

A Mini Review on Gene Expression Rita B*

Abstract

A DNA molecule is more than just a long, monotonous string of nucleotides. Instead, it is divided into functional units known as genes. All cells use information encoded in their DNA to control or regulate protein synthesis. Gene expression refers to the process of turning on a gene to produce RNA and protein. All known life—eukaryotes (including multicellular organisms), prokaryotes (bacteria and archaea), and viruses—use gene expression to generate the macromolecular machinery for life. Gene expression is the most fundamental level at which the genotype gives rise to the phenotype in genetics. The regulation of gene expression is a highly complex process. Strictly speaking, "gene expression" refers to the process of a gene being activated until a mature protein is found in its corresponding compartment to perform its function and contribute to the expression of a cell's phenotype. The purpose of the expression studies is to detect and quantify messenger RNA (mRNA) levels of a specific gene. The rapid activation of gene expression in response to stimuli is largely controlled by RNA polymerase II-dependent transcription. Gene expression microarrays are being used to study RNA expression and may be used to derive profiles/signatures associated with tumour and normal tissue radio response. The events that occur during the transcription cycle in eukaryotes that are important for the rapid and specific activation of gene expression in response to external stimuli are discussed in this review.

Keywords: Gene expression; Eukaryotes; Prokaryotes; Messenger RNA; Transcription; Microarrays

G. Pulla Reddy College of Pharmacy,
Osmania University, Hyderabad, Telangana,
India

Corresponding author: Rita B

✉ badigeru.rita@gmail.com

G. Pulla Reddy College of Pharmacy,
Osmania University, Hyderabad, Telangana,
India.

Citation: Rita B (2021) A Mini Review on Gene Expression. Insights Biomed Vol.6 No.7:34

Received: July 05, 2021; **Accepted:** July 23, 2021; **Published:** July 30, 2021

Introduction

Proteins must be synthesized at the correct time for a cell to function properly. All cells use information encoded in their DNA to control or regulate protein synthesis. Gene expression refers to the process of turning on a gene to produce RNA and protein. Gene expression regulation conserves both energy and space. Because it would take a significant amount of energy for an organism to express every gene all of the time, it is more energy efficient to turn the genes on only when they are needed. Furthermore, expressing only a subset of genes in each cell saves space because DNA must be unwound from its tightly coiled structure in order to be transcribed and translated. Gene expression is the most fundamental concept in genetics. The genotype is represented by the genetic information stored in DNA, whereas the phenotype is the result of that information's "interpretation." Such phenotypes are frequently expressed through the synthesis of proteins that control the structure and development of the organism or act as enzymes catalyzing specific metabolic pathways [1].

Gene expression is the most fundamental level at which the genotype gives rise to the phenotype, i.e. observable trait, in genetics. The genotype is represented by the genetic information stored in DNA, whereas the phenotype is the result of that information's "interpretation." Such phenotypes are frequently manifested by the synthesis of proteins that control the structure and development of the organism [2].

Genes can be conveniently grouped under two classes:

1. Constitutive genes
2. Inducible genes

A constitutive gene is one that is transcribed at a relatively constant level regardless of the cell's environmental conditions. An inducible gene is one whose expression is either responsive to environmental changes or dependent on cell cycle position [3].

Expression of gene

Because of the complexity of each step in the pathway from

gene to protein, they have had to be studied in isolation, and the majority of our knowledge in this area has come from classical biochemistry. Gene regulation is the process by which a cell controls which genes, among the many genes in its genome, are "turned on" (expressed). Because of gene regulation, each cell type in your body has a unique set of genes [4].

Prokaryotic gene expression is primarily controlled at two levels: transcription and translation. Regulation is also influenced by mRNA breakdown and protein modification. A metabolic pathway through a chain of reactions is a broad technique in which chemical changes occur in a living organism. The enzymes are in charge of each step. The production of an enzyme occurs once more [5].

The synthesis of mRNA is referred to as transcription. Transcription is controlled at or near a gene's promoter region. The cell can modulate the amount of message transcribed through the structural gene by controlling the ability of RNA polymerase to bind to the promoter. If RNA polymerase has bound, it can modify transcription once again. Jacob and Monod (1961) introduced the operon model to describe gene activity regulation for the first time. In order for a cell to maintain homeostasis; gene expression must be properly regulated. Genes are frequently clustered together and co-transcribed in prokaryotes, resulting in small sets of genes directing a given cellular function being either all ON or all OFF. The mRNA sequence is decoded to specify the amino acid sequence of a polypeptide during translation. The name translation refers to the fact that the mRNA sequence's nucleotide sequence must be

translated into a completely different "language" of amino acids. The central dogma of molecular biology is this directional flow of information. An operon is a group of genes that are all controlled by the same regulatory region and are located in tandem. Cells' responses to extracellular signals typically necessitate changes in the expression of many genes, potentially involving several distinct metabolic pathways [6].

We can create 'gene expression profiles' that characterize the dynamic functioning of each gene in the genome by measuring transcription levels of genes in an organism under different conditions, at different developmental stages, and in different tissues [7].

Discussion and Conclusion

Cells can rapidly adjust their protein levels on the degradative side of the balance by enzymatically breaking down RNA transcripts and existing protein molecules. Both of these actions result in a reduction in the amount of certain proteins. This breakdown is frequently linked to specific events in the cell. Cells must be able to respond to changes in their environment in order to survive. This adaptability is dependent on the regulation of the two main steps of protein production, transcription and translation. Cells have the ability to control which genes are transcribed and which transcripts are translated, as well as biochemically process transcripts and proteins to alter their activity. Both prokaryotes and eukaryotes regulate transcription and translation, but eukaryotes' regulation is far more complex.

References

- 1 Velculescu VE, Zhang L, Vogelstein B, Kinzler KW (1995) Serial analysis of gene expression. *Science* 270: 484-487.
- 2 Brazma A, Vilo J (2000) Gene expression data analysis. *FEBS letters* 480: 17-24.
- 3 McAdams HH, Arkin A (1997) Stochastic mechanisms in gene expression. *Proc Nat Acad Sci* 94: 814-819.
- 4 Emilsson V, Thorleifsson G, Zhang B, Leonardson AS, Zink F, et al. (2008) Genetics of gene expression and its effect on disease. *Nature* 452: 423-428.
- 5 Orphanides G, Reinberg D (2002) A unified theory of gene expression. *Cell* 108: 439-451.
- 6 Agresti A, Bianchi ME (2003) HMGB proteins and gene expression. *Curr Opin Genet Develop* 13: 170-178.
- 7 Vohradsky J (2001) Neural network model of gene expression. *FASEB J* 15: 846-854.