Using Bioinformatics Techniques to Identify Gene Expression and Potential Genetic Pathways in Preeclampsia

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The genetic disorder preeclampsia is characterized by severe hypertension and proteinuria during pregnancy. Our project investigated the role of lncRNA (long non-coding RNA) in the genetic pathology of this dangerous illness. We began by using data downloaded off of the Gene Expression Omnibus to determine the lncRNAs that were upregulated or downregulated between the three phenotypes of the disorder: normal, early onset preeclampsia and late onset preeclampsia. We then used information gathered from the database LncRNA2Target v2.0 to determine the targets of the previously selected lncRNAs. Then, we generated six genetic maps in order to observe the connections between these genes. At the conclusion of our experiment we found pathways suggesting links between symptoms like hypoxia and proliferation of trophoblasts with preeclampsia. We also used the open-source software Cytoscape to create a network analysis to determine potential pathway “hubs.” Our research suggests differences between the early and late onset phenotypes of the disease. We hope that the research we have conducted will advocate for better clinical knowledge of the disease and help the generate improved diagnostics and treatments. In addition, our project also demonstrates further applications for bioinformatic techniques as well as lncRNA.

Awards Won: