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Understanding the Meaning of Transcriptome and its Advances in Recent times

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INTRODUCTION

Transcriptome is the study of the transcriptome, which is the complete set of RNA transcripts produced by the genome in specific cells under specific conditions or using high-throughput techniques such as microarray analysis. By comparing transcriptomes, it is possible to identify genes that are differentially expressed in different cell groups or in response to different treatments. In the early 1990s, the first attempt was made to study the entire transcriptome. Since the late 1990s, technological advances have constantly changed this field, making transcriptomics a widely used field in life sciences. Microarrays that quantify a set of present sequences and RNA Seq that capture all transcripts using high-throughput sequences are two important modern approaches in this area.

DESCRIPTION

The amount of data generated by each transcriptome experiment has increased as technology has advanced. As a result, data analysis technology is continually improving, enabling more accurate and efficient analysis of larger volumes of data than ever before. The more transcriptomes are collected and shared by researchers, the more useful the transcriptome database will be. It is almost impossible to decipher the information contained in the transcriptome.

Transcriptomics-specifically whole transcriptome sequencing is a technically difficult and extremely beneficial research technique, but it is not yet ready for application in mainstream medicine. Existing clinical transcriptome analysis applications are limited to panel tests that use microarrays or qRT-PCR to examine the activity of a subset of genes known to provide prognostic information about a disease, informing clinical decisions about how much, or how little, treatment a patient requires. The RNA sequence is the same as the DNA sequence to which it was transcribed. As a result, researchers can determine when and where each gene is turned on or off in the cells and tissues of an organism by examining the complete collection of intracellular RNA sequences (transcriptomes).

DNA (Deoxyribonucleic Acid) is a long coiled molecule that contains the information needed to build and maintain cells and constitutes the human genome. These instructions are written in the form of four chemical “base pairs” located in 20,000 to 25,000 genes. To carry out the instructions, the DNA must be “read” and transcribed, that is, replicated into RNA (ribonucleic acid). The transcriptome is a type of gene reading, and the transcriptome is a collection of all gene readings in a cell. RNA comes in many forms. The most common form known as messenger RNA (mRNA) is essential for protein synthesis. mRNA is transcribed by genes, and mRNA transcripts are transcribed into the ribosome, a molecular mechanism.

In contrast to the microarray method, the sequential method directly sequences the cDNA. Initially, Sanger sequences were used in cDNA or EST libraries, but this method is relatively inexpensive, expensive, and generally unstandardized. Tag-based methods have been developed to overcome these limitations. This includes genes [deleted] SAGE for continuous expression, gene cap analysis [deleted] CAGE and the most consistent signature sequence (MPSS) These tag-based sequences are extremely powerful and can provide accurate digital “genetic” levels. However, most are based on expensive Sanger sequencing technology, and it is not possible to separate a significant portion of the short tags from the reference genome. In addition, only part of the text is analyzed and the isoforms are usually not separated from each other. This drawback reduces the use of traditional sequencing technology in interpreting transcriptome formation [1-4].

CONCLUSION

Transcriptomics are possible every decade or more and are

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characterized by the development of new writing methods that obsolete previous methods. The first attempt to partially map the human transcriptome was published in 1991 and reported the sequence of 609 mRNA in the human brain. In 2008, 2 million manuscripts collected from 16,000 genetic materials were published and in 2015, hundreds of transcriptomes were published. In the meantime, regional transcriptomes are often created for a variety of diseases, tissues, or individual cells. This explosive increase in transcriptomics is driven by the rapid development of new technologies, sensitivity and cost-effectiveness. Transcript mix has paved the way for a complete understanding of how genes are expressed and connected. Over the last three decades, the success of the methodology has continuously changed the profile of the transcriptome and redefined what can be studied. Integrating transcriptome data with other omics further integrates the concept of cellular complexity and facilitates complete biomedical research practices.

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CONFLICT OF INTERESTS

The author has nothing to disclose and also state no conflict of interest in the submission of this manuscript.

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