International Journal of Biochemistry and Cell Biology 116 (2019) 105596

Contents lists available at ScienceDirect

International Journal of Biochemistry and Cell Biology

journal homepage: www.elsevier.com/locate/biocel

Single cell genomics

Single-cell analysis has an old history but has undergone a rapid transformation in the past decade. Three and a half centuries ago, Robert Hooke found pores in a thin cutting of cork under the microscope and termed them 'cells', which were then recognized as the most fundamental building blocks of all life on earth. Since then, single-cell analysis became established and has been continuously evolving. From the invention of the microscope to the development of antibodies for the labeling of cellular states and subsets to the discovery of fluorescent proteins for live imaging, and later to the establishment of transgenic approaches for cell lineage tracing, single-cell techniques have driven biological discovery for centuries. Yet the molecular and biochemical aspects of the cell have been primarily assessed when cells are treated as groups but not as individuals. This is problematic as hidden cell-to-cell variations exist even in the seemingly homogeneous cellular populations. As a result, the diverse cellular characteristics are often buried in the bulk measurement of millions of cells together. It was not until recently that single-cell analysis merged with the newly developed technologies in genomics and spurred a worldwide pursuit of single-cell studies, investigating the genome, transcriptome, and epigenome on a deeper level.

The most mature of these technologies is single-cell RNA-sequencing which is almost routine in profiling cellular heterogeneity nowadays. Now the technological development has shifted to another trend: to measure epigenetic states including DNA methylation, chromatin accessibility, chromosome conformation or even the combination of methods to simultaneously measure two or more modalities in single cells. On the other hand, single-cell whole-genome DNA sequencing can provide valuable information about functional mutation and copy number variations of cells. Modern single-cell genomics technologies are evolving at a faster pace than ever, which has also imposed a new demand on statistical and computational methods to extract meaningful information from the data and deliver new biological insights and knowledge.

With this background, we are excited to present in this Special Issue "Single Cell Genomics" the advances of single-cell analytical techniques and bioinformatic methods. The issue will also showcase the utility of single-cell genomics in basic research and preclinical or clinical applications. The editors would very much like to thank the authors and referees of the articles in this Special Issue for their contributions.

Acknowledgements

Hong Kong Research Grant Council - Collaborative Research Fund (C4054-16G).

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https://doi.org/10.1016/j.biocel.2019.105596

Available online 30 August 2019