

Teaching notes: Epigenetic control of gene expression in eukaryotes

These teaching notes relate to section 3.8.2.2 of our A-level Biology specification. This resource describes key teaching points in the accompanying PowerPoint presentation.

PowerPoint presentation

Introduction - key points (slide 1)

The content of the specification relates specifically to eukaryotes.

Control of gene expression in prokaryotes – the Jacob and Monod model – is not specification content and the examining team cannot expect students to be familiar with it.

What is epigenetics? (slide 2)

This is a basic definition of epigenetics, as given in the specification.

The nature of genes (slide 3)

This slide presents a quick recap of material learnt in Year 1.

In Year 1, students learnt more about:

- the transcription of genes to produce functional mRNA molecules that were then translated by ribosomes to form polypeptides
- the involvement in protein synthesis of tRNA molecules that are also encoded by genes.

Genes and transcription factors (slide 4)

In Year 2, students learn that genes are 'switched on' when transcription factors bind to a DNA region called the gene's promoter.

Binding of transcription factors is needed for the activation of RNA polymerase.

DNA composition (slide 5)

A reminder of the involvement of organic bases in the structure of DNA nucleotides.

In vertebrate animals, the organic base most commonly methylated is cytosine, though adenine can also be methylated.

Methylation of cytosine (slide 6)

Methylation involves addition of a methyl group (CH_3) to the C5 of a cytosine residue.

Methyltransferase is the enzyme that catalyses this methylation reaction.

Methylated CpG repeats 'silence' genes (slide 7)

Repeated CpG sequences, referred to as **CpG islands**, are common at the 5' end of many genes.

During development, methylation of these CpG islands 'silences' the affected genes by preventing activation of RNA polymerase.

DNA is wound around histones (slide 8)

The chromosomal DNA of eukaryotes is wrapped around molecules of the protein **histone**, forming bead-like **nucleosomes**.

In this slide, students can see:

- an 'open' part of the chromosome, in which the DNA and histones can be seen separately
- a condensed part of the chromosome, in which the DNA and histones are too tightly wound to be seen clearly.

The 'winding' may be tight or loose (slide 9)

This slide demonstrates that DNA can be wound around tightly-packed histones or around loosely-packed histones. What causes this is dealt with in the next slide.

You can introduce here that if a gene (coloured yellow here) is located in a tightly-coiled region of the chromosome, transcription factors and RNA polymerase cannot 'get at it' to begin its transcription.

'Tails' on histone molecules (slide 10)

The key concept here is that acetylation of histone molecules results in them becoming loosely packed.

You could ask students where they have come across acetylcoenzyme A (acetylcoA) before (the precise answer, expected in an examination, is in the link reaction of aerobic respiration).

The effect of acetylation (slide 11)

For visual learners, the process is summarised in a final diagram.

Further reading:

Katherine Hentges (2008), *Cell differentiation: how cells arise*, Biological Sciences Review 20 (4)

Final note

No questions for students are supplied to accompany this topic due to the small size of the topic.