

EDITORIAL

Single Cell Sequencing Coming of Edge

As the biology and medical science are developing, we are realizing cell heterogeneity makes pathophysiology mechanism very comprehensive. For instance, tumor cell heterogeneity is an obstacle for the treatment of the diseases. The solid organs are composed of millions of cells in which there are many different cell types. Thanks to the rapidly developing high-throughput sequencing technology, every single cell genomics in one experiment can be observed. The single cell sequencing era is coming. Now we can capture and analyze the difference among cells and the interaction between cells and microenvironments. Although there are many high impact studies published using single cell sequencing, this method is still an emerging technology. Many problems need to be solved, for instance, different methods have different sequencing depths and the question arises how to choose a suitable method for our experiment should be considered before the start. In this issue, we want to systemically introduce the single cell sequencing and review recent advances in this field. I believe this special issue will provide valuable inspirations for the readers.

The first letter article *Discrepant mRNA and Protein Expression in Immune Cells* by Li *et al.* [1] demonstrated an interesting and important phenomenon in immune research using single cell RNA sequencing (scRNA-seq). The disconnect between the levels of mRNA and surface protein expression has confused many researchers. In this study, the authors suggested that scRNA-seq should be combined with other sequencing methods in single-cell studies (*e.g.*, CITE-seq) in certain circumstances. The first review entitled *Single-cell RNA Sequencing in Immunology* by Cao *et al.* [2] systemically introduced the history, development, methodology of scRNA-seq and its application in immunology. The advantages of single-cell sequencing include (1) accuracy and sensitivity over traditional methods, and the ability to accurately analyze gene expression in each cell; (2) detection of the transcriptomics of rare cells or newly found cells without known markers; (3) ability to analyze and interpret the intercellular relationship in the microenvironment; and (4) ability to distinguish and compare among cell populations objectively. This review summarized the mainstream applications of single cell sequencing, for instance, cell anatomy, redefining cellular markers and so on. The next two reviews introduced recent advances of single cell sequencing in stem cell research and cardiovascular diseases.

In *Single-cell Sequencing in the Field of Stem Cells*, Chen *et al.* [3] introduced new discoveries of single cell sequencing in pluripotent stem cells, tissue-specific stem cells and cancer stem cells. Variation and heterogeneity between cells are the basic characteristics of stem cells. This review might help readers to understand the importance of investigating stem cells as different individuals. The cardiac system is a combination of a complex structure, various cells, and versatile specified functions and sophisticated regulatory mechanisms.

The review entitled *Single-cell RNA Sequencing: In-depth Decoding of Heart Biology and Cardiovascular Diseases* by Dr. Chen [4] reviewed recent advances in single cell studies of cardiovascular system and summarized new insights provided by scRNA-seq in heart developmental sciences, stem-cell researches as well as normal or disease-related mechanisms.

In the last article of this issue, Gao *et al.* [5] compared two mainstream scRNA-seq platforms in the review *The Comparison of Two Single-cell Sequencing Platforms: BD Rhapsody and 10x Genomics Chromium*. Although these two platforms follow a similar basic strategy, there are still some differences between them in terms of mechanisms, operations and output results from same experiments. In most labs, it is not practical to choose both platforms. Therefore, we have to be familiar with their similarities and differences. I think this review is able to provide valuable information.

I believe all the articles and reviews in this issue will attract your attention and give you inspiration for your further research.

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