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
O^c / I / I^s
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
CAP binding sequence

CBS

winter annual

vernalisation

FLC

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