control and experimental plants. A conclusion is done, that increasing of plant ontogenesis with use different growth regulators is achieved by activating of unsame type groups of genes

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THE MOLECULAR MECHANISM OF HYDROGEN BOND FORMATION BETWEEN T-A BASE PAIRS WITHIN A PROMOTER AND A SIGMA FACTOR

The canonical viewpoint on DNA packaging in higher eukaryotes is that DNA in the nucleus is wrapped around a protein core of two molecules of each of the core histones H2A, H2B, H3 and H4 [8, 9]. Both DNA replication and chromatin assembly occur simultaneously during the S-phase of the cell cycle. It is generally assumed that the parental nucleosomes are transiently disrupted before S-phase and are subsequently assembled onto two DNA daughter strands by an unknown mechanism [9]. *De novo* assembly of nucleosomes occurs by the deposition of a tetramer of the core histones H3 and H4 followed by the deposition of a pair of dimers of the histones H2A and H2B to reconstitute the nucleosome. The formation of the nucleosome in larger eukaryotes is accomplished by the binding of the histone H1 to the core histones H3, H4, H2A and H2B.

Nucleosome core particles that contain a 'core particle' of the fixed length of DNA [146 base pairs, bp] wrapped 1.65 times around an octamer of 'core' histone proteins are the most thoroughly described in the literature. Although the core histones are arranged as the 2(H3-H4) tetramer and two H2A-H2B dimers positioned on both sides of the tetramer, deeper knowledge of the structure about the origin and preferential positioning stability of the nucleosome along the DNA chain is still unsettled or at least fragmentary. It is suggested that the individual nucleosome is a particle of a flattened cylinder 10.5 nm in diameter and 5.7 nm in height (i.e., the nucleosome possesses in the disk-shaped form that has sizes approximately 6 nm × 11 nm × 11 nm) [8].

The function of four different core histones H2A, H2B, H3, and H4 is to package of DNA into the cell nucleus but little is known about the functional role of each of them in the higher eukaryotic histone octamer. Earlier we have described a model for histone arrangements in the nucleosomes of higher eukaryotes [4–6].

Transcription involves synthesis of an RNA by RNA polymerases. Firstly, RNA polymerase must bind to the double-strand of DNA. The initiation stage requires the recognition of a short region of DNA douplex. The sequence of DNA that is necessary for this reaction is called the promoter. The basic initiation of transcription is performed by the multisubunit RNA polymerase, so called sigma (s) factor (s) [3], which directly contacts the promoter sequences. Sigma factors specifically recognize the distinguishable promoter DNA determinants that are responsible for the binding of RNA polymerases to DNA. Hence, the sigma factor determines which gene must be transcribed. Initiation occurs when an RNA polymerase binds to the promoter, and the site at which the first nucleotide is incorporated is called the startpoint. The identification of transcription factor binding sites is a fundamental problem in the understanding of a signal transduction platform for extracellular or intracellular signals and the regulation of all genome functions.

Prokaryotic and eukaryotic organisms contain a variety of sigma factors that specifically recognize different promoter sequences. Many studied genes have similar promoter sequences, with a consensus sequence of TTGACA at the -35 position and TATAAT at the -

10 position. The consensus sequence TATAAT also is called the Pribnow box. Another sequence of 7 bp

$$T_{82}\ A_{97}\ T_{93}\ A_{85}\ \begin{matrix} A_{63} \\ T_{37} \end{matrix}\ A_{83}\ \begin{matrix} A_{50} \\ T_{37} \end{matrix}$$

has a separation from the start point from 19 to 27 bp and is called TATA or Hogness box. Here the subscript denotes the percent occurrence of the most frequently found base [7].

It is essential to note that although there are many sigma factors in the cell, most of them in free forms do not bind to promoter sequences. In this connection we proposed that both the promoter and any polymerase must have unique fragment of DNA, called a gene lock and gene key [4–6]. Figure 1 present a model to explain how the promoter and sigma factor are disposed in on the chromosome and RNA polymerase and can interact during transcription reaction.

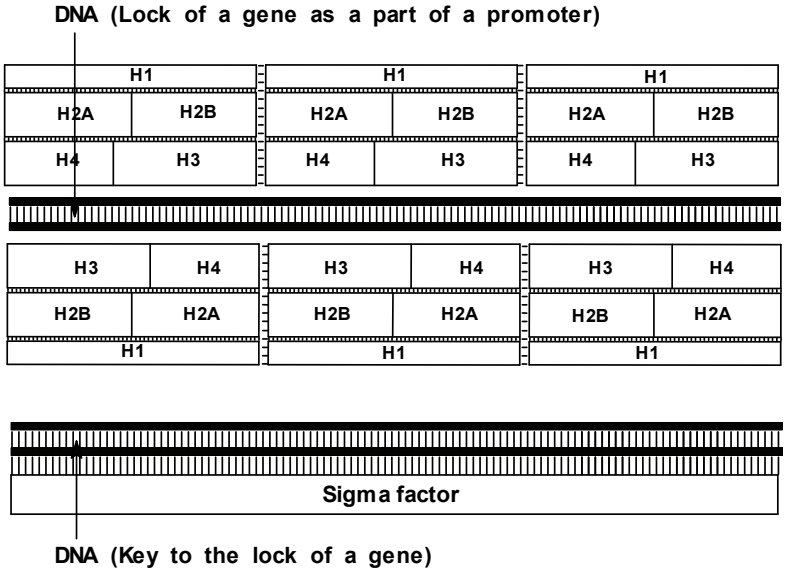

Figure 1. A general model to explain how a sigma factor of RNA polymerases (a gene key) can attach to the gene promoter (a gene lock). The sigma factor can possess in the linear sizes approximitely from 80 bp to 100 bp. It is believed that there are at list 100 contacts between the histone octaner and DNA [2] (not shown).

We propose that each gene/cluster lock (it is a part of a promoter) and each gene key (it presents a sigma factor) begin with adenine (A) or thymine (T) bases. The starting point of RNA/DNA synthesis is the formation of non-covalent hydrogen bonds between paired AT bp of the lock and the key at the beginning of doubled strands of DNA (TA or TATA) and also between one pair of AT bp that can be disposed at different distance to the end of the lock and the key as we can see, for example, in the case with TTGACA and TATAAT boxes. The hydrogen bond is formed between the hydrogen at N6 of the adenine and the oxygen at C2 of the thymine (Figure 2). This process leads to the separation of doubled strands of DNA in the lock into two single strands of DNA.

Many cellular substances are proposed to be signaling molecules between genetic information in nucleus and biochemical processes occurring in the cytoplasm. Nevertheless, the molecular mechanisms by which these putative substances initiate, for example, transcription is unknown. It is not clear how the cell knows which gene (for example from 20,000 to 25,000 in human genome [1]) should be transcribed at any given time. We propose that messengers between accession to genetic information and biochemical processes that occurs in accordance with this information are small molecules of DNA named as keys to the gene (i.e. a parole, also called a sigma factor). All cellular organelles are supplied by such genetic keys that are silenced before the destruction of these organelles. We believe each

gene/cluster has a lock which is also composed of DNA, and disposed on one nucleosomal triplet. Hence, all genes/clusters are closed for transcription and can be open only by such keys that are separated from cellular organelles during programmed synthesis or damaging (physically or in oxidative reactions) of cellular structures.

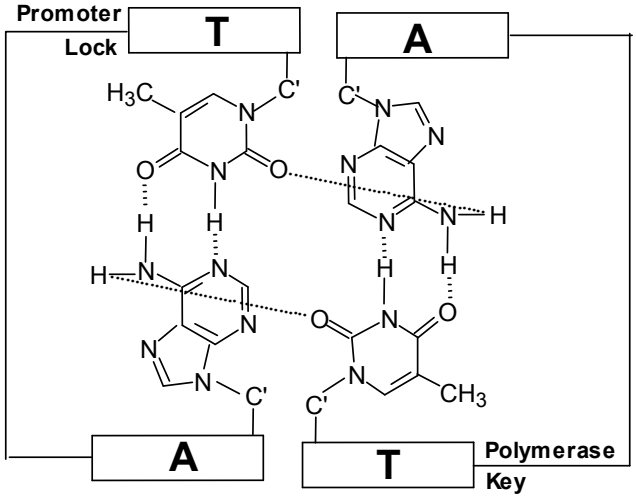

Figure 2. The formation of hydrogen bonds between TA base pair of the promoter and AT base pair of sigma factor.

The gene lock (a fragment of a promoter) and the gene key (a sigma factor) are collinear, but the base pairs within the sigma possess inverse position (Figure 3). Between the TATA box and TA bp are disposed only GC or CG base pairs. Hence, only coincidence TA bp between two fragment of DNA (within a promoter and a sigma factor) permits to form stable hydrogen bonds and initiate transcription.

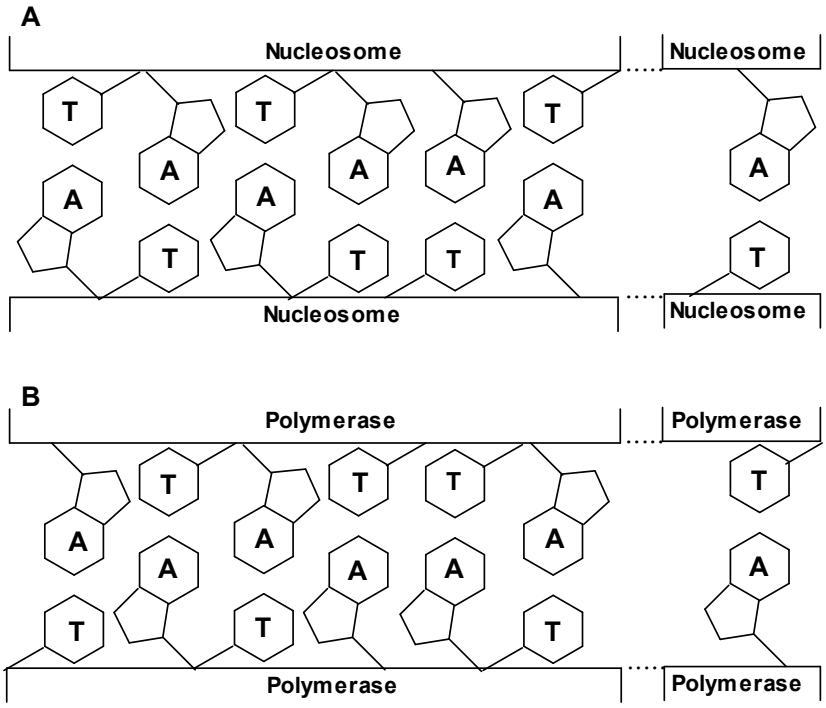

Figure 3. The fragments of a promoter (A) and a sigma factor (B) that contain AT bp. Between the TATA box and TA bp are disposed only GC or CG base pairs.

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In this report it is described the molecular mechanisms of a promoter (a gene lock) and a sigma factor (a gene key) interaction during transcription reaction. The hydrogen bond is formed between the hydrogen at N6 of the adenine and the oxygen at C2 of the thymine. This process leads to the separation of doubled strands of DNA in the gene lock into two single strands of DNA and transcription initiation.

В этом сообщении описаны молекулярные механизмы взаимодействия промотора (генный замок) и сигма фактора (генный ключ) в реакции транскрипции. Водородная связь образуется между водородом при N6 аденина и кислородом при С2 тимина. Этот процесс ведет к разделению двойной нити ДНК в генном замке на две отдельные нити ДНК и инициации транскрипции.

В цьому повідомленні описуються молекулярні механізми взаємодії промотора (генний замок) и сигма фактора (генний ключ) в реакції транскрипції. Водневий зв'язок утворюється між воднем при N6 аденіна и киснем при С2 тиміна. Цей процесс визиває розходження подвійної нитки ДНК в генному замку на дві окремі нитки ДНК і ініціацію транскрипції.