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Histopathology Cytology and Transcriptomic Approaches in Microbes

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Introduction

Over the past ten years, single-cell transcriptomics (scRNA-seq), particularly in the fields of developmental biology, cancer, immunology, and neuroscience, has become crucial for biomedical research. Cells must be recovered whole and viable from tissue according to the majority of commercially available scRNA-seq procedures. This has precluded many cell types from study and largely destroys the spatial context that could otherwise inform analyses of cell identity and function. Nowadays, a growing number of commercially available technologies enable "spatial transcriptomics," or the spatially resolved, high-dimensional analysis of gene transcription. The methods we provide here fall into three categories: those that scan the positions of cells before analysis, use spatial arrays of mRNA probes, or record the locations of hybridised mRNA molecules in tissue [1].

Description

Lung cancer continues to be the main cause of cancer-related death despite recent advancements in treatment, which highlights the significance of gaining a greater understanding of the disease's complex tumour microenvironment (TME) in order to find novel therapeutic alternatives. While other studies have looked at the gut microbiota as a potential contributor to disease and response to treatment, previous studies have described the mutational, transcriptional, and immunological profiles of lung cancer. 2 3 But very little is understood about the lung intratumor microbiome, largely because there was little research done in the past because it was thought that lung parenchymal tissues were sterile. 4 However, recent developments in 16S rRNA sequencing, a technique for bacterial investigation that is independent of culture [2].

Numerous biological systems, including cancers, intestinal villi, liver lobules, and embryos, depend on the spatial structure of their cells to function. In the last ten years, computational techniques have been developed that use spatial gene expression data to discover genes with spatial patterns and to designate neighbourhoods within tissues. High-throughput technologies have been created to quantify gene expression in space. We present a curated review of the literature on spatial transcriptomics going back to 1987, along with a thorough analysis of trends in the field, such as the use of experimental techniques, species, tissues studied, and computational approaches used. Our goal is to comprehensively document spatial gene expression technologies and data-analysis methods. Our Review places present practises in a historical framework, and we draw field-specific conclusions from it [3].

The spatial organisation of cells is essential for the operation of many biological systems, including malignancies, intestinal villi, liver lobules, and embryos. In the past ten years, computer methods have been created that leverage spatial gene expression data to identify neighbourhoods within tissues and find genes with spatial patterns. Technologies with high throughput have been developed to measure gene expression in space. We offer a meticulous study of the developments in the area, including the utilisation of experimental methods, species, tissues investigated, and computational methodologies.

In reaction to their surroundings, microbes change their transcriptome profiles. By comparing the transcription levels of particular genes, the physiological conditions encountered by a microbial community can be deduced via meta-transcriptomic sequencing. To determine the precise genes from which RNA readings come, this approach needs precise reference genomes. Such an approach should also prevent transcript count biases caused by variations in organism abundance. The "diametric ratio" method, which compares transcript ratios of genes with opposing transcription responses, was used to remove biases resulting from variations in organismal abundance. Sample-specific meta-genomic assembled genomes (MAGs) were used as reference genomes to precisely identify the origin of RNA reads.

With an average of 3 to 6 ARIs per year, acute respiratory infections (ARI) are a primary cause of morbidity and mortality in infants and young children. Because ARIs involve a wide variety of viruses, bacteria, and fungal pathogens, with frequent co-infection among them, identifying the diversity of pathogens responsible for them remains difficult. As the "gold standard" for ARI diagnosis, conventional diagnostic techniques like PCR, serological type, bacterial culture, and antibody detection are frequently employed. However, it is still challenging to simultaneously identify all probable ARI pathogens and capture novel or unusual respiratory infections, despite current efforts to integrate numerous pathogens in a single assay [4,5].

Conclusion

Since it is usually believed that the condition of individual cells

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will be comparable to that found in the population, microbiologists typically research populations rather than single cells. Recent research has revealed that individual cell behaviour can differ significantly from population behaviour, highlighting the necessity of expanding traditional microbiology research to the level of the single cell. Single-cell microbiology has tremendously benefited from recent technology developments, including flow cytometry, next-generation sequencing (NGS), and microspectroscopy, which have increased our understanding of the individuality and heterogeneity of bacteria in many biological systems. In particular, the use of various 'omics' in single-cell research has illuminated how individual cells perceive, react to, and adapt to their environment, how heterogeneity develops in response to external stress, and how it ultimately dictates how a cell behaves.

Microbiologists typically investigate the physiology, internal connections, and even genetic information of microbes. In the past, all of these studies have been conducted at the population level, often using millions to billions of cells for examination in bulk and presuming that each cell's state is comparable to that of the population as a whole. These results are certainly instructive, but they frequently ignore any potential population heterogeneity. Recent research, however, suggests that cell-to-cell heterogeneity in isogenic populations may be an order of magnitude more than previously believed, underscoring the need of extending conventional microbiology research to the single-cell level.

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Conflict of Interest

There are no conflicts of interest by author.

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