Acquiring Cellular Spatial Information Using Unique Light-Sensitive DNA Barcodes

Tech ID: 33730 / UC Case 2023-886-0

BACKGROUND

The function of a cell is closely tied to its spatial location within a tissue, and its organization alongside other cells is a key determinant in tuning its cellular function. While capturing the spatial structure of a tissue is central to understanding cellular function, current methodologies for single-cell RNA sequencing (scRNA-seq) require the dissociation of a tissue into individual cells, resulting in a loss of all positional information for each of those cells. Several methods have been developed to capture the transcriptome of single cells while retaining positional information; however, these genome-wide methods typically do not have spatial resolution at the level of individual cells, fail to capture positional information outside the designed capture spots/grids and are not able to make other molecular measurements from a cell. Additionally, these methods are limited to profiling fixed instead of live cells, so they cannot capture tissue dynamics in real time, and their mRNA capture efficiency is low compared to standard scRNA-seq methods.

DESCRIPTION

Researchers at the University of California, Santa Barbara have introduced the concept of single-cell Spatial Transcriptomics and Multiplexed Profiling, or *scSTAMP-seq*, which captures the transcriptomes of every cell within a field of view at the spatial resolution of individual cells. Cholesterol-tagged UV-sensitive oligonucleotides are incorporated into cell membranes and then spatially-imposed light gradients are applied to optically “stamp” the position of each cell prior to tissue dissociation and single-cell sequencing. scSTAMP-seq is completely modular and can be combined downstream with any single-cell sequencing technology or measurement, enabling rapid multiomic single-cell phenotypic profiling that can access the genetic diversity present in biological systems. This technology could be used to create kits to provide a sensitive and high-throughput mapping of the transcriptome and epigenome at single-cell resolution for applications in both fundamental and clinical research.

ADVANTAGES

- Enables high-throughput mapping of the transcriptome and epigenome at single-cell resolution
- Works on live and fixed cell cultures/tissues
- Can be used in conjunction with other NGS transcriptomic/epigenomic methods, including technologies that do not have single cell resolution and require pre-fixed tissue samples
- Lowers costs and simplifies library construction with easy multiplexing
- Easily adaptable to other laboratories

APPLICATIONS

- Genetic research
- Cancer biology
- Cell and gene therapy

PATENT STATUS

Country	Type	Number	Dated	Case
Patent Cooperation Treaty	Published Application	2024/173380	08/22/2024	2023-886

Additional Patent Pending

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OTHER INFORMATION

KEYWORDS

DNA, Cellular, Cancer, Gene therapy, Cell therapy, Genes, Genetic research, Cells

CATEGORIZED AS

- **Medical**
  - Disease: Cancer
  - Gene Therapy

RELATED CASES

2023-886-0

ADDITIONAL TECHNOLOGIES BY THESE INVENTORS

- Optogenetic Control of the Integrated Stress Response

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