Pratik, Transcriptomics 2018, 6:2
DOI: 10.4172/2329-8936.1000143

Transcriptomics: Open Access

Short Communication Open Access

Transcriptomics of Single Cell: New Discoveries to Become Basis for Future Studies

Pratik K*

Department of Electronics and Tele Communication, Allied Analytics LLP, India

***Corresponding author**: Pratik K, Content Writer, Department of Electronics and Tele Communication, Allied Analytics LLP, India, Tel: +91 20 66346060; E-mail: pratik.kirve@alliedanalytics.com

Received: August 01, 2018; **Accepted:** August 17, 2018; **Published:** August 20, 2018

Short Communication

Single-cell transcriptome profiling has been an indispensable tool used for determining cell type, transcriptomic signatures, and single cell transcriptomics of ncRNAs. This technique could bring about a paradigm shift in disease management and could even become the basis of further studies.

Transcriptomics: an overview

Transcriptomics is the process of using high-throughput techniques to study the expression levels of mRNAs in a cell. Transcriptome which is an umbrella term for all RNA molecules, play a vital role in studying human tissues at the cellular level, as it is a dynamic and good representative of the cellular state. This make it an indispensable tool to understand how genes are expressed and interconnected.

Trends and scope

Numerous studies have been conducted across the globe to discern the nuances of the genetic make-up alongside making new breakthroughs in the field of genetics. In line with this trend, private organizations such as Thermo Fisher Scientific, Inc. have taken significant proactive steps to make inroads in disease profiling and treatment using novel techniques. For instance, Thermo Fisher Scientific's Ion Torrent Transcriptome Profiling Grant Program focuses on the importance of a conducting gene-level expression analysis for discovering novel biomarkers, which essentially play a vital part in prognostics, cancer diagnostics, and experimental therapy. Moreover, research and development activities focusing on the role of transcriptomes in single cells have been gaining momentum lately, which makes this field lucrative for investment. According to a research firm, Allied Market Research, the global transcriptomics market is pegged to reach $7.95 billion by 2023, which could be attributed to the surge in funding by private and government organizations for R&D activities. Thus, current breakthroughs from major research activities in the field of transcriptomics would become the basis for future research.

Single-cell transcriptome profiling for cell type and cell lineages

According to two new studies published in the Science journal, single-cell transcriptome profiling can be used to determine the cell type and cell lineages of a whole complex animal. In both the studies, researchers have used Drop-seq, a high-throughput transcriptome-profiling platform, to study cell types in a model organism, *Schmidtea mediterranea*. This platform was developed in collaboration with Harvard University and the Broad Institute.

Furthermore, researchers from the Massachusetts Institute of Technology and the Whitehead Institute for Biomedical Research were able to identify the transcriptomes from each cell type of *S. mediterranea*. Moreover, they could sequence nearly 50,000 single cells alongside determining nearly 44 distinct major cell clusters and nearly 150 sub-clusters.

Researchers expressed that, "Much like the genome of an animal, we propose this atlas-like dataset of cell-type transcriptomes can serve as a resource fueling an immense amount of research, not only in planarians, but in other bilaterians with similar cell types".

In a similar study, researchers from Berlin's Max-Delbrück Center for Molecular Medicine, Germany were able to create a cell type atlas for *S. mediterranea* and even forming a lineage tree. They were able to sequence nearly 20,000 individual cells as well determine nearly 51 cell clusters and 23 cell lineages.

Transcriptomic signatures change with aging

With ageing, organisms develop a relationship between cancer and degenerative chronic diseases at the transcriptome level. However, the risk of developing cancer reduces with age among geriatric population, but the chances of contracting a degenerative chronic disease increases significantly [1].

Researchers at Christian-Albrechts-University, Kiel, Germany stated that this change could be due to a shift in gene transcription. They studied the transcriptomes of four vertebrate species to determine a transcriptomic signature for aging. In their study, they used two aging time points for developing transcriptomic signatures associated with aging and also found different regulated processes occurring with age.

These signatures outlined the up-regulation of the immune system along with the down-regulation of the cell cycle. Moreover, they represented processes of cell differentiation among the elderly. As reported in Nature Communications, they discovered that transcriptomic signatures change with age and become similar to those found in degenerative diseases and less like those found in cancer [2].

"These results reveal a fundamental trade-off between cancer and degenerative aging diseases that sheds light on the pronounced shift in their epidemiology during aging," wrote by Kaleta and his colleagues, in their paper.

Single cell transcriptomics of ncRNAs

It was recently discovered that single cell within tissues is heterogeneous in nature. Several researchers conducted a study to determine the functionality of this heterogeneity through single-cell variation of non-protein coding RNA expression. As non-coding RNAs

(ncRNAs) play a crucial role in genomic regulatory functions, studying variations in them could offer insights on single cell expression variation. In a review published in WIREs RNA, a group of scientists presented their findings on ncRNA expression at single cell level. The study outlined that ncRNA shows as much variability as protein-coding RNA. Moreover, some of the classes of ncRNA may show more single cell variability than others [3].

Many studies focus on the expression of long non-coding RNAs (lncRNA), a molecule with more than 200 or longer base pairs that play a significant role in development and association with various diseases in humans such as cancer and other cardiovascular diseases. Some studies outline the cell-specific restriction of LncRNA expression, indicating that these molecules influence differentiation in cell lineages. In addition, it has been found that patterns of cell-specific expression are labeled for species-specific lncRNAs. These research studies outline that cell-specific lncRNAs control the fate of species-specific cells. Further studies on the development of technologies for measuring a broad spectrum of ncRNAs and profiling them in research of single cell could set the stage for various studies in future as well as find cure to terminal diseases.

Conclusion

The recent studies regarding single cell transcriptomics form a basis for the future studies. Researchers can build their new research studies based on these findings and inspire new breakthroughs. In addition, there needs to be funding from investors and grants from universities to encourage new studies. These studies would help in learning more details about the cell differentiation in human cells and prevent diseases in the future.

References

1. Plass M, Solana J, Wolf FA, Ayoub S, Misios A, et al. (2018) Cell type atlas and lineage tree of a whole complex animal by single celltranscriptomics. Science 360: 1723.
2. Kaleta C, Irizar PA, Schäuble S, Esser D, Groth M, et al. (2018) Transcriptomic alterations during ageing reflect the shift from cancer to degenerative diseases in the elderly. Nature Communications 9: 327.
3. Katerina AB, Gawronski, Junhyong K (2017) Single cell transcriptomics of noncoding RNAs and their cell-specificity. Wiley Interdisciplinary Reviews: RNA 8: 1433.