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The art of Epitranscriptomics

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Introduction

Epitranscriptomics is a branch of science from epigenetics that studies the various roles and regulations of RNA, such as: RNA editing, RNA modification, and regulation of noncoding RNA. In short, epitranscriptomics is RNA epigenetics.[1,2]

Modification of RNA turned out to be beyond the expectations of scientists. Moreover, after the systematic constellation between next-generation sequencing (NGS), antibody immunoprecipitation, and medication.[3]

Some of the advantages of this reversible RNA modification can be felt in several ways, such as: playing an important role in the regulation of cellular fate determination, sex determination, differentiation, and other benefits.[4]

The ability of the researchers to create genome-wide maps to understand 95% of RNA modifications is currently very limited by the lack of available selective antibodies and medications.[5]

The third generation sequencing platform, for example: Oxford Nanopore Technologies (ONT), has successfully laid a fundamental foundation for epitranscriptomics.[6]

Scientists have benefited from ONTs, for example in the identification of new isoforms, direct identification of modified RNA and DNA, accurate transcriptome profiling, estimation of the 3′ poly(A) tail length, and studies of structural variation within various genomes.[7,8]

In addition, this ONT technology allows direct measurement of RNA and DNA molecules without prior amplification or fragmentation, thereby not limiting the length of RNA or DNA molecules that can be sequenced.[9]

Besides being useful for overcoming the limitations of the short-read sequencing process, this ONT technology platform can also directly measure the modifications of RNA and DNA in their native molecules.[10]

ONT is indeed able to overcome various problems that have not been solved by NGS technology. However, ONT also has limitations, namely the lack of standardized pipelines to carry out the ONT output analysis process. This limits the reach of the ONT to the rest of the scientific community.[11]

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Conflicts of interest

The authors have no conflicts of interest to declare.

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