Diabetic Complications Consortium

Application Title: "Spatial Representation of Single Cell RNA-sequencing Data in Embryonic Kidneys"

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1. Project Accomplishments:

The purpose of this project was to establish protocols and data to generate a virtual atlas of gene expression in the newborn mouse kidneys using in situ single cell mRNA sequencing. Very little progress has been made. The project was based on a collaboration with a startup company named Cartana, who were going to provide us with reagents and techniques to complete this project. Initially, there were delays caused by issues regarding material transfer agreements. This was complicated by work stoppage/slowdown at both Cartana and UTSW due to the Covid crisis. Once these issues were overcome, progress was once again halted when Cartana was purchased by 10X Genomics. 10X ordered all existing projects to be put on hold until a to be determined date. One month ago, we entered into an agreement with 10X to proceed with our proposed research. However, as the products produced by Cartana are not currently offered as a product by 10X, we once again have had to deal with contractual agreements as well as some alterations to our original experimental design. We believe all of the issues have now been addressed and the project is now scheduled to begin in the next 3-4 weeks. Once the work is completed, we will add info to the DiaComp web portal.

2. Specific Aims:

Specific Aim 1: Map E18.5 whole kidney single cell RNA-Seq to reference kidney

Specific aim1a: Perform in situ single cell sequencing with a set of logically chosen reference genes.

Results-A modified gene list has been generated. Although originally, we were allowed to create a list of up to 1024 genes, the new 10x product limits our choice to pre-designed gene sets and an additional 80 genes. Our new chip has been designed and we believe it will have the information needed to create our atlas.

Specific aim1b: Generate high definition, single cell expression map E18.5 kidney using Spatial Transcriptional Assignment Tool (STAT).

Results-The computer code for this tool has been generated. Once we receive the data from the in situ single cell sequencing, the database can be quickly created.

3. Publications:

None