The control of gene expression (AQA A2 Biology) PART 3 of 8 TOPICS

TOPICS: Alternation of the sequence of bases in DNA can alter the structure of proteins Gene expression is controlled by a number of features – most of the cell’s DNA is not translated Gene expression is controlled by a number of features – regulation of transcription and translation Gene expression is controlled by a number of features – gene expression and cancer Using genome projects Gene technologies allow the study and alteration of gene function allowing a better understanding of organism function and the new design of industrial and medical processes – recombinant DNA technology Gene technologies allow the study and alteration of gene function allowing a better understanding of organism function and the new design of industrial and medical processes – differences in DNA between individuals of the same species can be exploited for identification and diagnosis of heritable conditions Gene technologies allow the study and alteration of gene function allowing a better understanding of organism function and the new design of industrial and medical processes – genetic fingerprinting

# Gene expression is controlled by a number of features – regulation of transcription and translation:

In eukaryotes, transcription or target genes can be stimulated or inhibited when specific transcriptional factors move from the cytoplasm into the nucleus. As only target genes are transcribed, it means that specific proteins are made. Each type of body cell has different target cells so they give different characteristics i.e. a nerve cell is different to a red blood cell. Transcription factors can change the rate of transcription and the process is as follows:

* The transcription factors move in by diffusion into the nucleus from the cytoplasm.
* When in the nucleus they may bind to promoter sequence (the sequence which is the start of the target gene).
* The transcription factors either increase or decrease the rate of transcription depending if they have bound onto the promoter sequence.

Some transcription factors are called activators where they increase the rate of transcription. This is done by the transcription factors helping the RNA polymerase to bind to the promoter sequence to activate transcription. Others are called repressors where they decrease the rate of transcription. This is done by the transcription factors binding to the promoter sequence preventing RNA polymerase from binding. This stops transcription.

Oestrogen is a lipid-soluble steroid which can diffuse through a plasma membrane. It can initiate the transcription of target genes.

Oestrogen binds to the transcription factor in the cytoplasm making an oestrogen-oestrogen receptor complex and changes the shape of a DNA binding site elsewhere on the complex. This means that the transcription factor is now able to attach to the promoter sequence once it has entered the nucleus through a nuclear pore. When the transcription factor has bound to the promoter region Transcription begins.

In eukaryotes and some prokaryotes, translation of the mRNA produced from target genes can be inhibited by RNA interference known as RNAi. Short RNA molecules such as micro RNA, known as miRNA, and small interference RNA, known as siRNA, form an RNA Induced Silencing Complex, known as RISC, with proteins. The complexes each attach to their target mRNA sequence and preventing translation in different ways. This is how it is done for each small RNA molecules:

* **siRNA/miRNA in plants:**
* The bases on the siRNA attach to the bases on the mRNA by complementary base pairing.
* RNA hydrolase hydrolyses the mRNA strand into fragments preventing translation to occur as the whole polypeptide chain will not be made

**NB: It is not necessary to know that the fragments are degraded in the processing body. If you want to learn this there is no harm.**

* **miRNA in mammals:**
* The bases on the miRNA attach to the bases on the mRNA by complementary base pairing.
* Ribosomes are prevented from attaching to the mRNA strand stopping translation from occurring.

**NB: Again here, it is not necessary to know that mRNA is degraded or stored in the processing body.**

Epigenetics involves heritable changes in gene function, without changes to the DNA base sequence. These changes are caused by changes in the environment (more exposure to pollution) that inhibit transcription by:

* **Increased methylation of DNA:** A methyl group (known as an epigenetic mark) attaches to cytosine that has to be part of the nucleotide that is attached to guanine by a phosphodiester bond. **NB: You may be confused right now but look at the diagram below of one strand of DNA and notice which of the cytosine nucleotides the methyl group joins on to. Notice that the nucleotide on the far right of the strand and the third one from the left does not have a methyl group as they are not next to a nucleotide with guanine as the base.** As the structure has changed, it has become harder for enzymes to attach to the DNA stopping the expression of a gene. If the tumour suppressor gene is not transcribed it can cause cancer.

C

A

T

C

G

C

C

A

C

CH3

CH3

* **Decreased of associated histones:** An acetyl group - COCH3 - is another epigenetic mark which attaches to histone proteins to make the chromatin (mixture of DNA wound around histone proteins) less condensed for easy genetic expression to occur. The problem originates when histone deacetylase breaks the bond between the histone protein and acetyl group. The DNA becomes highly condensed making hard for enzymes to carry out the gene expression. **NB: Histone deacetylase can be abbreviated into HDAC but it is best that you stay with the full name.**
* Epigenetic changes to the DNA are fortunately reversible therefore they are good targets by drugs to stop the effects of epigenetic occurring. These drugs can either stop DNA methylation or can inhibit histone deacetylase allowing the acetyl groups to remain attached to the DNA.