Asmae Moursli, MD., Msc.
Phd student at Dr. Coulombe lab, IRCM. UdeM, Canada

Title: Single cell membrane epitope-proteome (SCMeP) method as a precise approach for investigating beta cell diversity and malfunction.

Cellular heterogeneity serves the need for functionally specialized cells, and it is mediated by a rich and complex proteomic network. Cell membrane proteins play a significant role in defining cell phenotypic diversity and thus contribute greatly to cell heterogeneity. Because cells undergo several changes over their lifetime, bulk studies do not accurately reflect the existing molecular mechanisms leading to cell heterogeneity in each cell population. In order to better understand and characterize cell diversity, single cell multi-omic approaches have shown promising results. In this respect, our project aims to develop and use a method allowing the correlation between single-cell surface epitopes and their associated proteomes. Because proteins cannot be amplified, the main hurdle in single-cell proteomics is the lack of protein abundance. To help circumvent part of these difficulties, the cornerstone of our methodology is based on the SCoPE2 approach developed by the Slavov Lab. This method exploits the combination of FACS and LC-MS/MS with Tandem Mass Tag barcode. Our main goal is to investigate the well-known challenges of cell diversity in the pancreatic Langerhans islets. Beta cells represent nearly 60% of Langerhans islet cells populations and they are very diverse compared to alpha cells. These cells are mainly affected in a number of pancreatic pathologies such as diabetes (DM) and neuroendocrine tumors (NET). Their surface membrane proteins/receptors are critical to their function and provide accurate information on their extracellular micro-environment which contributes to shape their phenotype. Several surface proteins have been described as major players in generating signaling pathways that dictate phenotypic functions of the beta cells. Because, cell membrane proteins composition and function is not fully characterized, exploring this signaling network at a single cell resolution is likely to provide yet more information that can be used as a novel therapeutic target or as a diagnostic biomarker.