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Editorial: Attention to finer-details: Progression from bulk to single-cell studies

ARTICLE INFO

ABSTRACT

This editorial is focused on the special issue titled as emerging field of single-cell technologies leading to comprehensive understandinh of biology.

Cells are building blocks of a comprehensive biological signaling network resulting in a functional living organism. Like most diseases, cancer represents a heterogenous cellular state with an amalgam of the normal and malignant cells in a tumor. Therefore, understanding of the cellular signaling at the single cell level is seminal for a comprehensive understanding of biology. Unsurprisingly, single cell based innovative technologies are increasingly taking center stage in recent biological analysis. Single cell analysis provides a deeper and clearer picture of normal, and disease related cellular states. This special issue is dedicated to bringing forth the recent advances in the field of single-cell technologies. It also focuses on translational aspects of this emerging field of scientific research with a direct impact on the advancement of biology. As a journal, we have compiled a list of primary research/review articles for this special issue. These manuscripts are prepared by ~5 different/ independent research groups across the globe with more than 25 contributing authors/coauthors. The primary theme of all contributing manuscripts is focused on single cell-based technologies spanning from single-cell transcriptomics, single-cell RNA-seq, to single-cell proteomics. For example, Petrosius and Schoof have provided a most current and up-to-date landscape of single-cell proteomics research and its technical standing compared to the more advanced counterparts like single-cell genomics and transcriptomics. Although the field of single-cell proteomics is rapidly evolving due to constant technical advancement in the proteomics sample preparation and mass spectrometry areas, it is already exciting to understand the protein functions at the single-cell regardless of the normal or disease conditions. Furthermore, single-cell proteomics has a direct therapeutic potential as we can now understand the functional unit of a cell i.e., proteins. Article by Srivastava et al. has focused on the recent understanding of skin biology as well as melanoma utilizing bulk RNA sequencing and related single-cell transcriptomics approaches. Given melanoma is a heterogeneous disease it is important to have a single cell-based analysis of cancer signaling resulting in a malignant transformation of the normal skin cells. This article provides a closer view of single-cell RNA-seq approaches to decipher complex melanoma biology. Furthermore, a research article

titled as tetramer-aided sorting and single-cell RNA sequencing facilitate transcriptional profiling of antigen-specific CD8+ T cells by Rajasekaran et al. has focused on how single cell-based cell sorting could be instrumental in gene signature and predicting cancer immunotherapy response/resistance. More specifically, the authors have shown how pMHC tetramer-aided sorted human CMV pp65 antigen-specific CD8+ T cells could be used as a model for transcriptional studies of antigen-specific CD8+ T cells at single cell level and utilized to predict antigen-specific response (ASR) with a direct therapeutic implication in the field of immunotherapy. The next article in the special issue focused on Multiple Myeloma (MM). It is a form of leukemia with heterogeneous in nature. Gandhi et al. has summarized current perspectives on inter-ethnic variability in MM using single-cell focused approaches. More specifically, this article discusses the emerging single-cell technologies and applications in MM, role of non-coding RNAs with respect to MM, and lastly how single-cell based research approaches hold a great promise in the overall understanding on a clonal diversity in MM. Lastly, a study focused on Non-Small Cell Lung Carcinoma (NSCLC) with publicly available scRNA-seq datasets by Sultana et al. utilized bioinformatics based approaches to understand the nuances of the cancer signaling at the single-cell level and implicated to potential biomarkers which could be used for diagnosis and treatment. This is an interesting study because the authors have implemented advanced bioinformatics methods and machine learning tools to understand the publicly available dataset at the single-cell level. Overall, this special issue is dedicated to bringing attention to the rapidly evolving field of single-cell technologies and its seminal role in the understanding of single-cell biology.

Author's contribution

Pankaj Dwivedi conceptulize, wrote, and edited the editorial.

Declaration of Competing Interest

The author declare no conflict of interest.

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