12.S: Regulation of Gene Expression (Summary)

- Regulation of gene expression is essential to the normal development and efficient functioning of cells
- Gene expression may be regulated by many mechanisms, including those affecting transcript abundance, protein abundance, and post-translational modifications
- Regulation of transcript abundance may involve controlling the rate of initiation and elongation of transcription, as well as transcript splicing, stability, and turnover
- The rate of initiation of transcription is related to the presence of RNA polymerase and associated proteins at the promoter.
- RNApol may be blocked from the promoter by repressors, or may be recruited or stabilized at the promoter by other proteins including transcription factors
- The lac operon is a classic, fundamental paradigm demonstrating both positive and negative regulation through allosteric effects on trans-factors.
- In eukaryotes, cis-elements that are usually called enhancers bind to specific trans-factors to regulate transcriptional initiation.
- Enhancers may be modular, with each enhancer and its transcription factor regulating a distinct component of a gene’s expression pattern, as in the yellow gene.
- Sticklebacks provide examples of recent evolutionary events in which mutation of an enhancer produced a change in morphology and a selective advantage.
- Chromatin structure, including reversible modifications such as acetylation of histones, and methylation DNA CpG sites also regulates the initiation of transcription.
- Chromatin modifications or DNA methylation of some genes are heritable over many mitotic, and sometimes even meiotic divisions.
- Heritable changes in phenotype that do not result from a change in DNA sequence are called epigenetic. Many epigenetic phenomena involve regulation of gene expression by chromatin modification and/or DNA methylation.
Key Terms:

gene expression
transcriptional regulation
operon
lactose
glucose
lac operon
lacZ
lacY
lacA
galactosidase
permease
trans-acetylase
P / promoter
O / operator
CBS
CAP-binding site
cis-elements
trans-regulators
lacI
homotetramer
repressor
allosteric
cAMP binding protein

adenylate cyclase
constitutive
\( \Omega^c / \Gamma / I^p \)
F-factor / episome
GC boxes
CAAT boxes
TATA boxes
GAL4-UAS
Driver/responder
transcription start site
enhancers/silencers
transcription factors
hemoglobin/heme/globin
pseudogene
gene families
stickleback
primordium
chromatin remodeling
acetylation/deacetylation
methylation/demethylation
CpG sites
epigenetics
<table>
<thead>
<tr>
<th>CAP</th>
<th>winter annual</th>
</tr>
</thead>
<tbody>
<tr>
<td>CAP binding sequence</td>
<td>vernalization</td>
</tr>
<tr>
<td>CBS</td>
<td>FLC</td>
</tr>
</tbody>
</table>

**Contributors**

- [Dr. Todd Nickle and Isabelle Barrette-Ng](https://bio.libretexts.org/Bookshelves/Genetics/Book%3A_Online_Open_Genetics_(Nickle_and_Barrette-Ng)/12%3A_Regulat...) (Mount Royal University) The content on this page is licensed under CC SA 3.0 licensing guidelines.