

How Gene Expression Shapes Us

According to the National Human Genome Research Institute (Brodyn, 2025) gene expression is the “process by which information encoded in a gene is turned into a function”. Gene expression primarily occurs through the transcription of RNA molecules, which either code for proteins or produce non-coding RNA molecules with various functions. It can be thought of as an “on/off switch” that controls when and where RNA molecules and proteins are produced (Brody, 2025). The gene expression process is tightly regulated and varies significantly across different conditions and cell types. The RNA and protein products of many genes also play a role in regulating the expression of other genes. To determine when, where, and to what extent a gene is expressed, the functional activity of its product can be measured, or the phenotype linked to the gene can be observed.

Gene expression transcription is the process by which an RNA molecule is synthesized from a DNA template, marking the first step in gene expression. Transcription begins when RNA polymerase binds to the gene’s promoter region, aided by transcription factors (Albert, 2002). The DNA double helix unwinds, exposing the template strand, and RNA polymerase synthesizes a complementary RNA strand in the 5' to 3' direction, based on the DNA sequence. Once the RNA polymerase reaches the terminator sequence, transcription ends, and the newly formed RNA is released. In eukaryotes, the mRNA undergoes post-transcriptional modifications, including the addition of a 5' cap, splicing to remove non-coding introns, and the addition of a poly-A tail to stabilize the mRNA. The final processed mRNA is then transported from the nucleus to the cytoplasm for translation into a protein. In prokaryotes, transcription is simpler and often coupled with translation since they lack a nucleus and mRNA processing steps (Brown, 2002).

Before mRNA can be translated into a protein, it undergoes several processing steps to ensure its stability and functionality. First, a 5' cap is added to the beginning of the mRNA, providing protection from degradation and assisting in the initiation of translation (Jurado, 2014). Next, splicing removes non-coding regions called introns and splices together the coding regions, or exons, to form a continuous mRNA

sequence. Lastly, a poly-A tail is added to the 3' end of the mRNA, which helps stabilize the molecule and aids in translation efficiency. These modifications are essential for ensuring that the mRNA is properly processed and ready for translation (Jurado, 2014).

In the process of translation, the processed mRNA is transported from the nucleus to the cytoplasm, where ribosomes read the mRNA sequence and translate it into a specific protein (Clancy & Brown, 2008). The ribosome reads the mRNA in sets of three nucleotides called codons, each of which codes for a particular amino acid. tRNA molecules, which carry specific amino acids, recognize the mRNA codons by pairing their complementary anticodons with the codons on the mRNA. As the ribosome moves along the mRNA, the tRNA molecules bring the corresponding amino acids, and the ribosome links these amino acids together to form a growing polypeptide chain. This polypeptide will eventually fold into a functional protein (Clancy & Brown, 2008).

After translation, the newly synthesized protein often undergoes post-translational modifications to become fully functional (Goulabchand et al, 2014). These modifications can include phosphorylation, where phosphate groups are added to the protein, altering its activity or function; glycosylation, where sugar molecules are attached to the protein, affecting its stability, folding, or cell signaling properties, where certain parts of the protein are removed to activate or modify its function (Goulabchand et al, 2014). These modifications are crucial for the protein's proper activity, regulation, and localization within the cell, enabling it to carry out its specific biological functions effectively.

Gene expression is tightly regulated at multiple stages to ensure that cells produce the right proteins in the right amounts at the appropriate times. This regulation is critical for processes like development, cellular responses to external signals, and maintaining homeostasis (Lee & Young, 2013). At the transcriptional level, transcription factors play a key role in determining which genes are activated or repressed. These proteins bind to specific regions of DNA, such as enhancers or promoters, to either increase or decrease the transcription of a gene (Lee & Young, 2013). Enhancers are regulatory sequences that can be located far from the gene they control and enhance transcription by attracting transcription factors and other proteins that activate the

gene (Kolovos et al, 2012). Conversely, silencers are DNA sequences that can repress transcription when bound by certain repressive transcription factors.

In addition to these DNA-based controls, mRNA stability also plays an important role in regulating gene expression. The lifespan of an mRNA molecule in the cytoplasm can be controlled by various mechanisms, such as the addition or removal of certain elements in its structure (like the 5' cap or poly-A tail), which influences how long it remains available for translation into a protein. Regulatory proteins can bind to the mRNA, preventing or facilitating its degradation, thus controlling how much of the protein is synthesized (Passmore, 2022).

These regulatory mechanisms ensure that cells can fine-tune gene expression in response to internal and external cues, allowing organisms to adapt to changing conditions, differentiate into specialized cell types, and carry out complex developmental processes.

Diet and genetics are closely connected, as an individual's genetic makeup can influence how their body processes and responds to different nutrients. Genetic variations can impact metabolism, nutrient absorption, and even the risk of developing certain conditions related to diet, such as obesity, diabetes, or cardiovascular diseases (National Research Council (US) Committee on Diet and Health, 1989). For example, some people may have genetic predispositions that make them more efficient at metabolizing fats or carbohydrates, while others may struggle with digesting lactose or certain types of food. Additionally, variations in genes related to taste receptors can affect food preferences and dietary choices. On the other hand, the food we eat can also influence gene expression, known as nutrigenomics. Certain nutrients, like vitamins and minerals, can affect the activity of genes, turning them on and off, which may influence health outcomes (National Research Council (US) Committee on Diet and Health, 1989). A balanced diet rich in healthy fats, antioxidants and fiber can help protect against gene damage and support overall health, while poor nutrition can greater genetic risks for diseases.

In conclusion, gene expression is a complex, highly regulated process that dictates the synthesis of RNA and proteins, ultimately controlling cellular functions and an organism's development. From transcription and post-transcriptional modifications to translation and post-translational changes, each step in the gene expression process plays a crucial role in ensuring the proper functioning of cells and tissues. The regulation of gene expression, influenced by transcription factors, mRNA stability, and other cellular mechanisms, allows organisms to respond dynamically to both internal and external stimuli. Additionally, the interplay between genetics and diet underscores the importance of nutrition in influencing gene activity, highlighting the role of nutrigenomics in health.

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