

Eukaryotic Gene Regulation

Part A Gene expression

Every cell* in your body contains exactly the same set of genes. The differences between cell types are therefore due to differences in which genes are expressed (i.e. "switched on") and which are not (i.e. "switched off").

Gene expression refers to the process of producing the functional product of a gene. In most cases this involves to produce RNA and then to produce a protein. In some cases though, RNA is the final product (e.g. in the case of).

Gene expression is regulated by transcription factors: that bind to the regulatory region of a gene.

*except mature red blood cells (which contain no genes) and gametes (which are haploid and only contain half of your genome)

Items:

Part B Transcription factors

Transcription factors regulate gene expression by regulating the binding of RNA polymerase to region of a gene. Transcription factors can either act as "activators" or as "repressors".

An activator binds to a specific sequence in region of a gene. This binding allows RNA polymerase to bind to region, which activates transcription.

A repressor binds to a specific sequence in region of a gene. This binding stops RNA polymerase from binding to region, which represses transcription.

A single gene may have multiple enhancers and silencers, which allows its expression to be regulated differently in different contexts (e.g. controlled by different transcription factors in different cell types).

Items:

Part C Terms & definitions

Match the term to the description in the table below.

Term	Definition
<input type="text"/>	the region of a gene that is transcribed
<input type="text"/>	the region of a gene that is not transcribed, but includes the promoter, enhancers, and silencers
<input type="text"/>	the region that RNA polymerase binds to
<input type="text"/>	a region that activators bind to
<input type="text"/>	a region that repressors bind to
<input type="text"/>	a protein that binds to a regulatory region of a gene to regulate its expression

Items:

transcription factor

promoter

enhancer

coding region

silencer

regulatory region

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Bacterial Gene Regulation

A Level

Part A Operons

In bacteria, genes are often found in clusters called operons. An operon is a cluster of genes that share a single . These genes are transcribed into a single which is then translated into multiple .

An operon also contains an : a regulatory region that repressors (transcription factors) bind to to repress transcription. This region is equivalent to a region in eukaryote genes.

In many cases, the repressor (produced by a separate regulatory gene) is constantly being produced. In these cases, the operon will only be expressed if another molecule (an) is present. This molecule binds to the repressor to stop it from binding to the operator.

Items:

Part B The *lac* operon

The *lac* operon is an operon found in many bacteria (including *E. coli*) which enables digestion of lactose. The *lac* operon contains three genes (*lacZ*, *lacY*, and *lacA*), which each encode a different protein (LacZ, LacY, LacA) involved in lactose digestion.

A nearby gene (*lacI*) is constantly expressed to produce a protein (LacI) that binds to the operator of the *lac* operon. However, when lactose is present, lactose binds to this protein to stop it from binding to the operator. This allows RNA polymerase to bind to the *lac* operon promoter to drive expression of the three *lac* operon genes.

Fill in the table below to identify the regulatory gene, the repressor, and the inducer in this system.

Remember that genes are written in italics and lower case, whereas proteins are written with an upper case first letter.

General term	<i>lac</i> operon
regulatory gene	<input type="text"/>
repressor	<input type="text"/>
inducer	<input type="text"/>

Items:

RNA polymerase

lactose

lacA

lacI

lacY

lacZ

LacA

LacI

LacY

LacZ

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Gameboard:

STEM SMART Biology Week 19

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Genes vs Operons

A Level



Part A Eukaryotic gene structure

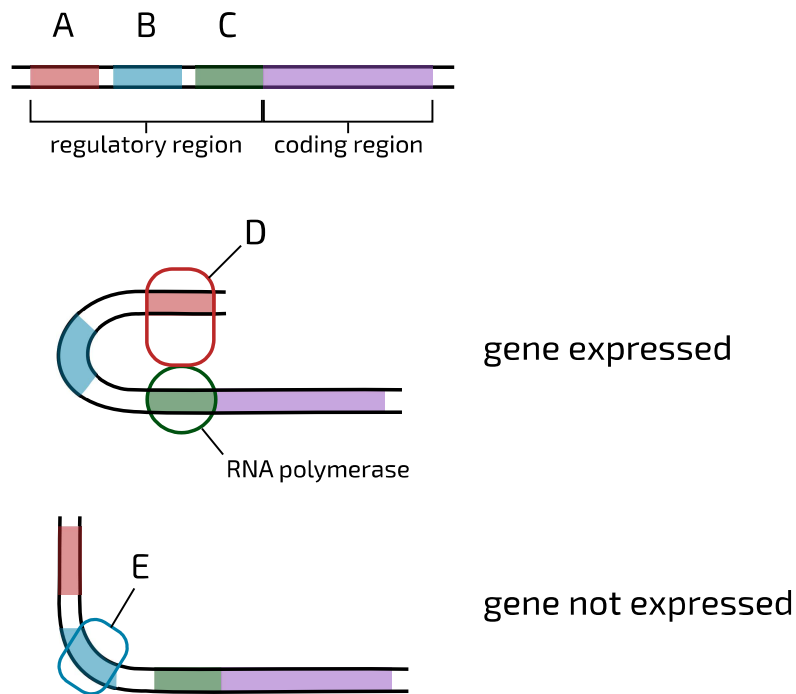


Figure 1: The structure of a eukaryotic gene, with different regions highlighted. Top: simple structure of the gene, showing the regulatory region (regions A-C) and the coding region. Middle: the same gene in its expressed state. Binding of molecule D to region A allows the binding of RNA polymerase to region C. Bottom: the same gene in its not-expressed state. Binding of molecule E to region B prevents RNA polymerase binding to region C.

Match the label from **Figure 1** to the region/molecule in the table below.

Label	region/molecule
A	<input type="text"/>
B	<input type="text"/>
C	<input type="text"/>
D	<input type="text"/>
E	<input type="text"/>

Items:

enhancer

silencer

promoter

repressor

activator

Part B Bacterial operon structure

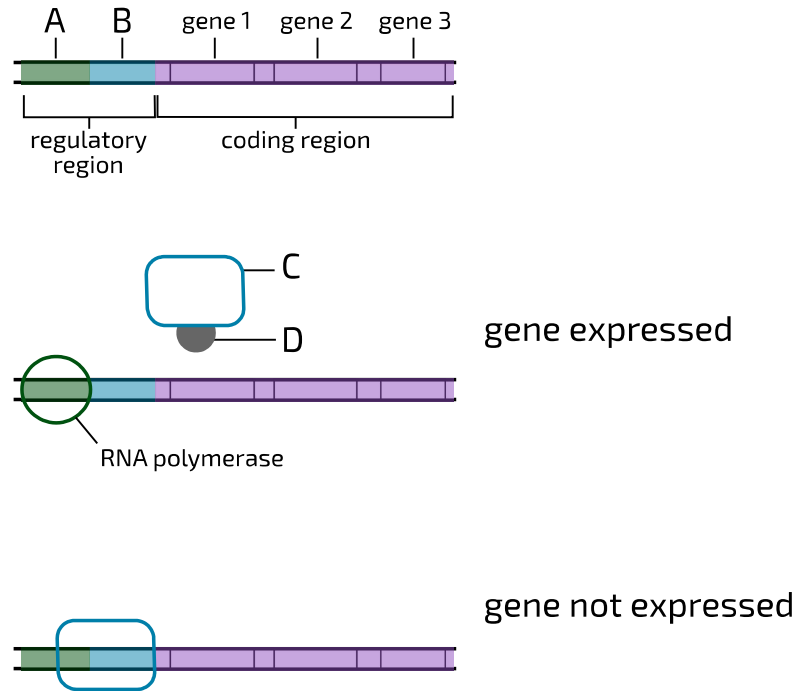


Figure 2: The structure of a bacterial operon, with different regions highlighted. Top: simple structure of the operon, showing the regulatory region (regions A-B) and the coding region (genes 1-3). Middle: the same gene in its expressed state. Binding of molecule D to molecule C prevents molecule C binding to region B, which allows the binding of RNA polymerase to region A. Bottom: the same gene in its not-expressed state. Binding of molecule C to region B prevents the binding of RNA polymerase to region A.

Match the label from **Figure 2** to the region/molecule in the table below.

Label	region/molecule
A	<input type="text"/>
B	<input type="text"/>
C	<input type="text"/>
D	<input type="text"/>

Items:

promoter

operator

repressor

inducer

activator

Part C Eukaryotic genes vs bacterial operons

What is the difference between eukaryotic genes and bacterial operons?

- ☐ Eukaryotic genes have enhancer regions where activators can bind, whereas bacterial operons do not.
 - ☐ Eukaryotic genes are transcribed by RNA polymerase, whereas bacterial operons are not.
 - ☐ Eukaryotic genes have regions where repressors can bind, whereas bacterial operons do not.
 - ☐ Eukaryotic genes usually have one promoter per gene, whereas bacterial operons have multiple promoters for one gene.
 - ☐ Eukaryotic genes are active by default, whereas bacterial operons are inactive by default.
 - ☐ Eukaryotic genes usually have one promoter per gene, whereas bacterial operons have one promoter for multiple genes.
-

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Epigenetics

A Level

Epigenetics refers to chromatin structure and organisation. Epigenetic changes (i.e. chromatin modifications) within a cell can regulate gene expression by making it easier or more difficult for transcription factors to bind to regulatory regions.

Part A Chromatin structure

In eukaryotic cells, DNA is wrapped around proteins called to form a structure called chromatin. During prophase, the chromatin coils up and condenses to form visible structures called , but for the most of the cell cycle it exists in its less condensed form.

The extent to which a region of DNA is wrapped around histones affects the expression of genes in that region. If a region of DNA becomes tightly wrapped around the histones, this will expression levels as it becomes difficult for transcription factors to bind. Conversely, if a region of DNA becomes less tightly wrapped around the histones, this can expression levels as it becomes difficult for transcription factors to bind.

Items:

Part B Acetylation & methylation

Acetylation is the addition of an acetyl group to a molecule. Histones become less positively charged when they are acetylated. This causes DNA to become tightly wrapped around the histones because DNA is charged. Acetylation, therefore, gene expression. The opposite happens when histones are deacetylated (i.e. when acetyl groups are removed from histones).

Methylation is the addition of a methyl group to a molecule. DNA methylation involves the addition of a methyl group to a nucleobase. In most cases, this gene expression by making it difficult for transcription factors to bind to regulatory regions. The opposite happens when DNA is demethylated (i.e. when methyl groups are removed from DNA).

These acetyl groups and methyl groups are sometimes referred to as "epigenetic tags". They alter the overall organisation/structure of chromatin without changing the genetic sequence of bases. Epigenetic changes can be triggered by genetic factors or by environmental factors.

Items:

Part C Development & reproduction

Over the course of embryo development, a zygote divides and differentiates into all the cell types of the organism. This process of differentiation involves in potency as cells become more specialised. This involves epigenetic changes to specific genes, as genes not required for each cell type undergo DNA methylation and/or histone .

Epigenetic tags must be removed during sperm and egg production, so that the zygote of the next generation can be . However, in some cases, not all epigenetic tags are removed and may be inherited by the offspring. This means that some environmentally-caused variation may be inherited by the offspring.

Items:

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Regulation Explanations

A Level



Part A A gene switching on

Which of the following could explain why a gene (which was previously not being expressed) is now being expressed in a cell? Select all that apply.

- ☐ the histones at this region of DNA have become acetylated, causing this region of DNA to be less tightly-wrapped around histones
- ☐ repressors have bound to the silencer region of the gene
- ☐ a silencer of this gene has become methylated, preventing repressors from binding
- ☐ activators have bound to the enhancer region of the gene
- ☐ the promoter of this gene has become methylated, preventing RNA polymerase from binding
- ☐ the histones at this region of DNA have become **de**acetylated, causing this region of DNA to be more tightly-wrapped around histones

Part B Tumour growth

Which of the following could explain why a tumour starts to form within a tissue? Select all that apply.

- ☐ a mutation in the regulatory region of a tumour-suppressor gene causes the gene to be constantly expressed
 - ☐ a mutation in the regulatory region of a coding region of a tumour-suppressor gene causes the protein to no longer function
 - ☐ a mutation in the regulatory region of a proto-oncogene causes the gene to be constantly expressed
 - ☐ the promoter region of a tumour-suppressor gene becomes methylated, preventing RNA polymerase from binding
 - ☐ the histones associated with a proto-oncogene become deacetylated, causing this region of DNA to be more tightly-wrapped around histones
 - ☐ the histones associated with a proto-oncogene become acetylated, causing this region of DNA to be less tightly-wrapped around histones
-

Part C Colour patches

A cat is heterozygous for a gene involved in fur colour (i.e. contains allele 1 and allele 2). Cats that are homozygous for allele 1 are black, whereas cats that are homozygous for allele 2 are ginger. The heterozygous cat has patches of black fur and patches of ginger fur.

Which of the following could explain why the heterozygote has this phenotype?

- ☐ a mutation occurs in the zygote that causes allele 1 to no longer produce a functional protein
 - ☐ allele 1 undergoes methylation whereas allele 2 undergoes acetylation
 - ☐ allele 1 is dominant and allele 2 is recessive
 - ☐ in some cells allele 1 is methylated and allele 2 is not, while in other cells allele 2 is methylated and allele 1 is not
 - ☐ allele 2 is dominant and allele 1 is recessive
 - ☐ a mutation in the gene for RNA polymerase causes it to no longer bind to allele 1 in some cells, and no longer bind to allele 2 in other cells
-

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Transcription Calculations

A Level



In a hypothetical haploid cell, gene A is 3.6 kilobase pairs (kbp) long, and RNA polymerase transcribes genes at a rate of 50 bases per second.

Part A RNA molecules with one polymerase

Assuming only one RNA polymerase can transcribe the gene at a given time, how long will it take the cell to produce 2 000 RNA molecules from gene A?

Part B RNA molecules with multiple polymerases

If one hundred RNA polymerase molecules can simultaneously transcribe the gene, how long will it take the cell to produce 2 000 RNA molecules from gene A?

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