

# Regulation of Gene Expression in Prokaryotes, Eukaryotes and Its Recent Advancements

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Gene regulation is a fundamental process that governs the expression of genetic information, allowing organisms to respond to environmental stimuli, adapt to changing conditions, and maintain cellular homeostasis. Prokaryotes and eukaryotes, representing two distinct domains of life, have evolved diverse mechanisms to regulate gene expression. This review provides a comparative analysis of gene regulation in prokaryotes and eukaryotes, highlighting both similarities and differences in regulatory strategies. In prokaryotes, gene regulation primarily occurs at the transcriptional level through the interaction of transcription factors with specific promoter regions, regulating RNA polymerase activity. Operons, clusters of genes transcribed together under the control of a single promoter, enable coordinated expression of functionally related genes. Post-transcriptional mechanisms, such as RNA stability and translation efficiency, further modulate gene expression in prokaryotes. In contrast, eukaryotic gene regulation is more complex, involving multiple layers of control. Transcriptional regulation in eukaryotes is governed by a diverse array of transcription factors, chromatin modifications, and DNA methylation patterns, influencing accessibility of DNA to the transcriptional machinery. Post-transcriptional and post-translational mechanisms, including alternative splicing, mRNA stability, and protein degradation pathways, add another level of regulation in eukaryotic cells. Evolutionarily conserved components of gene regulatory networks underscore the fundamental principles governing cellular processes across diverse organisms. Understanding the similarities and differences in gene regulation between prokaryotes and eukaryotes provides valuable insights into the evolutionary constraints and adaptive strategies that shape gene expression dynamics in living systems. Such knowledge has implications for fields ranging from basic biology to biotechnology and medicine.

## Introduction

**Gene** - It is a segment of DNA that has information coded in it in the form of a nucleotide sequence.

**Gene expression** - the process by which the information encoded in a gene is turned into a functional product known as a protein.

**Gene regulation** - mechanism used by the cells to increase or decrease the production of genes by turning on and off

## Regulation of gene expression in prokaryotes

**The Operon concept:** In prokaryotes, genes are organized in a groups called operon. It was proposed by F. Jacob and L. Monod in 1961. The operon concept is outstanding for its simplicity, specificity and precision in the regulation of transcription according to the needs of a cell.

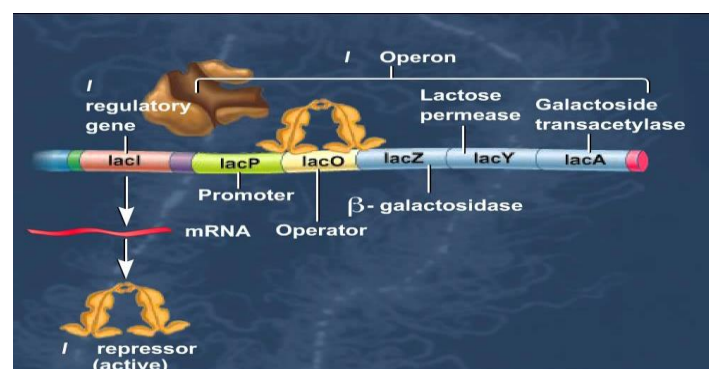
### Types of operons

Inducible operons - e.g. Lac operon

Repressible operons - e.g. trp operon

### Lac operon

The *lac* operon is an **operon**, or group of genes with a single promoter (transcribed as a single mRNA). The genes in the operon encode proteins that allow the bacteria to use lactose as an energy source. Glucose requires fewer steps and less energy to break down than lactose. If lactose is the only sugar available, the *E. coli* will go right ahead and use it as an energy source. To use lactose, the bacteria must



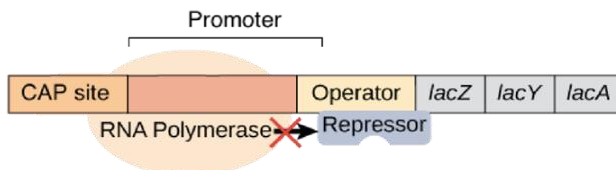
express the *lac* operon genes, which encode key enzymes for lactose uptake and metabolism. By measuring the concentrations of lactose and glucose and activation of *lac* operon transcription are regulated by two proteins

- lac repressor - acts as a lactose sensor.
- catabolite activator protein (CAP) - acts as a glucose sensor.

## Function of Lac operon

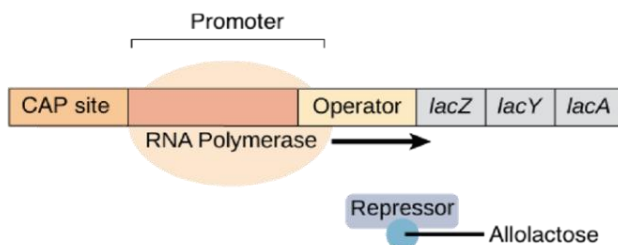
### When Lactose absent

The lac operon remains inactive the lac repressor protein is synthesized and binds tightly to the operator region (lacO) and stops transcription.



### When Lactose present

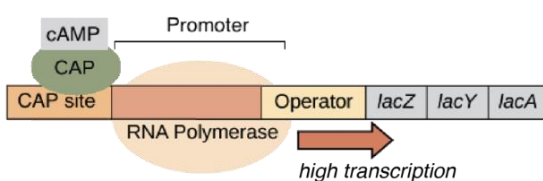
Allolactose binds to the lac repressor, causing a change in the protein's shape and making it unable to attach to the operator region allowing RNA polymerase to initiate transcription.



### How does Glucose affect the Lac Operon?

When lactose is present, the *lac* repressor loses its DNA-binding ability. This clears the way for RNA polymerase to bind to the promoter and transcribe the *lac* operon. As it turns out, RNA polymerase alone does not bind very well to the *lac* operon promoter. It might make a few transcripts, but it won't do much more unless it gets extra help from catabolite activator protein (CAP). CAP is not active on its own. Its activity is regulated by the concentration of cyclic AMP (cAMP) in the cell, which depends on the glucose concentration in the cell.

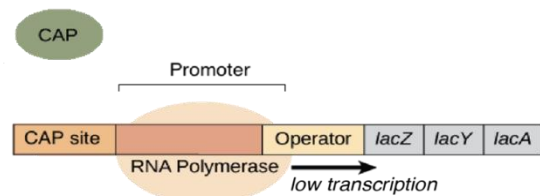
### Low glucose



When glucose levels are low cAMP is produced. The cAMP attaches to CAP allowing it to bind DNA. CAP helps RNA polymerase bind to the promoter resulting in high level of transcription.

### High glucose

When glucose levels are high no cAMP is made. CAP cannot bind DNA without cAMP so transcription occurs only at a low level.



### What is trp operon?

The trp operon, found in *E. coli* bacteria, is a group of genes that encode biosynthetic enzymes for the amino acid tryptophan. The trp operon is expressed (turned "on") when tryptophan levels are low and repressed (turned "off") when they are high. The trp operon is regulated by the trp repressor. When bound to tryptophan, the trp repressor blocks expression of the operon. The five genes are located next to each other in what is called the trp operon. Tryptophan biosynthesis is also regulated by attenuation (a mechanism based on coupling of transcription and translation). The trp repressor does not always bind to DNA. Instead, it binds and blocks transcription only when tryptophan is present. When tryptophan is around, it attaches to the repressor molecules and changes their shape so they become active. A small molecule like tryptophan, which switches a repressor into its active state, is called a corepressor.

### High tryptophan

In this system, the trp repressor acts as both a sensor and a switch. It senses whether tryptophan is already present at high levels and it switches the operon to the "off" position, preventing unnecessary biosynthetic enzymes from being made.

### Low tryptophan

When there is little tryptophan in the cell, the trp repressor is inactive (because no tryptophan is available to bind to and activate it). It does not attach to the DNA or block transcription, and this allows the trp operon to be transcribed by RNA polymerase.

## Regulation of Gene expression in Eukaryotes

### Chromatin structure

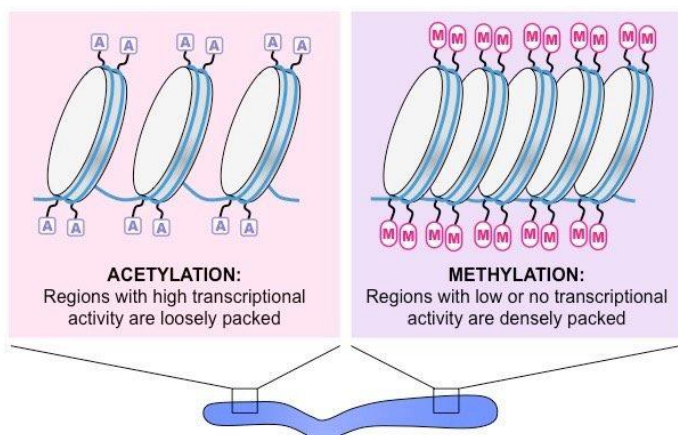
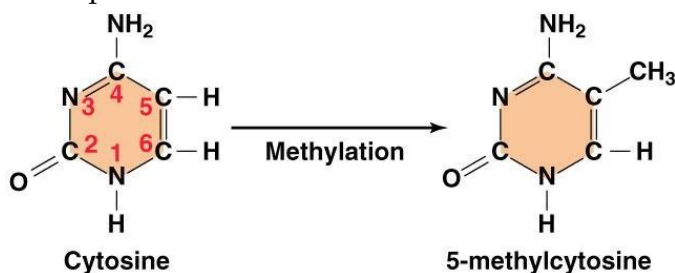
The structure of chromatin (DNA and its organizing proteins) can be regulated. More open or "relaxed" chromatin makes a gene more available for transcription.

- Heterochromatin - darker DNA (H) = tightly packed
- Euchromatin - lighter DNA (E) = loosely packed

Degree of packing of DNA regulates transcription tightly wrapped around histones and there is no transcription and the genes turned off.

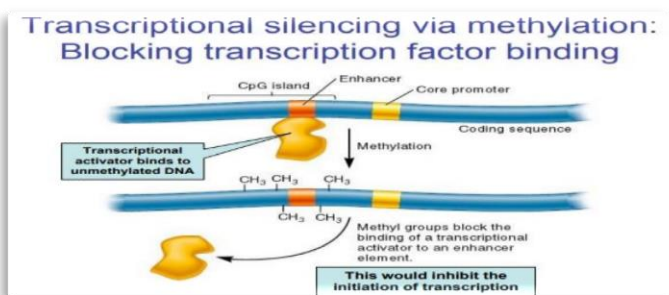
## DNA methylation

It is the attachment of methyl groups ( $-\text{CH}_3$ ) to cytosine. It changes the activity of DNA without changing the sequence. When located in gene promoter DNA methylation repress the gene transcription.



## Gene silencing

Mechanisms responsible for repression of genes involve changes in levels of DNA methylation and alterations in covalent modifications of histone proteins, which lead to chromatin compaction, making genes inaccessible to the transcription.



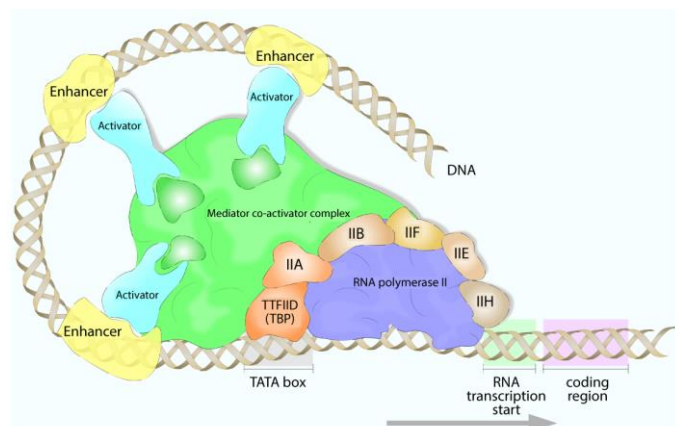
## Transcription initiation

Transcription initiation is the phase during which the first nucleotides in the RNA chain are synthesized. Transcription is a key regulatory point for many genes. A sets of transcription factor proteins bind to specific DNA sequences and promote or repress its transcription.

### Transcription factors and Post transcription control

TF is a set of proteins that controls the rate of transcription of genetic information from DNA to messenger RNA, by binding to a specific DNA

sequence. Binds to promoter, enhancer and silencer DNA in specific ways. Transcription factors are activators boost a gene's transcription while the Repressors decrease transcription. Post-



transcriptional control can occur at any stage after transcription. Once RNA is transcribed, it must be processed to create a mature RNA that is ready to be translated.

## Translation

A process where the mRNA is converted into protein. Translation of an mRNA may be increased or inhibited by regulators. For instance, miRNAs sometimes block translation of their target mRNAs (rather than causing them to be chopped up). Inc RNAs can modulate chromatin structure and function and the transcription of neighboring and distant genes, and affect RNA splicing, stability and translation.

### Advancements in the regulation of gene expression

#### Redox and light regulation of gene expression in photosynthetic prokaryotes

***Rhodobacter capsulatus*:** This bacterium uses two signal transduction gene Reg A and Reg B. Under oxygen deficiency phase the phosphate on Reg B is transferred to Reg A for photosynthesis, nitrogen fixation etc. On oxygen abundant phase, second regulator Crt J reacts to redox and repress the photosynthesis. App A a blue light absorber flavoprotein for longer photocycle and acts as antirepressor for Crt J. Once excited, App A binds to Crt J thereby inhibiting the repressor activity of CrtJ.

#### Cold stress regulation of gene expression in plants

***Arabidopsis thaliana*:** *Arabidopsis* ICE 1 gene in chilling-sensitive plants such as tomato and rice enhance the chilling tolerance. chilling-tolerant of *Arabidopsis* at vegetative stages not at reproductive stage at pollen maturation. Roots and leaves also exhibit different gene expression changes during cold



acclimation: 86% of the cold-induced genes are not shared between roots and leaves. These results suggest that the cold-regulated transcriptional networks might also differ in different tissues ICE 1 gene responsible for cold acclimatization. MYB15, an upstream negative regulator of ICE 1. Expression of cold tolerance is expressed different in different tissues. Transgenic analyses have shown that over expression of Arabidopsis ICE1 gene in chilling-sensitive plants such as tomato and rice enhance the chilling tolerance of these plants.

#### **Drought stress adaptation: metabolic adjustment and regulation of gene expression**

Stress-response gene expression is regulated largely by transcription factors, which in turn are subjected to very intricate regulation at the chromatin level, RNA level and protein level. Stress-induced chromatin remodeling may mediate acclimation responses and help a plant to cope better with subsequent stress situations. Micro-RNA-mediated gene silencing of stress response TFs under non-stress conditions and their activation by downregulation of miRNA expression have emerged as another important means of regulating downstream stress-response gene expression.

#### **Post-transcriptional Regulation of Gene Expression in Plants during Abiotic Stress**

The reviewed study suggests that plant genes are controlled at every step of the post-transcriptional process, from mRNA processing to protein translation, in response to abiotic stress. There is no preference for one regulatory mechanism over another when it comes to a given stress, as similar stressors might elicit distinct methods of post-transcriptional regulation. Both before and after mRNA processing,

mRNA stability appears to be a significant method of control. More research is necessary to fully understand the specific role that RNA binding proteins play throughout the processing of mRNA. Fascinating instances of the various ways that sRNAs may control mRNA stability are demonstrated by responses to abiotic stress. Stress-induced sRNA represses negative stress tolerance regulators on the one hand, and suppression of these regulators on the other. Stress triggers the production of a sRNA, which leads to the build-up of positive stress tolerance regulators. Since that sRNA may control both translation and RNA stability, their function may have gone. The majority of instances of translational regulation in reaction to stress pertain to the 5'UTR. However, compared to other features in the 5' and 3'UTRs, such as secondary structure or sites for recognition by regulatory RNA binding proteins, uORFs are particularly simple to discover and investigate, suggesting the possibility of bias.

#### **Conclusion**

In summary, prokaryotes regulation often occurs at the level of transcription through mechanisms such as operons and transcription factors allowing rapid adaptation to changing environments. Eukaryotic gene regulation is more complex, involving multiple layers of control including transcriptional, post-transcriptional, translational and epigenetic regulation, allowing for precise temporal and spatial control of gene expression. Despite their differences, both prokaryotic and eukaryotic gene regulation mechanisms are essential for the maintenance of cellular homeostasis and adaptation to varying environmental conditions.

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