



Exploring Epigenetics

Teacher Notes: Modelling gene regulation

Overview

Students work in small groups to create a model showing the structure of chromosomes. Different groups then proceed to model the effect on transcription, and therefore gene regulation, of:

- (1) transcription factors,
- (2) DNA methylation, and
- (3) histone acetylation

There are 3 versions of instructions in the student sheets document, depending on which process of transcriptional regulation is being modelled by each group.

All groups evaluate their models and then discuss their models with the class.

Discussion should include:

- **How** their mechanisms of transcriptional regulation change gene expression, and
- **Evaluation** of how effective their models are at showing these processes

Learning objectives

- (1) The structure of chromosomes
- (2) Mechanisms of transcriptional regulation

The alteration of transcription in response to environmental variables can occur through the mechanisms of:

- Transcription factors
- Histone acetylation
- DNA methylation

- (3) Evaluating the utility of models

These are given in greater depth in the student document.



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Preparation

There are a small number of confectionery items that need to be purchased for this activity:

- Multicoloured / strawberry laces: *DNA*
- Marshmallows: *histone proteins*
- Wooden skewers / kebab sticks
- A pompom: *RNA polymerase*
- Soft / sticky sweets: *acetyl groups*
- Polos: *methyl groups*
- Sour keys: *transcription factors*

If you assess it to be safe then students could construct their models on paper plates and later eat them.



Instructions

Each group will create a model showing the structure of chromosomes.

Each group will be assigned a different mechanism and construct a model which shows how it regulates transcription:

- transcription factors
- DNA methylation
- histone acetylation on transcription and therefore gene regulation. All groups evaluate their models.

Groups then demonstrate their models to the class and explain how their mechanism of transcriptional regulation alter gene expression. They should also evaluate how effective their models are at showing these processes.





Expected outcomes

Would having tightly wound chromatin or loosely wound chromatin increase the rate of transcription?

By using a hands-on modelling approach to teach about chromosome structure, students are able to visualise that tightly wound chromosomes do not permit RNA polymerase to access the start codons as easily as if the DNA is more loosely coiled around histones.

What are the functions of the enzymes DNA polymerase and RNA polymerase?

Students often confuse these 2 enzymes, due to the similarity in their names. It is worth explicitly considering their roles, so that students are able to compare and contrast the enzymes.

DNA polymerase is involved in DNA replication. It interacts at different points in the DNA sequence and produces a complementary strand of DNA to the template strand being used. It incorporates the bases adenine, thymine, cytosine and guanine into the DNA strand synthesised.

RNA polymerase is involved in transcription. It interacts with DNA at the start codon for a gene and produces a complementary strand of RNA to the template strand being used. It incorporates the bases adenine, uracil, cytosine and guanine into the mRNA strand synthesised.

What is the value in using models?

Models allow visualisation, particularly of inaccessibly small entities, which enables students to build a coherent narrative of the steps involved in subcellular processes.

How effective is the model at showing chromosome structure and how a transcription factor can affect transcription? What does it show, what information is missing?

Comments will to some degree depend on the models made by the students. They could be along the lines of:

The components that contribute to chromosome structure (histones and DNA) are shown and their basic position during interaction is evident. The presence of the skewer through the marshmallows (histones) makes it harder to show the difference between tightly wound chromosomes and DNA that is loosely coiled around the histones.

The transcription factor (sour key) can be shown interacting with the DNA at the start of the gene coding region and guiding the RNA polymerase into position for transcription. This helps to show the enzyme's role is in catalysing the interaction of different molecules.

Whilst the model shows the interaction between the components, it gives no idea of the scale (size) of the elements involved. It is also unable to provide information on the subcellular location where the process takes place.

How effective is the model at showing chromosome structure and how histone acetylation affects transcription? What does it show, what information is missing?

Comments will to some degree depend on the models made by the students. They could be along the lines of:

The components that contribute to chromosome structure (histones and DNA) are shown and their basic position during interaction is evident. The presence of the skewer through the marshmallows (histones) makes it harder to show the difference between tightly wound chromosomes and DNA that is loosely coiled around the histones.

The acetyl groups (soft / sticky sweets) can be shown interacting with the histones. As a result the DNA (strawberry laces) becomes less tightly coiled around the histones (marshmallows), which enables both transcription factors (sour key) and RNA polymerase (pompom) to access the DNA more easily.



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Whilst the model shows the interaction between the components, it gives no idea of the scale (size) of the elements involved. It is also unable to provide information on the subcellular location where the process takes place.

How effective is the model at showing chromosome structure and how DNA methylation affects transcription? What does it show, what information is missing?

Comments will to some degree depend on the models made by the students. They could be along the lines of:

The components that contribute to chromosome structure (histones and DNA) are shown and their basic position during interaction is evident. The presence of the skewer through the marshmallows (histones) makes it harder to show the difference between tightly wound chromosomes and DNA that is loosely coiled around the histones.

The methyl groups (polos) can be shown interacting with the DNA. As a result the DNA (strawberry laces) becomes less accessible for both transcription factors (sour key) and RNA polymerase (pompom).

Whilst the model shows the interaction between the components, it gives no idea of the scale (size) of the elements involved. It is also unable to provide information on the subcellular location where the process takes place, or the sequence CpG where the DNA methylation most commonly occurs.

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Does the model make it easier to understand how genes can be regulated to increase and decrease gene expression without the sequence of DNA being changed?

Comments will depend on how effectively students have modelled and understood their models of how; (i) transcription factors, (ii) DNA methylation, and (iii) histone acetylation, effect transcription and therefore gene regulation.

Hopefully students will find that the illustrative power of their models outweighs the detail not included. Certainly much research suggests that 'dual coding' of information (as text and as models) will help the understanding and memorisation of novel concepts.