MINI REVIEW

Structural similarities and differences between the Clinical and the Mouse Pancreas

Peter M. Douglas*

Department of Cellular and Physiological Sciences, University of British Columbia, Vancouver, BC, Canada

INTRODUCTION

The mammalian pancreas' function is dependent on intricate interactions between different cell types, gene expression profiles have traditionally been characterised using bulk mixtures. The transcriptomes of nearly 12,000 individual pancreatic cells from four human donors and two mouse strains were determined using a droplet-based, single-cell RNA-seq approach. All endocrine cell types, including uncommon epsilon-cells; exocrine cell types; vascular cells; Schwann cells; quiescent and active stellate cells; and four types of immune cells could be grouped into 15 clusters that matched previously defined cell categories. We discovered ductal cell subpopulations with unique expression profiles and confirmed their presence using immunohistochemistry staining. Furthermore, we discovered variability in the regulation of genes related to functional maturation and levels of cholesterol in human beta-cells [1].

Finally, we used single-cell data to deconvolve bulk gene expression collections in order to uncover disease-associated differential expression. Our database can be used to find new cell type-specific transcription factors, signaling receptors, and medically significant genes [1].

Drainage of the pseudocyst is the most appropriate treatment for gigantic pancreatic pseudocysts due to their huge size. The goal of draining pseudocysts can be accomplished through a variety of therapy techniques. An endoscopic ultrasound-guided cystogastrostomy is one of the most regularly used procedures, and this case demonstrates it as a viable therapeutic choice for big pancreatic pseudocyst [2].

Received 22-Jan-2022 Manuscript No IPP-23-731 **Editor Assigned** 24-Jan-2022 PreQC No IPP-23-731(PQ) **Reviewed** 11-Feb-2022 QC No IPP-23-731 **Revised** 18-Feb-2022 Manuscript No IPP-23-731(R) **Published** 25-Feb-2022 DOI 10.35841/1590-8577-23.2.731
Correspondence Peter M. Douglas
Department of Cellular and Physiological Sciences
University of British Columbia
Vancouver, BC, Canada
E-mail douglas.p@ubc.ca

Organogenesis' complexity makes in vitro creation of organs from a patient's pluripotent stem cells (PSCs) difficult, which is the ultimate goal of regenerative medicine. PSCs implanted into Pdx1(-/-) (pancreatogenesis-disabled) mouse blastocysts developmentally compensated for the loss of the pancreatic "developmental niche," resulting in a pancreas made virtually exclusively of PSCs. We injected mouse or rat PSCs into rat or mouse blastocysts, respectively, to test the potential for xenogenic techniques in blastocyst complementation. This resulted in interspecific chimaeras, showing that PSCs can contribute to xenogenic development between mouse and rat. The body size and species-specific organogenesis of these mouse/rat chimaeras were predominantly controlled by the host blastocyst and/or foster mother. We next implanted rat wild-type PSCs into Pdx1(-/-) mouse blastocysts, resulting in mice with a fully functional rat pancreas. These findings demonstrate the feasibility of interspecific blastocyst complementation and the in vivo creation of organs from donor PSCs in a xenogenic environment [3].

We employed iterative weighted gene correlation network analysis to create a Gene co-expression network (GCN) from 11 temporally and genetically characterized mouse cell populations to gain a better understanding of pancreatic-cell development. The GCN was then used to gain three new biological insights, as it had 91 unique modules. First, we discovered that during pancreas development, the clustered protocadherin genes are differently expressed. Pcdhy genes are expressed preferentially in pancreatic endoderm, nascent islets, and mature -cells. Second, we discovered 81 zinc finger protein (ZFP) genes that are selectively expressed throughout endocrine specification and -cell maturation after identifying sub-networks of transcriptional regulators for each embryonic stage. Finally, we used the GCN to pick three ZFPs for future investigation using CRISPR mutagenesis in mice. There were fewer pancreatic endocrine cells, changes in exocrine cell shape, and significant changes in gene expression in the pancreas implicated in protein translation, hormone secretion, and developmental pathways. Our findings suggest that developmentally orientated GCNs could be

Citation: Douglas PM. Structural similarities and differences between the Clinical and the Mouse Pancreas. JOP. J Pancreas. 2022;23(2):731

useful for learning more about gene control throughout organogenesis [4].

Important events in the organogenesis of the mouse pancreas have been defined thanks to extensive research. These findings were used to create human embryonic stem cell (hESC) differentiation methods with the goal of producing functional glucose-responsive, insulin-producing human cells. Despite significant advancements in hESC differentiation, existing mouse developmental biology-based procedures can only create human -cells in vivo. New differentiation markers and recently developed reagents may offer a once-in-a-lifetime opportunity to create a high-density expression map of human foetal pancreas and pancreatic islets, which might be used as a reference point for in vitro hESC differentiation [5].

REFERENCES

1. Baron M, Veres A, Wolock SL, Faust AL, Gaujoux R, Vetere A, et al. A single-cell transcriptomic map of the human and mouse pancreas reveals inter- and intra-cell population structure. Cell Syst 2016; 3:346-360.e4. [PMID: 27667365].

2. Kobayashi T, Yamaguchi T, Hamanaka S, Kato-Itoh M, Yamazaki Y, Ibata M, et al. Generation of rat pancreas in mouse by interspecific blastocyst injection of pluripotent stem cells. Cell 2010; 142:787-99. [PMID: 20813264].

3. Benitez CM, Goodyer WR, Kim SK. Deconstructing pancreas developmental biology. Cold Spring Harb Perspect Biol 2012; 4:a012401. [PMID: 22587935].

4. Osipovich AB, Dudek KD, Greenfest-Allen E, Cartailler J, Manduchi E, Case LP, et al. A developmental lineage-based gene co-expression network for mouse pancreatic β-cells reveals a role for Zfp800 in pancreas development. Development 2021; 148:dev196964. [PMID: 33653874].

5. Pan FC, Brissova M. Pancreas development in humans. Curr Opin Endocrinol Diabetes Obes 2014; 21:77-82. [PMID: 24569548].

Citation: Douglas PM. Structural similarities and differences between the Clinical and the Mouse Pancreas. JOP. J Pancreas. 2022;23(2):731