CASE STUDY

Profiling the Tumor Microenvironment of Neuroblastoma using ChipCytometry™

Who

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Product Focus

ChipCytometry™ Platform
ChipCytomety™ Custom Panel

Background and Objective

More precise and effective treatments are needed to treat patients with cancer. CAR T-cell therapy – where a patient's T cells are removed from their blood and genetically engineered in the laboratory to find and kill cancer cells – has the potential to deliver life-changing benefits. Patients with neuroblastomas have particularly poor prognoses and may greatly benefit from novel therapies.

A primary aim of my PhD research is to analyze the complex interactions occurring in the tumor-immune microenvironment in tissue samples from patients with various types of cancer. I have a joint appointment at UCL Cancer Institute and Autolus Limited under the supervision of Professor Teresa Marafioti and Dr. Mathieu Ferrari. Our goal is to investigate how to improve the design of future CAR T-cell therapies to ultimately improve patient outcomes.

Study Summary and Results

We used frozen tissue sections embedded in optimal cutting temperature (OCT) compound from patients with neuroblastomas. Tissue sections were loaded on microfluidic chips and protein abundance for 34 targets were quantified using a custom panel for immune cells, with a focus on T cell markers. We characterized key cell types and analyzed their spatial relationship within the tumor.

"We plan on utilizing ChipCytometry and custom protein panels to continue to profile clinical samples. With CAR T-cell therapy specifically, we are interested in applying our discovered cell profiles to improve the design of new therapies."

— Margarida Neves, M.Sc.

Initially, we deployed various open-source tools for computational pathology to analyze ChipCytometry™ datasets including QuPath, Scanpy, and Squidpy. The ability to export ChipCytometry™ data in open-source OME-TIFF file format has facilitated analysis by allowing us to test various pipelines. At the same time, our group is working with a bioinformatician to develop new computational modules to expand analysis into new areas.

Next Steps

Our custom ChipCytometry™ panel was an incredibly useful tool for spatial analysis of cell types based on protein expression. We are currently writing a manuscript to describe our findings. Our data highlights the necessity of understanding the spatial context of cells in the tissues to allow for more accurate biological comprehension of the data.

Our group will also perform transcriptional profiling with GeoMx Digital Spatial Profiler from NanoString. Each of the two platforms – ChipCytometry™ and GeoMx Digitial Spatial Profiler – will offer a unique set of complementary data that provides a more complete picture of the state and function of cells in the tumor microenvironment. We anticipate that our multi-omic approach will yield interesting insights into the molecular mechanisms at play in neuroblastoma and ultimately allow us to develop more effective CAR T-cell therapies.

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