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High throughput single cell multiomics platform (Abstract)

CRADA 561 (PNNL 79524)

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Scienion US Inc

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Abstract

In this collaborative project, PNNL and Scienion will co-develop an integrated microfluidic technology to co-measure the transcriptome and proteome in single cells. The technology will enable us to efficiently separate proteins from mRNA transcripts between two microchips, barcode the molecules, and measure them separately with next-generation sequencing and mass spectrometry, respectively.

Multicellular organisms contain diverse cell types and tremendous cell-to-cell heterogeneity that dictates a multitude of biological functions in both physiological and pathological environments. Even in the case of microbes, these genetically identical organisms can randomly differentiate into many subpopulations that assume different roles for the survival of the community. Bulk-scale measurements are insufficient to resolve such complexities. The development and applications of high throughput single-cell omics technologies have transformed our understanding of cellular heterogeneities and their differential responses to internal signaling events or external stimulations.

Despite these advances, most current single-cell omic technologies provide information on only one type of biomolecule. Perse, such measurements provide incomplete information because the cell phenotype is determined by multiple layers of biomolecules and the interplay between genome, epigenome, transcriptome, and proteome. For example, mRNA abundance in one cell can not be precisely referred to the corresponding DNA and protein in other cells because of the potential subtle difference in genotype (e.g., somatic mutation or copy number variation) or phenotype (external microenvironment and cell-cell interactions). As such, parallel measurement of multiple biomolecules in the same single cells can offer unique advantages compared with measuring them separately in different single cells.

Scienion is a world-leading biotech company focusing on precision liquid handling and its application in single-cell whole-genome sequencing and RNA sequencing. PNNL is the leading institution in ultrasensitive mass spectrometry, microfluidics, and untargeted single-cell proteomics (scProteomics). This collaboration will facilitate a unique fusion between scTranscriptomics capability at Scienion and scProteomics capabilities at PNNL to, for the first time, perform both untargeted transcriptomics and proteomics from the same single cells.

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