In Stevia Rebaudiana, New MicroRNAs were Discovered, and their Targets werePredicted

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EDITORIAL NOTE

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. He 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 significant researchers at Christian-Albrechts-University, Kiel, Germany stated that this change could be due to a gene transcription. He 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.

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.

For RNA cloning, we suggest beginning with polyadenylated RNA (poly(A)+ RNA), which contains courier RNA (mRNA) insteadof complete RNA. 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. He were able to sequence nearly 20,000 individual cells as well determine nearly 51 cell clusters and 23 cell lineages.

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