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Single-Cell Mrna Sequencing Reveals Role Of Dendritic Cells

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Single-Cell mRNA Sequencing Helps Reveal The Role Of "Precocious" Dendritic Cells In Inflammatory Response

Study Demonstrates the Importance of Single-Cell Sequencing to Identify Rare Cell Populations Normally Hidden in Bulk Sample Studies

BOSTON and SOUTH SAN FRANCISCO, Calif., June 30, 2014 — In work published in Nature this month, scientists at the Broad Institute and Fluidigm Corporation used the C1™ Single-Cell Auto Prep System to prepare cells for single-cell sequencing - enabling the discovery of a subpopulation of "precocious" cells expressing antiviral genes earlier than the majority of dendritic cells exposed to the same antigen. Normally, the ability to detect the actions of these "precocious expresser" cells would be lost due to averaging across many millions of cells in bulk cell studies. With this discovery, made possible with contributions from the Single-Cell Genomics initiative of Fluidigm and the Broad, researchers will be able to explore how these "precocious" cells escalate the body's immune response when the body is under attack.

The Nature paper also highlighted the role of cellular heterogeneity and its importance in cell-to-cell communication during an immune response. In typical studies, cells are studied together in one environment, allowing the cells to communicate and signal to one another. However, the unique properties of Fluidigm's C1 Single-Cell Auto Prep System allowed the researchers to isolate the cells from one another to identify the specific cells expressing antiviral genes. Because these cells were isolated, the non-expressing cells did not surmount a response, indicating that cell-to-cell communication plays a critical role in promoting immune response.

In addition to the discovery of a rare subpopulation of cells, this research represented a new benchmark for sheer volume of single-cell data. The 1,774 cells represented in this paper provide one of the largest single-cell genomic datasets published to date and one of the largest mRNA sequencing datasets available anywhere.

In order to identify and characterize these rare "precocious" cells, which make up only 1% of dendritic cell populations, researchers needed to scale up to a high number of cells. To do this, they first needed to solve two key problems: how to prepare single-cell libraries for thousands of cells, and how to sequence such large sample numbers affordably.

To prepare the huge number of single-cell libraries, the researchers relied on the C1 Single-Cell Auto Prep System, which had just been introduced to the marketplace at the time these experiments began. The C1 system's microfluidic technology enabled the researchers to rapidly and reliably isolate, process, and profile individual cells for genomic analysis. During the study, the group discovered that they could achieve stable data with single cells at less than one million reads (compared to run rates of at least 5 to 10 million reads when conducting bulk mRNA sequencing). The ability to obtain reliable data faster greatly reduced the cost of running the experiment.

For access to the complete paper -- Single-cell RNA-seq reveals dynamic paracrine control of cellular variation, Nature.2014 Jun 19;509(7505):363-9 -- please visit: http://info.fluidigm.com/Shalek_Et_Al.html.

SINGLE-CELL GENOMICS INITIATIVE

In 2012, the Broad Institute's Genomics Platform and Fluidigm Corporation (NASDAQ:FLDM) established the Single-Cell Genomics initiative dedicated to accelerating the development of research methods and discoveries in mammalian single-cell genomics. The Single-Cell Genomics initiative also acts as a hub for collaboration among single-cell genomics researchers in many pioneering fields, including stem cells and cancer biology. The initiative is housed at the Broad Institute in Cambridge, Massachusetts, and features a complete suite of Fluidigm single-cell tools, protocols and technologies, most notably the C1 Single-Cell Auto Prep System and the Biomark™ HD System.

TECHNOLOGY

The Fluidigm C1 Single-Cell Auto Prep System is based on the company's innovative microfluidic technology that enables researchers to rapidly and reliably isolate, process, and profile individual cells for genomic analysis. Scientists can extract, reverse transcribe, amplify, and ultimately detect and analyze cell activity using one technology thereby reducing the variability caused by multi-platform technical errors.

In the experiments that supported this newly announced research, up to five C1 systems were incorporated to work with a total cell count of 1,774 individual cells producing successful single-cell libraries from biologically meaningful experiments. This paper is the 10th peer-reviewed publication featuring the C1 system.

About Fluidigm

Fluidigm (NASDAQ:FLDM) develops, manufactures, and markets life science analytical and preparatory systems for growth markets such as single-cell biology and production genomics. We sell to leading academic institutions, clinical laboratories, and pharmaceutical, biotechnology, and agricultural biotechnology companies worldwide. Our systems are based on proprietary microfluidics and multi-parameter mass cytometry technology, and are designed to significantly simplify experimental workflow, increase throughput, and reduce costs, while providing excellent data quality. Fluidigm products are provided for Research Use Only. Not for use in diagnostic procedures.

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