

Types of RNA and the process of Transcription

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A gene is the functional unit of inheritance. The DNA sequence that codes for tRNA or rRNA molecule is also called a gene. A **cistron** is a segment of DNA that codes for a polypeptide, the structural gene in a transcription unit could be said as **monocistronic** (mostly in eukaryotes) or **polycistronic** (mostly in bacteria or prokaryotes).

In eukaryotes, the monocistronic structural genes have interrupted coding sequences, hence the genes in eukaryotes are split. The coding sequences or expressed sequences are called **exons**. Exons are said to be those sequence that appear in mature or processed RNA. The non-coding sequences or unexpressed sequences are called **introns**. The exons are interrupted by **introns**. Introns also known as intervening sequences do not appear in mature or processed RNA. The split-gene arrangement further complicates the definition of a gene in terms of a DNA segment. Inheritance of a character is also affected by promoter and regulatory sequences of a structural gene. Hence, sometime the regulatory sequences are loosely defined as regulatory genes, even though these sequences do not code for any RNA or protein.

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In bacteria, there are three major types of RNAs:

1. mRNA (messenger RNA)
2. tRNA (transfer RNA) and
3. rRNA (ribosomal RNA)

All three RNAs are needed to synthesise a protein in a cell. The mRNA provides the template, tRNA brings aminoacids and reads the genetic code, and rRNAs play structural and catalytic role during translation. There is single DNA-dependent RNA polymerase that catalyses transcription of all types of RNA in bacteria.

Initiation:

RNA polymerase binds to promoter and initiates transcription (**Initiation**). It associates transiently with **initiation-factor** (σ). Initiation-factor gives specificity to RNA polymerases. It uses nucleoside triphosphates as substrate and polymerises in a template depended fashion following the rule of complementarity. It somehow also facilitates opening of the helix and continues elongation.

Elongation:

The RNA polymerase is only capable of catalysing the process of elongation.

Termination:

Only a short stretch of RNA remains bound to the enzyme. Once the polymerase reaches the terminator region, the nascent RNA falls off, so also the RNA polymerase. This results in **termination** of transcription.

The RNA polymerase associates transiently with **termination-factor** (ρ) and terminate the transcription. Association with these factors alter the specificity of the RNA polymerase.

In bacteria, since the mRNA does not require any processing to become active, and since transcription and translation take place in the same compartment (no separation of cytosol and nucleus), many times the translation can begin much before the mRNA is fully transcribed. Consequently, the transcription and translation are coupled in bacteria.

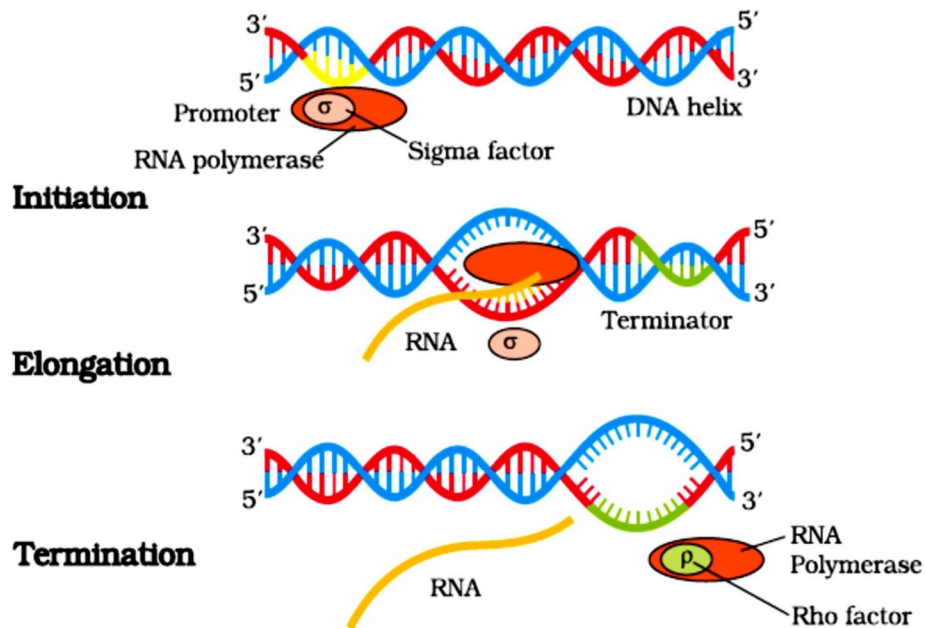


Figure Process of Transcription in Bacteria

In eukaryotes, there are two additional complexities –

(i) There are at least three RNA polymerases in the nucleus (in addition to the RNA polymerase found in the organelles). There is a clear cut division of labour. The RNA polymerase I transcribes **rRNAs** (28S, 18S, and 5.8S), whereas the RNA polymerase III is responsible for transcription of **tRNA**, **5srRNA**, and **snRNAs (small nuclear RNAs)**. The RNA polymerase II transcribes precursor of mRNA, the **heterogeneous nuclear RNA (hnRNA)**.

(ii) The second complexity is that the primary transcripts contain both the exons and the introns and are non-functional. Hence, it is subjected to a process called **splicing** where the introns are removed and exons are joined in a defined order. hnRNA undergo two additional processing called — capping and tailing.

In **capping** an unusual nucleotide (methyl guanosine triphosphate) is added to the 5'-end of hnRNA.

In **tailing**, adenylate residues (200-300) are added at 3'-end in a template independent manner.

It is the fully processed hnRNA, now called mRNA, that is transported out of the nucleus for translation.

The significance of such complexities: The split-gene arrangements represent probably an ancient feature of the genome. The presence of introns is reminiscent of antiquity, and the process of splicing represents the dominance of **RNA-world**.

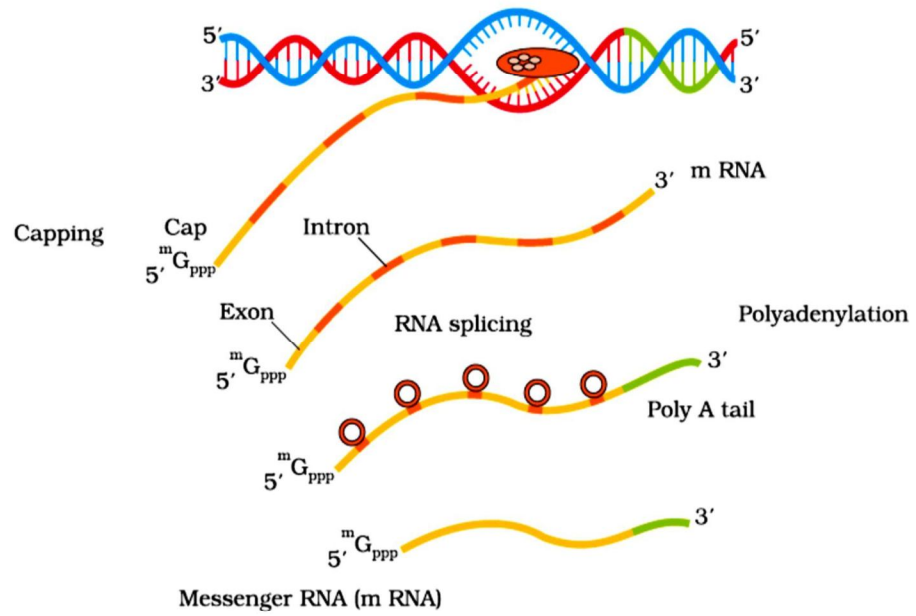


Figure Process of Transcription in Eukaryotes