Transcription

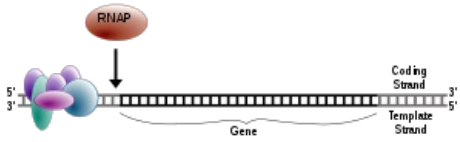
Transcription is the transfer of genetic information from *DNA into an RNA* molecule . It is overwhelmingly a transcription of information from one gene , used to create one **specific protein** , which the cell needs at a given moment. The RNA strand is formed on the principle of **complementarity** to the DNA strand.

After the information is transcribed, thanks to the mRNA , it is transferred to the **proteosynthetic apparatus** , where **proteosynthesis** begins according to the described order .

Initiation and transcription

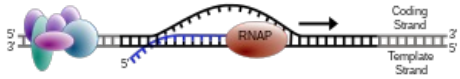
Transcription is an **enzymatic proces**s where **RNA polymerase** (DNA-dependent RNA polymerase) is used as an enzyme . The strand is examined from the **5' end to the 3' end**. RNA polymerase looks for a starting sequence of nucleotides in DNA, the so-called **promoter** (an enzyme subunit - the so-called sigma factor - is responsible for its recognition). Although the DNA molecule is double-stranded, the promoter is asymmetric, which means that:

- there is always a *transcription from only one thread* – **the working thread (also negative (-), anti-coding or nonsensical) ;**
- *the second thread is not important* for the transcription of this gene - **the memory thread (also positive (+), coding or meaningful) .**



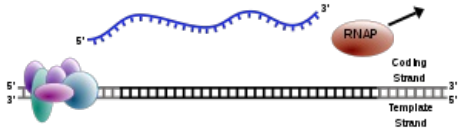
Initiation of transcription.

After recognition of the promoter and breaking of the hydrogen bonds, the **RNA strand is synthesized according to the complementarity of the bases to the working DNA strand** . ⚠



Elongation of transcription.

instead of T is U! Once the polymerase encounters a *stop sequence* in the chain, **transcription stops** and the released RNA can travel on. The basic enzymes involved in transcription are ***DNA-dependent RNA polymerases I.- III.***



Termination of transcription.

Designation	Location	Product
I.	Seed	pre-rRNA
II.	Kernel	pre-mRNA (hnRNA)
III.	Kernel	pre-tRNA, 5S rRNA

A number of proteins participate in the transcription of eukaryotes - the so-called **transcription factors (TF)** , which are distinguished by Roman numerals and letters. Transcription is initiated by binding of TF IID to the **TATA box** region . This is followed by the attachment of another TF, RNA polymerase and other TFs. Transcription in eukaryotes produces **precursor-type RNAs** , i.e. those that only become definitive functional molecules through post-transcriptional modifications.

Regulatory sequence

Promotor

It faces the **5' end** of the working DNA strand before transcription begins. It is of variable length, usually around 30–40 bp. Its function is to **mark the beginning of transcription** and participates in the **regulation of its intensity** . So-called *signal sequences* are often found in the promoter region :

- 30–40 bp before the start of transcription, the so-called *TATA box* ← contains a higher amount of T and A;
- another known signal sequence is the *CCAAT box* ← usually at position 75–80 bp (for genes equipped with this signal sequence, its presence is a condition for efficient transcription).

There are a number of genes that do not contain either a TATA or a CCAAT box - these are mostly genes found in every cell = **housekeeping genes** (e.g. genes determining enzymes of the citrate cycle).

Enhancers = "amplifiers"

They are stretches of DNA that can be **quite distant** from the gene they affect . These are short sequences whose function is not affected by the distance from the controlled gene. They can act both in the 5' → 3' direction and vice versa, their effect is similar to that of the **promoter.**

Posttranscriptional modifications

In **bacteria and prokaryotes** , no post-transcriptional modifications of mRNA generally occur.

On the other hand, for eukaryotic cells, the situation is much more complicated.

The primary transcript undergoes so-called **splicing** , when non-coding sequences are removed from it. Lasso-like twisting of the primary transcript cuts out **introns** (parts of the chain that do not code for any amino acids). The coding sections (**exons**) are then joined into the final chain. Again, specific sequences that mark the boundaries between introns and exons apply here. Clipped introns are immediately degraded.

The primary transcript is equipped at the 5' end with a so-called **cap** formed by a special nucleotide (7-methylguanosine, attached by three phosphoric acid residues) and at the opposite 3' end is equipped with a so-called **polyadenyl end** (several hundred adenine residues).

Editing – a process in which certain nucleotides are added or chemically changed to mRNA.

See Post-transcriptional modifications for more detailed information .

Transcription factors

- are proteins that participate in the initiation **of transcription** (transcription of hereditary information from a gene (from DNA) to RNA).

They bind to individual elements of the promoter , thereby facilitating the binding of the respective RNA polymerase . **Prokaryotic** RNA polymerase does not require TF for its activity, transcription in **eukaryotes** is dependent on the presence of TF.

Through them, gene expression is adapted to the needs of the cell or the whole organism (e.g. hormones , hypoxia can stimulate the expression - transcription of certain genes). This adaptation can be quite fast, up to several thousand transcripts of a single DNA segment can be produced within an hour. Some TFs must first be activated by e.g. phosphorylation or removal of the inhibitor.

We distinguish:

1. **General TF** – occurrence in all types of cells ,
2. **Special TF** – occurrence only in certain cells,
3. **Basal TF** – factors necessary for induction of basal transcription (in cells with low transcriptional activity).

Function and biological role of transcription factors

Regulation of basal transcription

- **GTFs** (general transcription factors) – necessary for transcription
- many of them do not bind to DNA, but are part of a preinitiation complex that reacts directly with RNA polymerase II
- most common: TFIIA, TFIIB, TFIID (includes a subunit called *TATA binding protein* (TBP) - binds specifically to the TATA box sequence), TFIIE, TFIIF and TFIIH

Cell development

- based on signals, they regulate cell differentiation and determination
- the TF Hox family is important for proper body alignment
- TF encoded by SRY (Sex-determining region of Y) – determination of human sex

Response to intercellular signals

- part of the signaling cascade (activation x suppression)
- e.g. estrogen **signaling** : TF is part of the estrogen receptor, which after activation travels to the nucleus, where it regulates the transcription of certain genes

Response to the external environment

- TFs also regulate signaling cascades of exogenous origin
- **Heat shock factor** (HSF) – activates genes enabling survival at higher temperatures
- **Hypoxia inducible factor** (HIF) – survival in an environment with a lack of oxygen

Cell cycle control

- **TFs** that are oncogenes (e.g. myc) and tumor suppressors (e.g. p53) – role in cell growth and apoptosis

Transcription in prokaryotes

- The basic features are the same as in eukaryotes, but they differ in temporal continuity, in the regulation mechanism, promoter nucleotide sequences, ribosome structure...
- DNA segment that is transcribed as a single RNA molecule is called a **transcription unit**
  - It can contain 1 gene (as in eukaryotes) or a whole series of genes
  - Co-transcribed genes usually encode related enzymes
- Synthesis is mediated by **RNA polymerase in the direction 5´→ 3**

- Composed of several polypeptides, the most important is the **sigma factor** = participates in transcription initiation (recognizes the signal sequence of the promoter and binds RNA polymerase there) • 3 stages: initiation, elongation, termination

- **Initiation**

→ Transcription begins with binding between the **sigma factor and the promoter**

→ A short section of the double helix is despiraled by the action of RNA polymerase, the hydrogen bonds are broken and the strands are separated

• According to the template of the working strand, RNA is synthesized

→ **Promoters** have a uniform structure, they contain conserved nucleotide signal sequences = **consensus sequence**

- In position -35 is the sequence **TTGACA = pribnow box , where RNA polymerase** binds
- In the -10 position is the **TATA box** - it helps **unfold and separate the chains**

- **Elongation**

→ RNA synthesis in the direction 5´→ 3´ **without sigma factor**

→ It occurs at the site of the transcription bubble - it lengthens as the polymerase moves

nascent RNA

- Termination

→ Controlled by termination signal

- Unlike eukaryotes, prokaryotic DNA does not contain introns, so post-transcriptional modifications may not occur
- Prokaryotes do not have a nuclear membrane, so nascent mRNA binds directly to ribosomes

Links

Related articles

- DNA
  - DNA Structure
  - DNA Replication
- Transcription factors
- Translation
- Post-translational modifications
- RNA
  - mRNA

Resources

- STEFÁNEK, Jiří. *Medicine, diseases, studies at the 1st Faculty of Medicine, UK* [online]. [feeling. 11/02/2010]. < http://www.stefajir.cz >.
- SIPEK, Antonín. *Transcription and post-transcriptional modifications* [online]. [feeling. 18.04.2010]. < http://www.genetika-biologie.cz/transkripce >.

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