

Systems Biology to Gene Function of Plant Tolerance to Abiotic Stresses

Matthew C*

Department of Pharmaceutical Biotechnology Targeted Drug Delivery Research Center, School of Pharmacy, Mashhad University of Medical Sciences, Mashhad, Iran.

EDITORIAL NOTE

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. These results reveal a fundamental between cancer and degenerative aging diseases that sheds light on the pronounced in their epidemiology during aging,” wrote by Kalera and his colleagues, in their paper. Single cell transcriptomics. 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. Play a crucial role in genomic regulatory functions, studying variations in them could insights on single cell expression variation. In a review published in WIREs RNA, a group of scientists presented their findings on RNA expression at single cell level. His study outlined that RNA shows as much variability as protein coding RNA. Moreover, some of the classes of RNA may show more single cell variability than others. Many studies focus on the expression of long non-coding RNAs (RNA), 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. 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.

Some studies outline the cell-specific restriction of RNA 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 RNAs. These research studies outline that cell-specific RNAs control the fate of species specific cells. Further studies on the development of technologies for measuring a broad spectrum of RNAs 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. 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. 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. He were able to sequence nearly 20,000 individual cells as well determine nearly 51 cell clusters and 23 cell lineages.

*Correspondence to: Matthew C, Department of Pharmaceutical Biotechnology, Targeted Drug Delivery Research Center, School of Pharmacy, Mashhad University of Medical Sciences, Mashhad, Iran. Email: leesweonmgn@gmail.com

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