

## 14.5: TRANSCRIPTION OF DNA

### OBJECTIVES

After completing this section, you should be able to

- describe, very briefly, how RNA is synthesized in the nucleus of the cell by transcription of DNA.
- identify the important structural differences between DNA and RNA.
- given the appropriate Kekulé structures, show how uracil can form strong hydrogen bonds to adenine.
- identify the base sequence in RNA that would be complementary to a given base sequence in DNA.

### KEY TERMS

Make certain that you can define, and use in context, the key terms below.

- messenger RNA
- RNA polymerase
- ribosomal RNA
- transcription
- transfer RNA

### STUDY NOTES

“Messenger RNA” (mRNA) carries the genetic information from the DNA in the nucleus to the cytoplasm where protein synthesis occurs. The code carried by mRNA is read by “transfer RNA” (tRNA) in a process called translation (see [Section 28.5](#)).

“Ribosomal RNA” (rRNA) is the term used to describe the RNA molecules which, together with proteins, make up the ribosomes on which proteins are synthesized.

Three types of RNA are formed during transcription: *messenger RNA* (mRNA), *ribosomal RNA* (rRNA), and *transfer RNA* (tRNA). These three types of RNA differ in function, size, and percentage of the total cell RNA (Table 14.5.1). mRNA makes up only a small percent of the total amount of RNA within the cell, primarily because each molecule of mRNA exists for a relatively short time; it is continuously being degraded and resynthesized. The molecular dimensions of the mRNA molecule vary according to the amount of genetic information a given molecule contains. After transcription, which takes place in the nucleus, the mRNA passes into the cytoplasm, carrying the genetic message from DNA to the ribosomes, the sites of protein synthesis. Elsewhere, we shall see how [mRNA directly determines the sequence of amino acids during protein synthesis](#).

Table 14.5.1: Properties of Cellular RNA in *Escherichia coli*

Type	Function	Approximate Number of Nucleotides	Percentage of Total Cell RNA
mRNA	codes for proteins	100–6,000	~3
rRNA	component of ribosomes	120–2900	83
tRNA	adapter molecule that brings the amino acid to the ribosome	75–90	14

For the hereditary information in DNA to be useful, it must be “expressed,” that is, used to direct the growth and functioning of an organism. The flow of genetic information in cells goes from DNA to mRNA to protein, by genes which specify the sequences of mRNAs, which in turn specify the sequences of proteins.

The first step in the processes that constitute DNA expression is the synthesis of RNA, by a template mechanism that is in many ways analogous to DNA replication. Because the RNA that is synthesized is a complementary copy of information contained in DNA, RNA synthesis is referred to as transcription. Transcription requires the DNA double helix to partially unwind in the region of mRNA synthesis. The region of unwinding is called a **transcription bubble**. The DNA sequence has patterns which indicate where RNA polymerase should start and end transcription. A DNA sequence at which the RNA polymerase binds to start transcription is called a **promoter**. The DNA sequence that indicates the endpoint of transcription, where the RNA polymerase should stop adding nucleotides and dissociate from the template is known as a **terminator** sequence. The promoter and terminator, thus, bracket the region of the DNA that is to be transcribed.

In bacteria, the promoter sequence contains two 6 bp region called **consensus** sequences. One sequence is centered about 10 bp upstream from the transcription start site. The second sequence is at about 35 basepairs upstream from the start of transcription. The consensus sequences at -10 and -35 are necessary for recognition of the promoter region by RNA polymerase.

The DNA sequence that is transcribed to make RNA is called the antisense strand (also called template, anticoding, or transcribed strand), while the complementary sequence on the other DNA strand is called the sense strand (also called the coding or informational strand). To initiate RNA synthesis, the two DNA strands unwind at specific sites along the DNA molecule. Ribonucleotides are attracted to the uncoiling region of the DNA molecule, beginning at the 3' end of the template strand, according to the rules of base pairing. Thymine in DNA calls for adenine in RNA, cytosine specifies guanine, guanine calls for cytosine, and adenine requires uracil. RNA polymerase—an enzyme—binds the complementary ribonucleotide and catalyzes the formation of the ester linkage between ribonucleotides, a reaction very similar to that catalyzed by DNA polymerase (Figure 14.5.1). Synthesis of the RNA strand takes place in the 5' to 3' direction, antiparallel to the template strand. Only a short segment of the RNA molecule is hydrogen-bonded to the template strand at any time during transcription. When transcription is completed, the RNA is released, and the DNA helix reforms. The nucleotide sequence of the RNA strand formed during transcription is identical to that of the corresponding coding strand of the DNA, except that U replaces T.

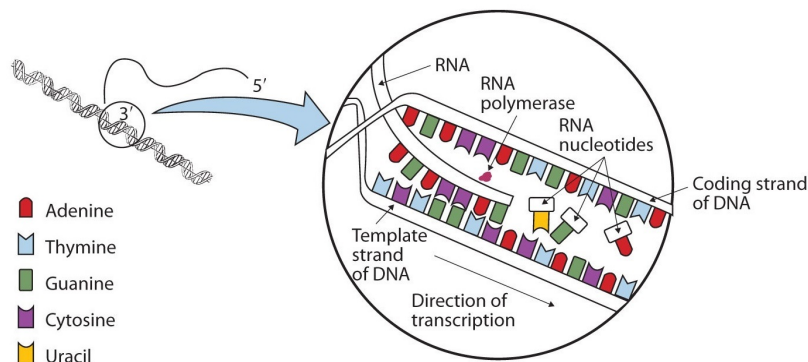


Figure 14.5.1: A Schematic Diagram of RNA Transcription from a DNA Template. The representation of RNA polymerase is proportionately much smaller than the actual molecule, which encompasses about 50 nucleotides at a time. (CC BY-SA-NC 3.0; Anonymous via LibreTexts)

The genes of eukaryotes (animals and plants) usually do not have continuous segments of coding DNA. Rather they have intervening sequences of DNA (introns) within a given gene that separate coding fragments of DNA (exons). In a process called **splicing**, a primary transcript is made from the DNA, and then splicesomes cut out the introns and join the exons to form a contiguous stretch to form messenger RNA, mRNA. Once formed the mRNA leaves the nucleus to be translated into a protein sequence.

New findings make it even more complicated to define a gene, especially if the transcripts of a "gene region" are studied. Cheng et al studied all transcripts from 10 different human chromosomes and 8 different cell lines. They found a large number of different transcripts, many of which overlapped. Splicing often occurs between nonadjacent introns. Transcripts were found from both strands and were from regions containing introns and exons. Other studies found up to 5% of transcripts continued through the end of "gene" into other genes. 63% of the entire mouse genome, which is comprised of only 2% exons, is transcribed.

### ? EXERCISE 14.5.1

A portion of the template strand of a gene has the sequence 5'-TCCATGAGTTGA-3'. What is the sequence of nucleotides in the RNA that is formed from this template?

#### Answer

Four things must be remembered in answering this question: (1) the DNA strand and the RNA strand being synthesized are antiparallel; (2) RNA is synthesized in a 5' to 3' direction, so transcription begins at the 3' end of the template strand; (3) ribonucleotides are used in place of deoxyribonucleotides; and (4) thymine (T) base pairs with adenine (A), A base pairs with uracil (U; in RNA), and cytosine (C) base pairs with guanine (G). The sequence is determined to be 3'-AGGUACUAAUCU-5' (can also be written as 5'-UCAACUCAUGGA-3').

### ? EXERCISE 14.5.2

What would be the DNA base sequence of the coding strand required to transcribe the following RNA sequence?

5'-AUGAGCGACUUUGCGGGAUUA-3'

#### Answer

5'-ATGAGCGACTTTGCGGGATTA-3'.

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