The Future of Organ Replacement: Using Bioinformatics To Determine the Best Protein Environment To Bioengineer the Optimum Renal Vasculature System Using hiPSCs

Sunil, Shreya (School: James Clemens High School)

The human kidney is the most transplanted organ in the United States, numbering more than 24,000 in 2021 alone! But kidney transplantation technology faces many challenges, including a shortage of kidneys and fears of potential organ rejection. Because of these limitations, stem cell treatment is becoming an alternative therapeutic approach. Through this research, an effort has been made to identify the protocol by which the best protein environment can be configured to bioengineer renal tissue using the patient's stem cells. The NCBI bioinformatics database was used to identify the transcription factors vital to the development of renal organoids. The best soluble factor combination to use are Activin A, Rectonic Acid, TGF-Alpha, and PDG Factor. The functions that they share, such as vascular endothelial growth and differentiation, serve as a vital component for the development of the vascular system of the kidney. Additionally, to efficiently differentiate hiPSCs into renal cells, they need the proper ECM proteins in the substrate to grow on. Embryonic gene expression values were analyzed for all integrin subunits and ECM proteins that are known to have a profound effect on the development of a kidney. The integrin subunits that provided the highest gene expression level in an embryonic stem cell during all three parameters were b1. The experimental results showed that the most efficient integrin subunit combination made by kidney cells during development is the ECM protein of Laminin-111 and Fibronectin. They consist of the beta subunit and act as regulators for different cellular pathways. These proteins can be used as the basis of the synthetic scaffold when differentiating cells in vitro and serve as a therapeutic treatment for patients battling kidney diseases.

Awards Won: