Measurement of Hundreds of Proteins in Single Cells by Microchip MIST Technology

Cellular diversity is an intrinsic trait of any multicellular system. Despite extensive study of cells, their complexity still poses major challenges to the identification of key cellular subsets and targets that are responsible for human diseases. Recently, single-cell functional proteome has emerged as a research field of intense interest owing to the significant role proteins play in cell type identification, signaling transduction, proliferation and apoptosis, transcription regulation, inflammation, and cell communication. The major obstacle to this field is the lack of appropriate tools that can survey the full sets of proteins of important functions. In this talk, I will introduce a single-cell MIST technologies developed in my research group for highly multiplexed protein assays toward functional proteomic studies, and I will discuss how such a transformative technology should be translated towards precision diagnosis. The technology is built upon a microchip that integrates a large-scale microarray. We have analyzed ~200 functional proteins important in brain cell classification and neurodegeneration. Bioinformatic analysis found differentially expressed proteins in AD pathology using Alzheimer’s Disease mouse models. We have also detected over 400 functional proteins in single immune cells, and we have studied how immune cells respond upon sepsis onset along the progression. Last, I will mention the new study on spatial proteomics by the MIST array. With the current success, we are heading towards mapping of the entire functional proteome in tissue samples.

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For more information on the NanoSystems Biology Cancer Center visit: http://nano.cancer.gov/action/programs/caltech/

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