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Transcriptomics:Open Access

Short Communication

A Short Note on Transcriptomics and its Applications

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DESCRIPTION

Transcriptomics establishes a connection between the genome, proteome and the cellular phenotype. It is an examination of the RNA transcripts generated by the genotype. Transcriptome refers to the process of producing transcripts during the biological transcription process. The collection of all RNA transcripts, both coding and non-coding, found in a single cell or in a population of cells is known as the transcriptome.

Applications of transcriptomics

Diagnostics and disease profiling: Numerous biological research fields, including detection of diseases and profiling have extensively used transcriptomic techniques. Using RNA-Seq techniques, transcriptional start sites have been extensively identified. Determination of these variants is essential for the interpretation of disease-association studies, since these regulatory elements are significant in human disease. RNA-Seq can also detect gene fusions, allele-specific expression and Single Nucleotide Polymorphisms (SNP) which are associated with disease. Retrotransposons are transposable elements that multiply within the genomes of eukaryotic organisms by a process called reverse transcription. The transcription of endogenous retrotransposons may affect the transcription of nearby genes through a variety of epigenetic pathways and results in diseases which can be revealed by RNA-Seq. The possibility for employing RNA-Seq to study immune-related diseases is fast growing as a result of the capability to sequence patient-derived T cell and B cell receptor repertoires and to dissect immune cell populations [1].

Human and pathogen transcriptomes: A well-established technique for measuring gene expression variations, discovering new virulence factors, forecasting antibiotic resistance and revealing host-pathogen immunological interactions is RNA-Seq of human pathogens. Transcriptomic research has mostly concentrated on the host or the pathogen. Recently, dual RNA-Seq has been used to profile RNA expression simultaneously in the pathogen and host during the infection process.

Responses to environment: Identification of the genes and processes that react to and mitigate biotic and abiotic environmental stresses is made possible by transcriptomics. The non-targeted approach of transcriptomics enables the discovery of fresh transcriptional networks in intricate systems.

Gene function annotation: Identification of the roles played by genes responsible for certain phenotypes have been made possible by all transcriptomic approaches. It is appropriate for gene expression research of non-model species with non-existent or underdeveloped genomic resources, since RNA-Seq read assembly is not dependent on a reference genome [2]. Additionally, RNA-Seq can be utilized to locate previously undiscovered protein coding regions in already sequenced genomes [3].

Non-coding RNA: Transcriptomics is most frequently used to study mRNA information of a cell. But the same methods also apply to non-coding RNAs that perform direct tasks rather than being translated into proteins, such as those involved in protein translation, DNA replication, RNA splicing and transcriptional regulation. Numerous of these non-coding RNAs have an impact on diseased conditions, such as cancer, cardiovascular and neurological disorders [4].

CONCLUSION

Transcriptomics is an examination of the RNA transcripts generated by the genotype. Detection of diseases and profiling has extensively used transcriptomic techniques. Determination of the variants is essential for the interpretation of disease-association studies, since these regulatory elements are significant in human disease. Transcriptomic research has mostly concentrated on the host or the pathogen. Identification of the genes and processes that react to and mitigate biotic and abiotic environmental stresses is made possible by transcriptomics. Identification of the roles played by genes responsible for certain phenotypes have been made possible by all transcriptomic approaches. Transcriptomics is most frequently used to study mRNA information of a cell.

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