



Exploring Epigenetics

Student sheets: Modelling gene regulation

Transcription Factors

Task

Your task is:

- (1) to create a model, using everyday confectionery, that illustrates the structure of chromosomes and mechanisms of transcriptional regulation, then
- (2) to evaluate how effectively the model illustrates these structures and processes.



Learning objectives

In order to complete this task you need to understand:

(1) The structure of chromosomes

- DNA in eukaryotic cells is found in the nucleus, associated with proteins called histones, to form chromatin, which makes up chromosomes
- Histones are proteins that have side branches containing the amino acid lysine. They are positively charged and are closely associated with DNA, which is negatively charged.
- At the start of cell division chromosomes are visible because the DNA is tightly coiled around histones
- During interphase chromosomes are not visible because the DNA is loosely coiled around histones, which allows RNA polymerase to transcribe genes and DNA polymerase to replicate the DNA





(2) Mechanisms of transcriptional regulation

- There are ways in which environmental factors can influence gene expression without changing (mutating) the base sequence of DNA
- **Transcription factors** (sometimes with co-factors) can bind to a promoter in the DNA sequence before the start codon of a gene increasing the rate of transcription in response to environmental variables
- Epigenetic modifications can modify the transcription of certain genes without changing the DNA sequence, through histone acetylation and DNA methylation.
- **Histone acetylation** is a process by which acetyl groups (COCH_3) can be added to the lysine side branches of histone proteins
- Increased histone acetylation reduces the positive charge of the histone proteins, so that negatively charged DNA is less tightly bound. This allows increased transcription.
- Decreased histone acetylation increases the positive charge of the histone proteins, so that negatively charged DNA is more tightly bound. This reduces or prevents transcription.
- **DNA methylation** is a process by which methyl groups (CH_3) are added to cytosine residues by an enzyme called methyltransferase. This happens most commonly where cytosine is linked by a phosphodiester bond to a guanine base (CpG) and can suppress transcription
- DNA methylation suppresses transcription by preventing transcription factors from binding to DNA and by decreasing acetylation of histones

(3) How to evaluate the utility of models

- Small entities, and the processes that they are involved in, which are not visible even using the greatest magnification and resolution offered by microscopy can be difficult to understand and visualise
- Models can help to overcome this barrier but will have limitations in their accuracy and ability to show complex interactions
- To evaluate models productively requires understanding of their strengths and limitations

SCoPE



Instructions – Transcription Factors

(1) The structure of chromosomes

Step 1

Take laces of 2 different colours and make 2 lengths of single-stranded DNA with a gene (shown by the different coloured lace)



Step 2

Wind the laces (single-stranded DNA) around each other to create a double-helical double-stranded length of DNA



Step 3

Wind the DNA around the histone proteins (marshmallows) to form chromatin

You can secure the chromatin model with a kebab skewer to help hold it together



Step 4

Use a pompom to show the RNA polymerase interacting with the DNA during transcription

Remember that DNA strands need to separate for RNA polymerase to access the DNA for transcription



Questions

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

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

SCoPE



(2) How transcription factors affect transcription

Step 5

Add a sour key to the DNA before the start of the gene to represent a transcription factor binding to the promoter region



Step 6

Some genes are only transcribed when a transcription factor (sometimes with a co-factor) is bound to the promoter

Here binding of the transcription factor is shown 'guiding' the RNA polymerase (pompom) to the DNA, initiating or increasing the rate of transcription



(3) Evaluating the model

Evaluate how well this model shows:

- (1) the structure of chromosomes
- (2) how a transcription factor can affect transcription

Questions

What is the value in using models?

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?

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?



Exploring Epigenetics

Student sheets: Modelling gene regulation

Histone Acetylation

Task

Your task is:

- (1) to create a model, using everyday confectionery, that illustrates the structure of chromosomes and mechanisms of transcriptional regulation, then
- (2) to evaluate how effectively the model illustrates these structures and processes.



Learning objectives

In order to complete this task you need to understand:

(1) The structure of chromosomes

- DNA in eukaryotic cells is found in the nucleus, associated with proteins called histones, to form chromatin, which makes up chromosomes
- Histones are proteins that have side branches containing the amino acid lysine. They are positively charged and are closely associated with DNA, which is negatively charged.
- At the start of cell division chromosomes are visible because the DNA is tightly coiled around histones
- During interphase chromosomes are not visible because the DNA is loosely coiled around histones, which allows RNA polymerase to transcribe genes and DNA polymerase to replicate the DNA





(2) Mechanisms of transcriptional regulation

- There are ways in which environmental factors can influence gene expression without changing (mutating) the base sequence of DNA
- **Transcription factors** (sometimes with co-factors) can bind to a promoter in the DNA sequence before the start codon of a gene increasing the rate of transcription in response to environmental variables
- Epigenetic modifications can modify the transcription of certain genes without changing the DNA sequence, through histone acetylation and DNA methylation.
- **Histone acetylation** is a process by which acetyl groups (COCH_3) can be added to the lysine side branches of histone proteins
- Increased histone acetylation reduces the positive charge of the histone proteins, so that negatively charged DNA is less tightly bound. This allows increased transcription.
- Decreased histone acetylation increases the positive charge of the histone proteins, so that negatively charged DNA is more tightly bound. This reduces or prevents transcription.
- **DNA methylation** is a process by which methyl groups (CH_3) are added to cytosine residues by an enzyme called methyltransferase. This happens most commonly where cytosine is linked by a phosphodiester bond to a guanine base (CpG) and can suppress transcription
- DNA methylation suppresses transcription by preventing transcription factors from binding to DNA and by decreasing acetylation of histones

(3) How to evaluate the utility of models

- Small entities, and the processes that they are involved in, which are not visible even using the greatest magnification and resolution offered by microscopy can be difficult to understand and visualise
- Models can help to overcome this barrier but will have limitations in their accuracy and ability to show complex interactions
- To evaluate models productively requires understanding of their strengths and limitations

SCoPE



Instructions – Histone Acetylation

(1) The structure of chromosomes

Step 1

Take laces of 2 different colours and make 2 lengths of single-stranded DNA with a gene (shown by the different coloured lace)



Step 2

Wind the laces (single-stranded DNA) around each other to create a double-helical double-stranded length of DNA



Step 3

Wind the DNA around the histone proteins (marshmallows) to form chromatin

You can secure the chromatin model with a kebab skewer to help hold it together



Step 4

Use a pompom to show the RNA polymerase interacting with the DNA during transcription

Remember that DNA strands need to separate for RNA polymerase to access the DNA for transcription



Questions

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

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



(2) How histone acetylation affects transcription

Step 5

Stick sweets to the marshmallow histones to represent the acetyl groups (COCH_3) being added to the lysine side branches of histone proteins



Step 6

Increased histone acetylation reduces the positive charge of the histone proteins, so that negatively charged DNA is less tightly bound

As the DNA is less tightly bound the RNA polymerase (pom-pom) is able to access the DNA more easily, so the rate of transcription increases



(3) Evaluating the model

Evaluate how well this model shows:

- (1) the structure of chromosomes
- (2) how histone acetylation affects transcription

Questions

What is the value in using models?

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

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?





Exploring Epigenetics

Student sheets: Modelling gene regulation

DNA Methylation

Task

Your task is:

(1) to create a model, using everyday confectionery, that illustrates the structure of chromosomes and mechanisms of transcriptional regulation, then

(2) to evaluate how effectively the model illustrates these structures and processes.



Learning objectives

In order to complete this task you need to understand:

(1) The structure of chromosomes

- DNA in eukaryotic cells is found in the nucleus, associated with proteins called histones, to form chromatin, which makes up chromosomes
- Histones are proteins that have side branches containing the amino acid lysine. They are positively charged and are closely associated with DNA, which is negatively charged.
- At the start of cell division chromosomes are visible because the DNA is tightly coiled around histones
- During interphase chromosomes are not visible because the DNA is loosely coiled around histones, which allows RNA polymerase to transcribe genes and DNA polymerase to replicate the DNA



(2) Mechanisms of transcriptional regulation

- There are ways in which environmental factors can influence gene expression without changing (mutating) the base sequence of DNA
- **Transcription factors** (sometimes with co-factors) can bind to a promoter in the DNA sequence before the start codon of a gene increasing the rate of transcription in response to environmental variables
- Epigenetic modifications can modify the transcription of certain genes without changing the DNA sequence, through histone acetylation and DNA methylation.
- **Histone acetylation** is a process by which acetyl groups (COCH_3) can be added to the lysine side branches of histone proteins
- Increased histone acetylation reduces the positive charge of the histone proteins, so that negatively charged DNA is less tightly bound. This allows increased transcription.
- Decreased histone acetylation increases the positive charge of the histone proteins, so that negatively charged DNA is more tightly bound. This reduces or prevents transcription.
- **DNA methylation** is a process by which methyl groups (CH_3) are added to cytosine residues by an enzyme called methyltransferase. This happens most commonly where cytosine is linked by a phosphodiester bond to a guanine base (CpG) and can suppress transcription
- DNA methylation suppresses transcription by preventing transcription factors from binding to DNA and by decreasing acetylation of histones

(3) How to evaluate the utility of models

- Small entities, and the processes that they are involved in, which are not visible even using the greatest magnification and resolution offered by microscopy can be difficult to understand and visualise
- Models can help to overcome this barrier but will have limitations in their accuracy and ability to show complex interactions
- To evaluate models productively requires understanding of their strengths and limitations

SCoPE



Instructions - DNA Methylation

(1) The structure of chromosomes

Step 1

Take laces of 2 different colours and make 2 lengths of single-stranded DNA with a gene (shown by the different coloured lace)



Step 2

Wind the laces (single-stranded DNA) around each other to create a double-helical double-stranded length of DNA



Step 3

Wind the DNA around the histone proteins (marshmallows) to form chromatin

You can secure the chromatin model with a kebab skewer to help hold it together



Step 4

Use a pompom to show the RNA polymerase interacting with the DNA during transcription

Remember that DNA strands need to separate for RNA polymerase to access the DNA for transcription



Questions

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

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

SCoPE



(2) How DNA methylation affects transcription

Step 5

Thread polo sweets around the DNA to represent the methyl groups (CH_3) being added to cytosine residues of the DNA

In cells this process is completed by an enzyme called added methyltransferase and occurs most frequently when cytosine is linked by a phosphodiester bond to a guanine base (CpG)



Step 6

Increased DNA methylation prevents transcription factors from binding to DNA and decreases acetylation of histones

Both of these mechanisms reduce or prevent transcription – shown by the RNA polymerase (pom-pom) not associated with the DNA

Decreased histone acetylation will increase the positive charge of the histone proteins, so that negatively charged DNA is more tightly bound, suppressing transcription



(3) Evaluating the model

Evaluate how well this model shows:

- (1) the structure of chromosomes
- (2) how DNA methylation affects transcription

Questions

What is the value in using models?

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

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?