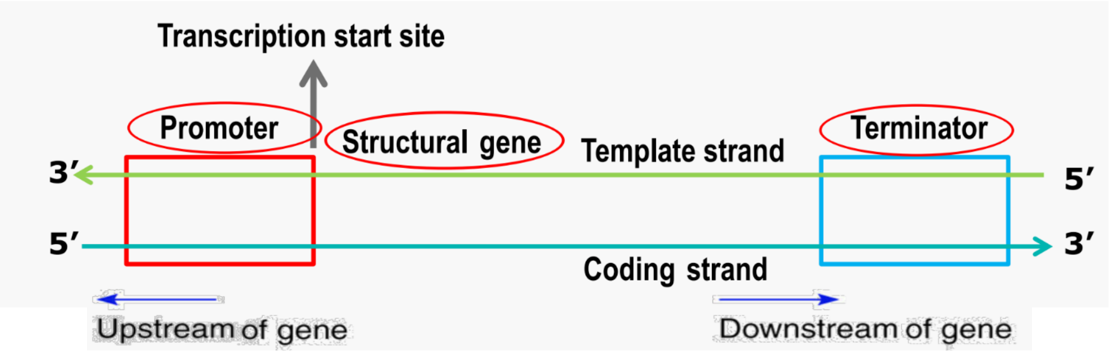
Transcription

- It is the process of copying genetic information from one strand of DNA into RNA.
- Principle of complementarity governs the process (except adenosine- in RNA uracil is present instead of thymine)
- The DNA depended RNA polymerase catalyses transcription, in the 5'→3' direction.
- DNA consist of two strands -

Template Strand (Antisense, Minus Strand)	**Coding Strand** (Sense Strand)
Strand with 3'→ 5' Polarity.	Strand with 5'→ 3' Polarity.
Acts as template (model to follow) to codes for RNA	Does not code for any region of RNA.
Have opposite sequence to newly synthesised RNA.	Have same sequence as newly synthesised RNA



- A transcription unit in DNA consist of:
  1) **Structural Gene :** Region between promoter & terminator where transcription takes place.
  2) **Promoter:** Binding site for RNA Polymerase to start the transcription.
     Located on 5' end (up stream) of Coding Strand.
     Defines template and coding strand by switching its position with terminator.
  3) **Terminator:** Located on 3' end (downstream) of Coding Strand.
     Terminator Region do not code for any codon hence terminate the transcription.

Que: If the sequence of template strand is "**CAGTACGATTCAGACT".** What would be the sequence of coding strand and RNA Strand?

Que : Why both the strands of DNA are not copied during Transcription?

Ans: (1) RNA molecules with different sequences will be produced and hence different proteins (with different amino acid sequence). One DNA segment would code for two different Protein which complicate genetic information machinery.

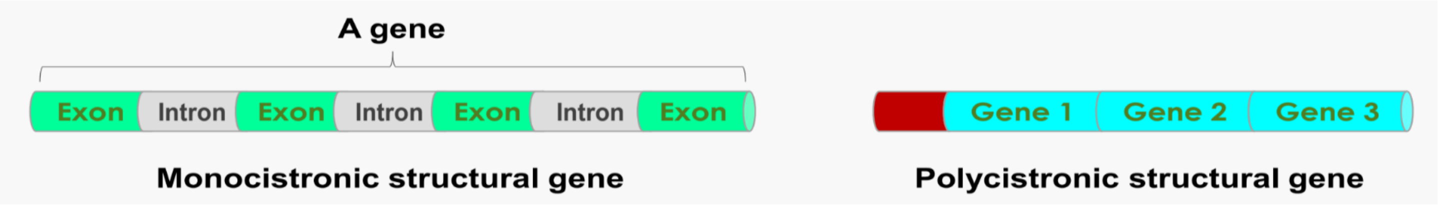
(2) Double stranded RNA molecules will be produced that would prevent translation.

Transcription Unit & The Gene

Gene is the functional unit of inheritance.

Cistron: A fragment of DNA coding for a polypeptide chain.

a) **Monocistronic structural gene (Split gene)**: Found in Eukaryotes. Consist of -
   (i) **Exons** -Coding (Expressed) sequences - appear in the matured RNA
   (ii) **Introns** -Non-coding sequences- do not appear in the matured RNA



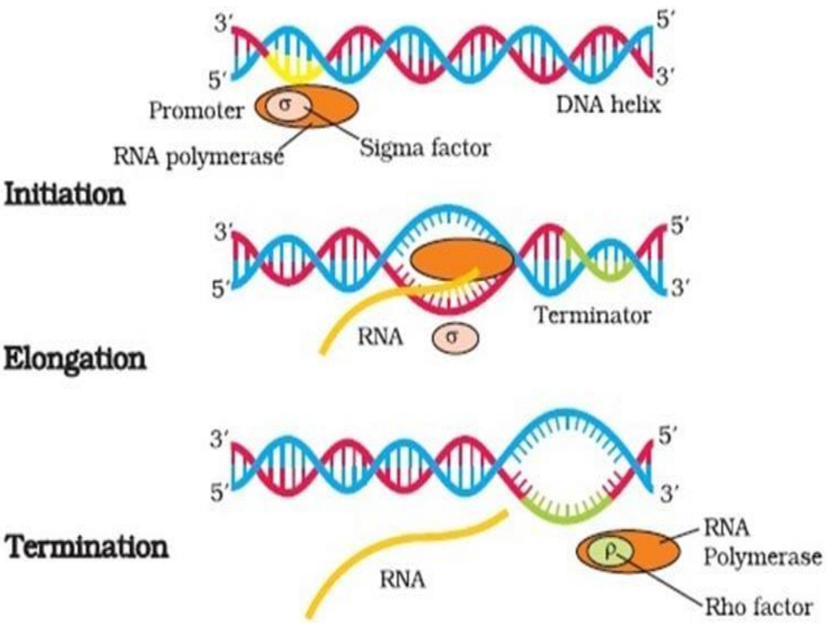
b) **Polycistronic structural gene:** Found in prokaryotes. In a transcription unit between promoter and terminator more than one cistrons are present.

❖ Inheritance of character is also affected by promotor & regulatory gene (it sequence do not code for any RNA or protein)

Transcription in Prokaryotes

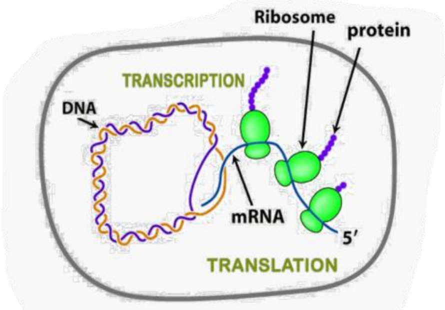
Types of RNA in Prokaryotes need to synthesise a protein in a cell. Single enzyme (RNA polymerase) responsible to transcribe all three RNA in a polycistronic gene.

1) **mRNA (messenger RNA)-** Provide template for translation.
2) **tRNA (transfer RNA)-** Brings amino acids and read genetic code hence called adapter molecule.
3) **rRNA (ribosomal RNA)-** Structural and catalytic role in translation.



Transcription includes 3 main processes:

1. **Initiation:** Sigma factor (σ) – Initiating factor binds transiently to RNA Polymerase which further binds to Promoter to start the transcription.
2. **Elongation:** Nucleotide triphosphate (ATP, GTP, CTP, UTP) a used as substrate following complimentary principle. RNA polymerase open DNA helix and continue elongation where a short stretch of RNA remains bound to enzyme.
3. **Termination:** Rho (ρ) – Terminating factor binds transiently to RNA polymerase to stop the transcription. Newly formed RNA falls off and RNA polymerase also detach from DNA



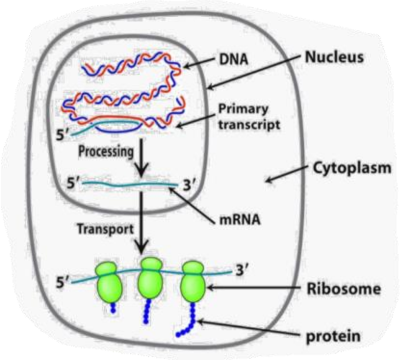
Bacterial cell (Prokaryote)

Transcription & Translation occur simultaneously in Prokaryotes in the same compartment.

i) mRNA do not need any processing to become active.

ii) There is no separation of cytoplasm and nucleus.

In Eukaryotes there is no coupling of transcription and translation. Translation occurs after Transcription



Eukaryotic Cell

Types of Ribosomal RNA in Prokaryotes

70S Ribosome

30S	50S
16srRNA	23srRNA 5srRNA

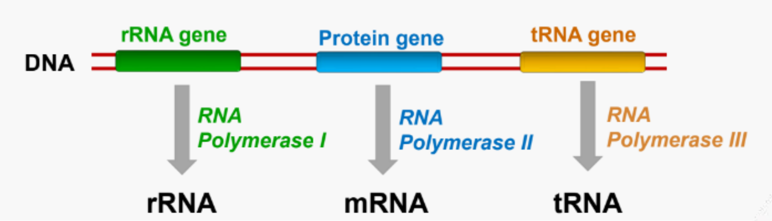
Types of Ribosomal RNA in Eukaryotes

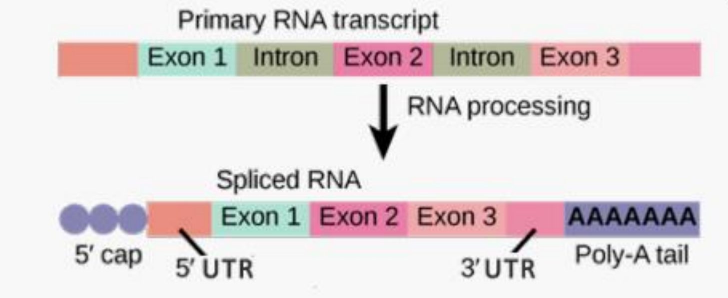
80S Ribosome

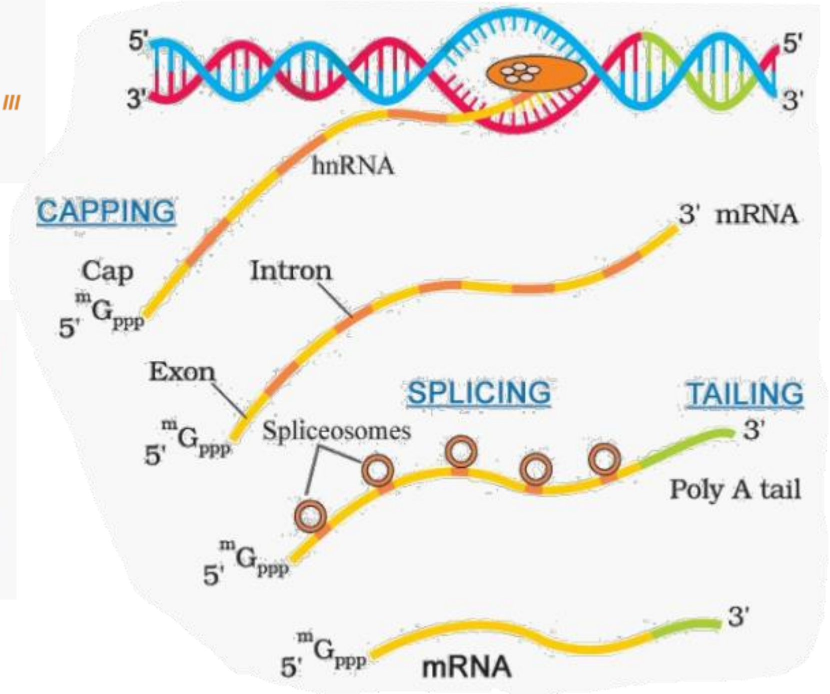
40S	60S
18srRNA	28srRNA 5.8srRNA 5 srRNA

Transcription in Eukaryotes- It follows same process of transcription with two additional complexities:

1) Three types of RNA polymerase use to transcribe:
   - i) **RNA polymerase I** – rRNA (28S, 18S &5.8S)
   - ii) **RNA polymerase II-** hnRNA (heterogenous nuclear RNA) precursor of mRNA.
   - iii) **RNA polymerase III-** tRNA, 5 srRNA, & snRNA (Small Nuclear RNA)
2) After Transcription the Primary Transcribe contain both Exons & Introns and are non-functional. Hence, introns must be removed. Subjected to







i) **Splicing-** Introns are removed by spliceosome and Exons are joined in a definite manner.

ii) **Capping:** A nucleotide methyl Guanosine triphosphate ($^{m}G_{ppp}$) is added as cap to 5’ end of hnRNA.

iii) **Tailing (Polyadenylation):** Adenylate (adenosine) residue (200-300) are added to 3’ end.

- Split gene arrangement probably represents ancient feature of Genome.
- Presence of introns represent antiquity & splicing represent RNA dominance in history.