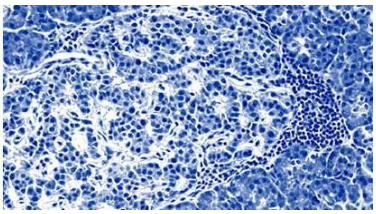
nPOD
Network for Pancreatic Organ Donors with Diabetes



Proteomic Based Detection and Identification of Enteroviruses in nPOD Cases

AUTHORS

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PURPOSE

As part of the JDRF nPOD-Virus group, our ongoing studies focus on utilizing proteomics and liquid chromatography-mass spectrometry (LC/MS) technologies to identify and characterize enterovirus proteins/peptides in disease stratified nPOD tissue samples. The goal is to use global and targeted methods to robustly demonstrate the presence of enteroviruses and proteomic signatures consistent with enterovirus infections.

METHODS

We have isolated and processed proteins from different types of pancreas tissue preparations from nPOD including flash frozen tissue chunks, fresh frozen OCT embedded tissue chunks, 20 µM tissue slices from fresh frozen OCT and laser capture micro-dissected tissue sections for LC/MS analysis. We have utilized an Orbitrap Fusion Lumos Mass Spectrometer to acquire high resolution, high mass accuracy and high sensitivity MS data using different scanning methods including data dependent acquisition (DDA), data independent acquisition (DIA), and parallel reaction monitoring (PRM) followed by qualitative and quantitative comparative analysis.

SUMMARY OF RESULTS

In our cumulative studies using disease stratified nPOD pancreas tissue samples, we identify enterovirus peptides from different serotypes including those that have been correlated with the etiology of type 1 diabetes. Some of the identification results have been validated by targeted mass spectrometry and in Western Blots. In addition, comparative label free quantitation analyses reveal the upregulation and activation of pathways that are associated with viral infections.

CONCLUSIONS

Our current data provides additional evidence that T1D pancreata are infected and potentially harbor various enterovirus proteins and pathways that are associated with the infection are also activated in infected tissues.