Transcription in prokaryotes and eukaryotes

All living organisms need to carry out protein synthesis, from the smallest bacterium, to the largest humpback whale. There are two main processes involved in protein synthesis, transcription and translation. Transcription is the production of an mRNA strand from a template strand of DNA. Though transcription differs between eukaryotes and prokaryotes there are many similarities relating to both processes. Translation is the conversion of the mRNA code into a polypeptide. In all cells, translation takes place within ribosomes.

As like most other biological functions, transcription in both eukaryotes and prokaryotes is controlled by enzymes and other various proteins. The main enzyme used in both types of organism is RNA polymerase.

Prokaryotes contain one type of RNA polymerase, Eukaryotic cells contain three different types of the enzyme: RNA polymerase I, II and III. Though RNA polymerase II is the only one used in the process of transcription. All RNA polymerases move from the 5′ end to the 3’end of the DNA strand.

DNA contains special sequences of nucleotides called promoter regions, these are lengths of DNA, with a specific sequence and occur just before the DNA that is going to be transcribed. They allow RNA polymerase or other proteins to bind to it. The DNA that is to be transcribed is called a transcription unit (Campbell et al, 2008).

In prokaryotes RNA polymerase can attach directly onto the promoter region. As it begins to transcribe it unwinds the DNA exposing roughly 10-20 bases allowing complimentary RNA bases to move in, RNA polymerase then moves along the DNA strand rewinding the previously unwound DNA and unwinding

the next section of DNA. As RNA polymerase moves a long the DNA it forms a sugar-phosphate backbone along the free RNA nucleotides forming a molecule of mRNA, this process is called elongation.

Prokaryotic transcription continues until a sequence of DNA called the terminator region is transcribed, at which point RNA polymerase drops off of the DNA strand and releases the mRNA strand. The new mRNA molecule is now free to be translated.

Eukaryotic transcription is very similar prokaryotic transcription, however, the control mechanisms are a lot more complex. Eukaryotic DNA also contains promoter regions, however RNA polymerase II is unable to directly bind to the DNA without the help of several binding proteins. Eukaryotic promoter regions often contain a nucleotide sequence containing the bases thymine and adenine around 25 bases down from the transcription unit beginning this is called a TATA box. The proteins that attach to the DNA allowing RNA polymerase to bind to the DNA are called transcription factors.

There are numerous types of transcription factors, one transcription factor is able to recognise the TATA box and then bind to it. Multiple other transcription units bind to the DNA at the same time as RNA polymerase, the resulting complex is called the transcription initiation complex. The DNA then partially unwinds, and transcription begins at the start on the template strand. Transcription continues along the DNA strand, transcribing the DNA sequence into pre-mRNA. Termination in eukaryotic cells occurs when a sequence of AAUAAA is transcribed . This is called a polyadenylation signal. About 10-30 nucleotides down from where this signal has been transcribed, a

protein responds to this signal and cleaves the pre-mRNA from the RNA polymerase.

Unlike in prokaryotes, translation cannot occur straight away. The pre-mRNA needs to be modified and turned into mature mRNA before translation can occur. The first modification to happen to pre-mRNA is the of a modified guanine molecule called 7-methyl guanosine (a G 5′ cap). Next is the addition of a poly-A tail to the 3′ end. This is the adding of 50-250 adenine bases through the action of an enzyme. The function of these additions appears to be to first facilitate the movement of the mRNA out of the nucleus, as well as stopping the digestion of the mRNA sequence by nuclease enzymes, they also act as a binding point for ribosomes (Campbell et al, 2008). These additions are not translated.

Pre-mRNA often goes through more complex modification before it can finally be translated, this modification is called RNA splicing. This is the removal of non-encoding sections of RNA: introns and the connection of coding sections of RNA called exons. Introns are in between the coding sequences of RNA, meaning that they need to be cut out before the exons can be joined together. RNA splicing is initiated by the binding of molecules called small nuclear ribonucleoproteins or snRNPs (Campbell et al, 2008). These are small molecules that are made up from RNA and protein. These snRNPs recognise and bind to specific nucleotide sequences at the ends of introns. Then multiple other protiens and snRNPs bind together and form a spliceosome. This reacts to various points along the RNA strand, cleaving out the introns, and joining the two exons together. Once the pre-mRNA is free of introns, it is now mature mRNA and ready to be transcribed.

It may seem rather redundant for DNA to code for all of these sections if it is just going to be removed at a further stage. However, introns are a very important aspect in eukaryotic genes, as depending on which sequences of RNA are treated as introns and exons, one gene can code for multiple polypeptides . This is alternative RNA splicing.

Translation is an amazing process, it allows for a multitude of polypeptides to be produced from a relatively small amount of DNA. The differences between prokaryotic and eukaryotic translation, such as RNA splicing, offer an explanation for why eukaryotes tend to be more complex than prokaryotes, yet the similarities, help to show our evolutionary past.