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Research Article

DNA signals processing

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Abstract
In this paper ribonucleic acid from deoxyribonucleic acid transcription signals were examined. The synthesis of a ribonucleic acid transcript from deoxyribonucleic acid is a very complex process, involving the enzyme ribonucleic acid polymerase and a number of associated proteins. The process of ribonucleic acid synthesis begins to recognize the promoter for transcription. The enzyme attaches at a specific site, the promoter, on the coding strand. Dependent transcription termination signals processing were studied. The main contribution of this paper is transcript signals using as research tool for better understanding nucleotide sequences inducing. Signal regulation processing for communication was evaluated.

Keywords: *RNA, transcript, regulation, signal, synthesis.*

1. Introduction

The general steps required to synthesize an RNA (ribonucleic acid) from DNA (deoxyribonucleic acid) - the primary transcript are initiation, elongation, and termination. Most is known about initiation. A number of DNA regions (generally located upstream from the initiation site) and protein factors that bind to these sequences to regulate the initiation of transcription have been identified. This process is the best understood in prokaryotes and viruses, but considerable progress has been made in deciphering mammalian cell transcription in recent years [1]-[4]. It is important to understand the basic principles of Ribonucleic acid synthesis, for modulation of this process results in altered rates of protein synthesis and hence a variety of metabolic changes, and this is how organisms adapt to changes of environment [5]-[7].

The RNA molecules synthesized in mammalian cells are often very different from those made in prokaryotic organisms, particularly the mRNA encoding transcripts. Prokaryotic mRNA can be translated as it is being synthesized, whereas in mammalian cells most RNA are made as precursor molecules that have to be processed into mature, active RNA. Erroneous processing and slicing of mRNA transcripts are a cause of disease, e.g. the coding strand. This is followed by initiation of RNA synthesis at the starting point, and the process continues until a termination sequences reached certain types of thalassemia.

In this paper transcript signals in RNA from DNA synthesis were studied.

2. RNA synthesis

The process of synthesizing RNA from a DNA template has been characterized best in prokaryotes. Although in mammalian cells the regulation of RNA synthesis and the processing of the RNA transcripts are different from that in prokaryotes, the process of RNA synthesis is quite similar in these 2 classes of organisms. Therefore, the description of RNA synthesis in prokaryotes will be application to eukaryotes even though the enzymes involved and the regulatory signals are different [8]-[10].

The sequence of ribonucleotides in an RNA molecule is complementary to the sequence of deoxyribonucleotides in one strand of the double stranded DNA molecule [11]. The strand that is transcribed into an RNA molecule is referred to as the coding strand of the DNA. The other DNA strand is frequently referred to as the noncoding strand of that gene. In case of a double-stranded DNA molecule containing many genes, the coding strand for each gene will not necessarily be the same strand of the a double – stranded DNA molecule helix (Fig. 1). Thus, a given strand of DNA double-stranded DNA molecule will serve as the coding strand for some genes and the noncoding strand of other genes. Note that the nucleotide sequence of an RNA transcript will be the same (except for U replacing T) as that of the noncoding strand.

DNA- dependent RNA polymerase in the enzyme responsible for the polymerization of ribonucleotides into a sequence complementary to the coding strand of the gene. This is followed by initiation of RNA synthesis at the starting point, and the process continues until a termination sequence is reached. A transcription unit is defined as that region of DNA that extends between the promoter and the terminator. The RNA product, which is synthesized in the 5' to 3' direction, is the primary transcript. In prokaryotes, this can represent the product of several genes, in mammalian cells, it usually represents the product of a single gene. The 5' terminal of the primary RNA transcript and the mature cytoplasmic RNA are identical. Thus, the star point of transcription corresponds to the 5' nucleotide of the mRNA. The primary transcripts generated by RNA polymerase II are promptly capped by 7-methylguanosine triphosphate-caps that persist and eventually appear on the 5'end of mature cytoplasmic mRNA. These caps are presuamably necessary for both the subsequent processing of the primary transcript to mRNA as described below and for its subsequent translation.

The DNA dependent RNA polymerase of the bacterium *Escherichia coli* exists as a core molecule composed of 4 subunits; 2 of these are identical to each other (the α submits), and 2 are similar in size to each other but not identical (the β subunit and β' subunit). The core ribonucleic acid polymerase utilizes a specific protein factor (the sigma [∂] factor that assists the core enzyme to attach more tightly to the specific deoxynucleotide sequence of the promoter region. Bacteria contain multiple ∂ factors, each of which acts as a regulatory protein that modifies the promoter recognition specificity of the RNA polymerase. The appearance of different ∂ factors can be correlated temporally with various programs of gene expression in procaryotic systems, such as bacteriophage development, sporulation, and the response to heat shock.

The process of RNA synthesis, depicted in Fig. 2, involves first the binding of the RNA holopolymerase molecule to the template at the promoter site. Initiation of formation of the RNA molecule at the 5' end then follows with the release of the ∂ factor, while the elongation of the RNA molecule from the 5' to its 3' end continues antiparallel to its template. The enzyme polymerazes the ribonucleotides in a specific sequence that is dictated by the coding strand and interpreted by Watson-Crick base pairing rules. Pyrophosphate prokaryotes and eukaryotes, a purine ribonucleotide is usually the first to be polymerized into the RNA molecule.

As the elongation complex containing the core RNA polymerase progresses along the DNA molecule. DNA unwinding must occur in order to provide access for the appropriate base pairing to the nucleotides of the coding strand. The extent of DNA unwinding is constant throughout transcription and has been estimated to be about 17 base pairs per polymerase molecule. Thus, it appears that the size of the unwound DNA region is dictated by the polymerase and is independent of the DNA sequence in the complex. This suggests that RNA polymerase has associated with it an "unwindase" activity that opens the DNA helix. The fact that the DNA double helix must unwind and the strands part at least transiently for transcription implies some disruption of the nucleosome structure of eukaryotic cells.

Termination of the synthesis of the RNA molecule is signaled by a sequence in the coding strand of the DNA molecule, a signal that is recognized by a termination protein, the rho (ρ) factor. After termination of synthesis of the RNA molecule, the core enzyme separates from DNA template. With the assistance of another ∂ factor, the core enzyme then recognize a promoter at which the synthesis of a new RNA molecule commences. More than one RNA polymerase molecule may transcribe the same coding strand of a gene simultaneously, but the process is phased and spaced in such a way that at any one moment each is transcribing a different portion of the DNA sequence.

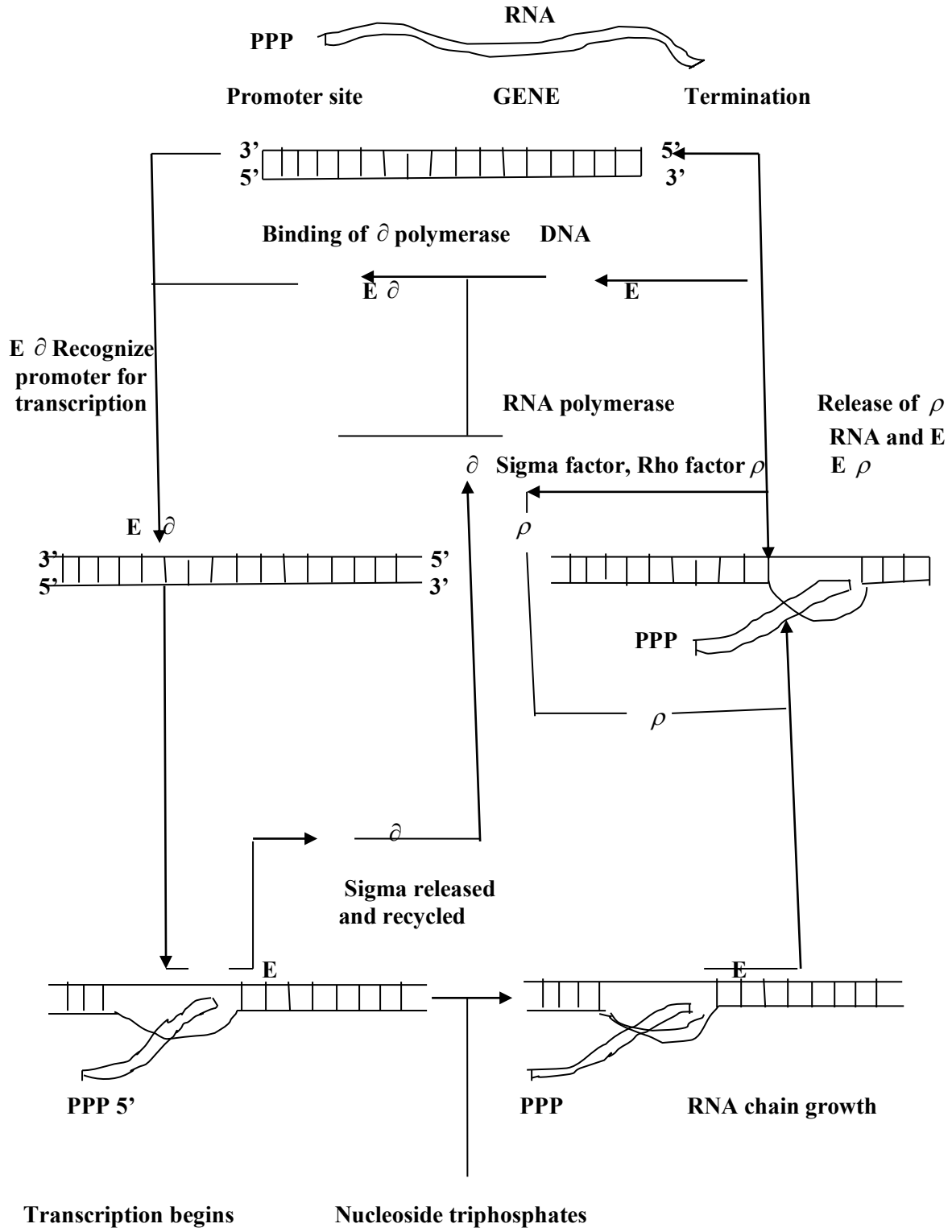

Fig. 1. The process of RNA synthesis. It begins at the upper left hand portion of the figure with the binding of sigma factor to be core polymerase to form a complex that can recognize the promoter for transcription. The process is completed as the RNA polymerase is released from the gene, and all of the catalytic components are free to recycle. enzyme

Mammalian cells possess several DNA – dependent RNA - polymerases, the properties of which are described in Table 1. Each of these DNA- dependent RNA polymerases seem to be responsible for the transcription of different sets of genes. Mammalian cells possess several DNA. The sizes of the RNA polymerases for the 3 major classes of eukaryotic RNA range are from MW 500,000 to 600,000. All of these enzymes share the basic subunit

structural organization of bacterial RNA polymerase. They all have 2 large subunits and a number of smaller subunits. Recent DNA cloning and sequencing work indicates that eukaryotic RNA polymerases have extensive amino acid homologies with prokaryotic RNA polymerases. The functions of each of the subunits are not yet understood. Many could have regulatory functions, such as serving to assist the polymerase in the recognition of specific sequences like promoters and termination signals.

One toxin from the mushroom *Amantia phalloides,* $\alpha-$amantin, is a specific inhibitor of the eukaryotic nucleoplasmic DNA- dependent RNA polymerase (RNA polymerase II) and as such has proved to be a powerful research tool (Table 1).

Table 1. Nomenclature and localization of animal DNA-dependent RNA polymerases

Class of enzymes	Sensitivity to $\alpha-$amantin	Products	Principal localization
I(A)	Insensitive	rRNA	Nucleolar
II(B)	Sensitive to low concentration ($10^{-8}-10^{-9}$ mol/L)	hnRNA (mRNA)	Nucleoplasmic
III(C)	Sensitive to high concentration	tRAN and SS RNA	Nucleoplasmic

3. Transcription signals

The DNA sequence analysis of specific genes obtained by recombinant DNA technology has allowed the recognition of a number of sequences important in gene transcription. From the large number of bacterial genes studied it is possible to construct consensus models of transcription promoter and termination signals.

These are random (stochastic) processes with expected value of signals set for $T_i \to \infty$:

$$\lim_{T_i \to \infty_{t_i}} \frac{1}{T_i} \sum_{i=0}^{T_i} [\xi(t_i)] = E\{[\xi(t)]\}$$

where t - time and T_i -period [12].

This is expression for the middle value of transcription promoter and termination signals.

Bacterial promoters are approximately 40 nucleotide pairs (4 turns of the DNA double helix) in length, a region sufficiently small to be covered by an *E. coli* RNA holopolymerase molecule. In this consensus promoter region are 2 short, conserved sequence elements. Approximately 35 base pair upstream of the transcription start site there is a consensus sequence of 8 nucleotide pairs. More proximal to the transcription start site, about 10 nucleotides upstream, is a 6-nucleotide pair AT-rich sequence. The latter sequence will have a low melting temperature because of its deficiency of GC nucleotide pairs. Thus, the TATA or Pribnow box is thought to case the dissociation between the coding and noncoding strands so that RNA polymerase bound to the promoter region can have access to the nucleotide sequence of its immediately downstream coding strand.

4. Dependent transcription termination signals

Rho-dependent transcription termination signals in *E. coli* also appear to have a distinct consensus sequence, as shown Fig. 2. The conserved consensus sequence, which also extends about 40 nucleotide pairs in length, can be seen to contain a hyphenated or interrupted inverted repeat, followed by a series of AT base pairs. As transcription proceeds through the hyphenated, inverted repeat, the generated transcript can form the intramolecular hairpin structure, also depicted in Fig. 3. Transcription continues into the AT region, and with the aid of a termination protein factor called rho (ρ)the RNA polymerase stops and dissociates, releasing the primary transcript.

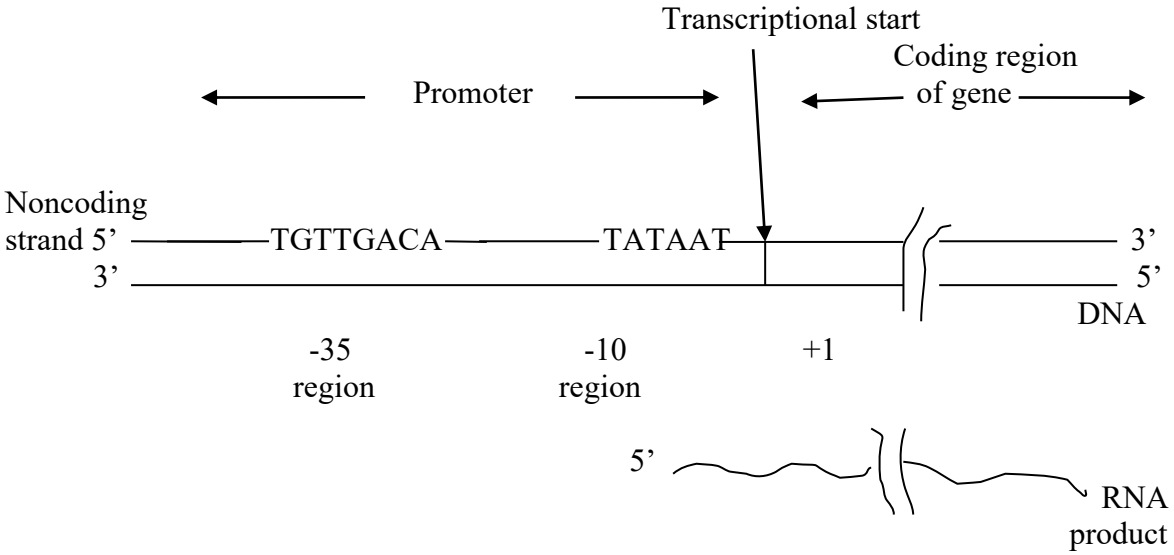

Fig. 2 Bacterial promoters share 2 regions of highly conserved nucleotides. These are centered 35 and 10 base pairs upstream from the start site of transcription, indicated as + 1

An extensive analysis of eukaryotic transcription signals has been conducted utilizing recombinant DNA techniques. It is clear that the signals in DNA which control transcription are of several types. Two types of sequence elements are promoter proximal. One of these defines where transcription is to commence along the DNA, and the other determines how frequently this event is to occur. In the thymidine kinase gene of herpes simplex, which utilizes the transcription system of its mammalian host for gene expression, there is a unique transcription start site, and accurate transcription from 32-16 nucleotides upstream from the start site. This region has the sequence of TATAAAAG and bears remarkable homology to the functionally related. Pribnow box (TATAAT) located about 10 base pairs upstream from prokaryotic mRNA start points. The RNA polymerase II probably binds to DNA in the region of the TATA box and then commences transcription of the template strand about 32 nucleotides downstream at a T, which is surrounded by purines (Fig. 4).Therefore, the TATA box seems to provide the "where" signal.

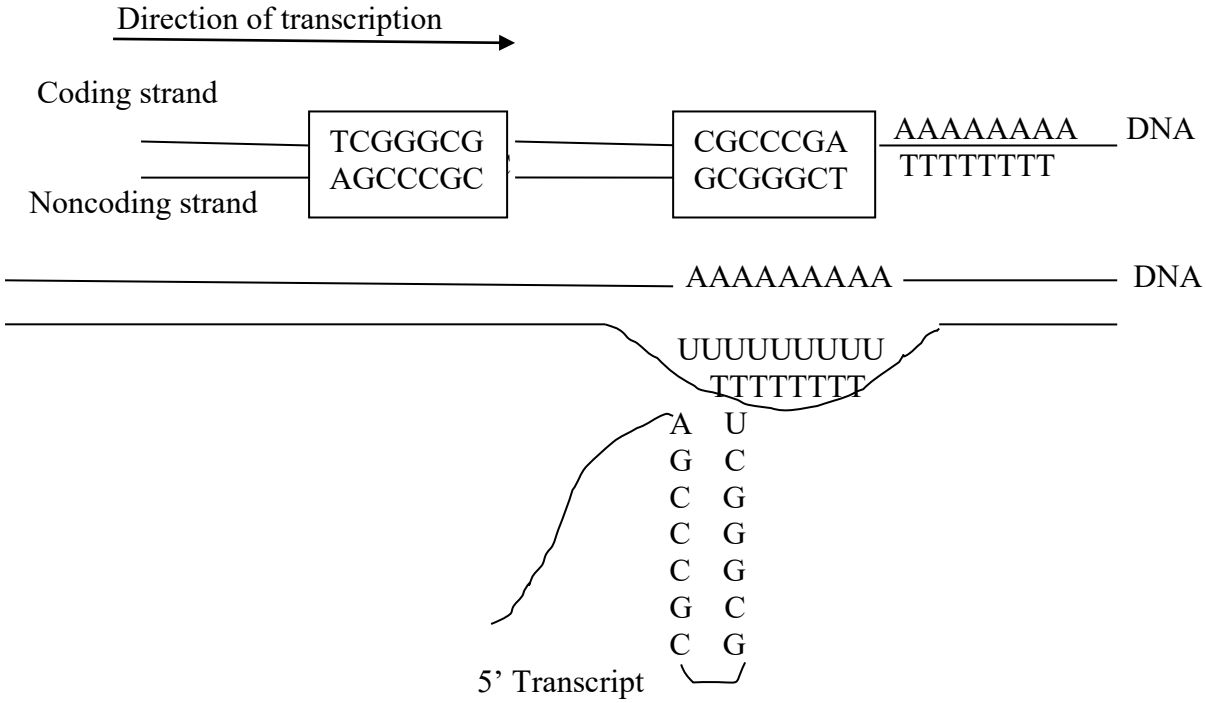

Fig. 3 The bacterial transcriptional termination signal in the gene contains an inverted, hyphenated repeat followed by a stretch of AT base pairs (above) that upon being transcribed can generate the secondary structure in the RNA.

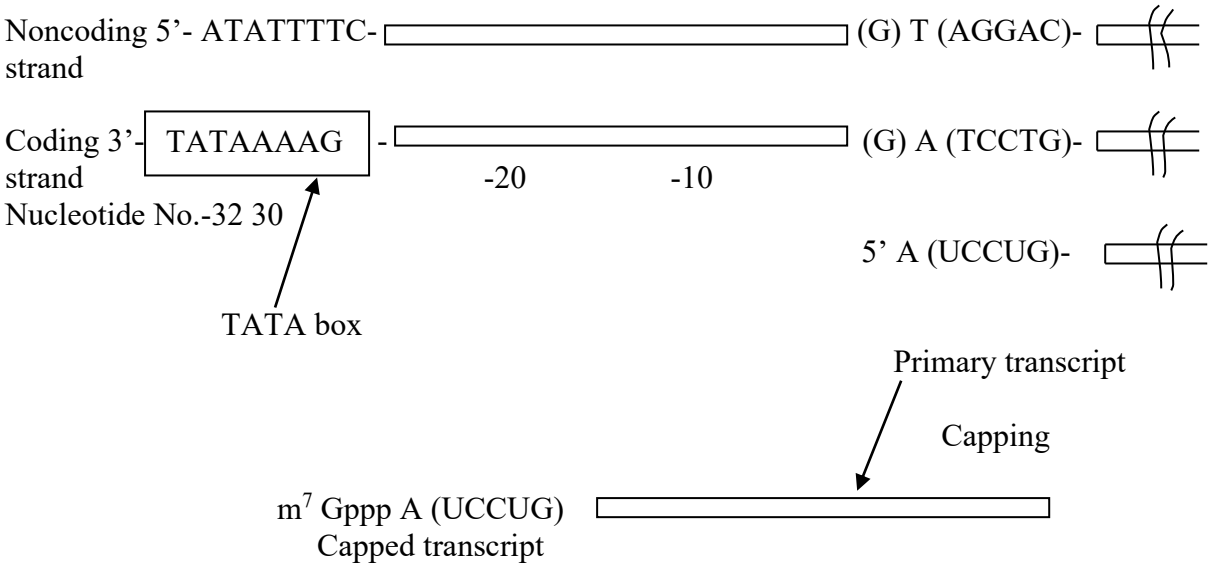

Fig.4 Transcription of the thymidine kinase gene. The DNA- dependent RNA polymerase II binds to the complement of the TATA box and commences transcription of the coding strand about 32 nucleotides downstream at a T that is surrounded by purines. The primary transcript is rapidly capped at the first nucleotide (5'-purine).

The transcription signals in mammalian cells are, not unexpectedly, more complex. polymerase stops and dissociates, releasing the primary transcript.

Two segments of nucleotides farther upstream from the start site form a single functional element that is responsible for determining how frequently this transcription vent occurs. Mutations in either of these regions, located between -61 to -47 and -105 to -80 by upstream from the start site of the thymidine kinase gene, reduce the frequency of transcriptional starts 10 to 20 fold. These basal promoter elements that confer to fidelity and frequency of initiation have rigid requirements for position and orientation. Single base changes have dramatic effects on function; spacing with respect to the start site is critical, and they generally do not work if the 5' to 3' orientation is reversed.

5. Discussion

1. There is a sequence of specific gene for transcription which is obtained by recombinant technology.
2. From large number of gene can construct consensus models of transcription promoter and termination signals.
3. The expected values of transcriptional signals occurs is derived.
4. The signals in DNA which control transcription are of several types, two of them have considered in the paper.
5. The study of RNA synthesis in prokaryotes can be applied to eukaryotes even though the enzymes involved and the regulatory signals are different.

6. Conclusion

In this paper transcription signal of RNA was examined. RNA synthesis from DNA by a specific gene was analyzed. This paper contributes signal regulation processing for transcript communication.

The dependent transcriptional determination signals were studied. The signal that is recognized by a termination protein, the rho (ρ) factor has been proceeded.

The expression for the middle value of transcription promoter and termination signals occur was derived.

The transcription of the thymidine kinase gene was examined in this paper.

Abbreviation

DNA- deoxyribonucleic acid
RNA - ribonucleic acid

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