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Breakthrough Technology: RIBOmap Explores Subcellular Localization of Protein Synthesis

Jessi White
BioSci Publisher
Corresponding author email: jessi.j.zhang@foxmail.com

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On June 30, 2023, the research paper titled "Spatially resolved single-cell translatomics at molecular resolution" published in "SCIENCE" generated significant enthusiasm among biologists. This paper introduces a novel method and approach for exploring protein synthesis and gene expression regulation within cells.

The research report describes a new method called RIBOmap, which detects the translation process of protein synthesis at spatial and single-cell resolution. By combining targeted sequencing strategies with three-dimensional in situ localization and highly multiplexed in situ sequencing reads, researchers were able to simultaneously detect the translation of thousands of genes' mRNA, providing detailed information about protein synthesis.

The significance of this research lies in its contribution to filling the gap in studying protein synthesis at the cellular and tissue levels. Gene regulation operates at both the transcription and translation levels, but traditional methods primarily focus on mRNA expression levels, paying less attention to the correlation between mRNA and proteins. The emergence of RIBOmap addresses this issue by directly detecting mRNA during translation, thus providing more accurate information about protein synthesis.

This study represents the first application of RIBOmap in HeLa cells, revealing the dependency of translation on the cell cycle and subcellular localization. Through the analysis of translation for 981 genes, significant differences in translation were found across various stages of the cell cycle and subcellular compartments. These findings highlight the importance of the cell cycle and subcellular localization in the regulation of translation, unveiling a more nuanced level of gene expression control.

Furthermore, the researchers applied RIBOmap to mouse brain tissue slices, successfully obtaining single-cell translation profiles within intact tissue. Through the analysis of 5 413 genes, they identified and characterized translation profiles of multiple brain cell types, revealing spatial patterns of protein synthesis across different cell types and brain regions. This provides new insights into intercellular interactions in brain function and developmental processes, and offers valuable clues for the in-depth study of brain disorders.

Another significant feature of RIBOmap is its ability to unveil the spatial distribution of translation at the subcellular level. Through co-localization analysis of genes, the researchers discovered translation modules that exhibited highly correlated subcellular spatial organization. These translation modules were closely associated with specific cellular functions and pathways, such as protein synthesis machinery, synaptic transmission, and organelle-related translation. These findings emphasize the importance of protein synthesis in subcellular localization and the coordination of translation within specific cellular regions.

The study also revealed a connection between the cell cycle and translation regulation. By analyzing the translation profiles of cell cycle-related genes, the researchers found that these genes displayed highly coordinated translation patterns at specific cell cycle stages. This aligns with the requirements and regulatory mechanisms of the cell cycle, indicating the significant role of the cell cycle in temporal and spatial control of translation.

In summary, RIBOmap, as an emerging technological platform, provides us with a fresh perspective to study the complexity of gene expression regulation and protein synthesis. Its strengths lie in its ability to provide spatial and single-cell resolution information on protein synthesis, taking into account the regulation of translation by the cell cycle and subcellular localization. Through its application in studying brain tissue, researchers have also demonstrated RIBOmap's capability to explore cell types and spatial patterns within complex tissues.

However, this research is still in the laboratory stage and faces certain limitations and challenges. For instance, the RIBOmap method currently requires further technical improvements to enhance its accuracy and sensitivity. Additionally, in practical applications, data analysis and interpretation present complexities and challenges. Researchers need to develop more computational tools and methods to handle and interpret large-scale spatial and single-cell translation data.

This study provides us with a powerful tool and platform to explore protein synthesis at the spatial and single-cell levels, granting us a fresh understanding of gene expression and protein synthesis. It opens up new avenues for studying biological processes such as cellular function, development, and diseases. With ongoing technological advancements and further developments in its application, RIBOmap has the potential to become an important tool for investigating gene expression regulation in cells and tissues, offering deeper insights into the mysteries of life.

This article is based on the research paper published in Science on June 30, 2023, titled "Spatially resolved single-cell translatomics at molecular resolution" (Science 380, eadd3067, 2023. DOI: 10.1126/science.add3067).