pathway, suggesting a role in hypertension. Another pathway, RAR activation, was affected in PE. Lastly, top affected networks involved cardiovascular development and function. It is known that preeclamptic women are at increased risk of cardiovascular disease later in life. The genes in this network could be involved with this risk. These results represent the pathways and networks responsible for PE etiology and further studies can confirm these results.

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