Probing cancer geography with FFPE-CycIF, an open-source, highly multiplexed imaging and analysis of cancer tissues at single-cell resolution

The tumor microenvironment plays an important role in disease progression and therapy resistance. Increased understanding of the heterogeneity in both the tumor and its microenvironment will be crucial to the development of more effective therapies. Recently, several studies employing leading-edge single-cell sequencing methods reveal enormous complexity in the tumor microenvironment. However, the spatial information and cell-to-cell interaction could not be preserved in these dissociated cells.

Our team has developed the Cyclic Immunofluorescence (CycIF), which increases the multiplexity of conventional immunofluorescence. The CycIF method has been applied in pre-clinical drug discovery, cancer, and stem cell biology.

We also have now developed FFPE cyclic immunofluorescence (FFPE-CycIF), a novel method that enables single-cell resolution imaging of up to 45 proteins in the same FFPE slide from various cancer tissues slides and tissue microarrays. Using this method, we quantitatively discerned tumor composition, evolution from healthy to high-grade disease across 13 cancers, and explored phenotypes, spatial distribution and cell-to-cell interactions of tumor-infiltrating lymphocytes (TILs). Our analyses reveal divergence of MAPK-pathway and Wnt/beta-catenin signaling in pancreatic cancer cells, resolves tumor heterogeneity in glioblastoma, and shows that a single tumor harbors regions of different histologic subtypes.

In this talk, we will describe several clinical applications of FFPE-CycIF, a novel method enabling multiplexed protein assessment of FFPE samples at single-cell resolution in a preserved spatial context.

The data from the research will be presented using Glencoe Software's digital pathology solution PathViewer 2.0 with OMERO Plus.