A close-up photograph of several white flowers with prominent yellow centers and stamens. The flowers are in focus, while the background is a soft, out-of-focus green, suggesting foliage. The lighting is bright, highlighting the delicate petals and the intricate details of the reproductive parts.

Zakia Bayguzhina

The Number RM in DNA. Non-coding DNA

Zakia Bayguzhina
The Number RM in
DNA. Non-coding DNA

*http://www.litres.ru/pages/biblio_book/?art=70295311
SelfPub; 2024*

Аннотация

The Human Genome project has shown that the most of human DNA is non-coding DNA, which is sometimes called “junk”. But nature is wise and so arranged that there is nothing superfluous, unnecessary in it. And it helps to understand “the number RM”, which is directly related to non-coding DNA.

Zakia Bayguzhina

The Number RM in DNA. Non-coding DNA

When science reaches a peak, it opens up a vast prospect of a further path to new peaks, new roads are opened along which science will go further.

S. I. Vavilov

One of the most mysterious and unusual molecules is DNA, the main molecule of life.

The search for the foundations of the living was long and difficult: with mistakes and hopes, with faith and disappointment.

And that's happened!

Between 1949 and 1951, biochemist Erwin Chargaff (1905-2002) and his group made a major discovery. They determined the quantitative ratio of purines and pyrimidines in DNA.

And in 1953, an article by Francis Crick (1916-2004) and James Watson (born 1928) was published in the journal Nature.

They constructed the spatial structure of DNA on the basis of X-ray diffraction studies obtained by Rosalind Franklin (1920-1958) and Maurice Wilkins (1916-2004), as well as the Chargaff rule.

There was only one page of text, but it was with this publication that the era of Molecular biology began.

James D. Watson and Francis Crick revolutionized biology. The structure of DNA was no longer a mystery. It turned out that the molecule was built ingeniously simple, like everything that nature has created.

The structure of DNA is as follows: two antiparallel polynucleotide chains are twisted about the axis. On the periphery of the molecule there are carbohydrate-phosphate chains, inside – nitrogen-containing heterocycles.

The nitrogenous bases of one antiparallel chain are connected to a specific base of the other chain, observing Chargaff's rule: adenine combines with thymine, guanine with cytosine. This arrangement is called complementary.

But how does this molecule work?

It is known that one of the functions of DNA is the storage of hereditary information, which is contained in genes.

Therefore, the study of the coding part of human DNA makes

it possible to understand the origin and development of many genetic diseases, including such as malignant neoplasms.

The development of these diseases is directly related to the work of genes.

The need for further study of this molecule would help to find a clue to the development of cancer. These and many other considerations led to the fact that scientists around the world decided to read human DNA: which nucleotides and in what sequence are located in the molecule, as well as the possible information embedded in them.

Therefore, it was too early to stop.

In 1990, it was officially announced the launch of a program to study the nucleotide sequence of all human DNA. The Human Genome has become an international research project in which many countries have participated.

Already in 2003, this work came to an end, but it was completed in 2022.

So, the difficult task was solved. But after reading the entire sequence of nucleotides, it did not bring clarity.

The Human Genome Project has shown that DNA contains about 3 billion 100 million pairs of nucleotides.

And among such a huge number, only 1-2% are nucleotides encoding proteins. But the main part is occupied by non-coding DNA.

There was hope, that after learning the sequences of nucleotides, all the questions would be resolved by themselves, and we would be able to find effective ways to treat genetic diseases, maybe even understand the origin of life.

There was disappointment, having spent so much effort, we found out that there are about 2% of genes, and most of the DNA is non-coding.

Some suggest calling this part of the DNA non-functional, but nature is arranged in such a way that there is nothing superfluous, non-functional in it. What doesn't work disappears, because nature simply gets rid of the unnecessary. This did not happen with the non-coding part of the DNA.

Maybe non-coding DNA has another function?

Let's try to figure it out.

So, non-coding DNA is the part of DNA that does not encode protein sequences.

It is known that non-coding DNA includes such sequences of nucleotides as telomeres – these are the end sections of linear chromosomes, promoters from which RNA synthesis begins, as well as functionally significant sequences of nucleotides and so on.

But there are areas that, it would seem, do not have biological functions. For example, repeating sequences that were built into DNA, viral elements, and others.

There is one interesting feature here. In primitive organisms,

for example, bacteria, coding regions occupy more than 88% of the genome.

This means that almost the entire bacterial genome has functions.

In vertebrates, including humans, the situation is different.

The non-coding part of human DNA is about 98%, that is, the ratio of non-coding regions is much higher than the number of genes encoding proteins.

Different organisms, but their hereditary apparatus unites them.

The non-coding DNA of eukaryotes can vary widely, even between closely related sequences.

Most of the differences are due to a decrease or increase in repetitive DNA, not the number of genes. Therefore, some researchers have suggested that repetitive DNA is junk DNA.

There is no need for such sequences in the simplest organisms, since they are represented by one cell, and it is wasteful for them to have a large genome.

A necessary condition for life is energy.

Every organism, every living thing adapts as best it can, finding different sources of energy: be it its own resources or something else. Energy gives life.

For example, plants use the energy of the sun. During

photosynthesis, complex substances are formed from inorganic substances (carbon dioxide and water) due to visible light.

As a result of photosynthesis, glucose is formed, which then participates in complex biochemical processes with the formation of macroergic molecules.

Microorganisms by the source of nutrition are phototrophs that use the energy of sunlight for biosynthetic reactions and chemotrophs that obtain energy by oxidizing inorganic substances and organic compounds.

It is clear that energy is needed for the vital activity of each individual cell.

How a living eukaryotic cell provides itself with the energy it needs is still unknown to the end.

Of course is important, the role of macroergic and other molecules that can store energy in various reactions.

For example, deoxyribonucleoside triphosphates (ATP, ATP, GTP, CTF) are a source of energy in such an important process as DNA replication. Other molecules also perform similar functions. But this is a small particle for a living cell, for its existence.

Perhaps there are still unknown sources?

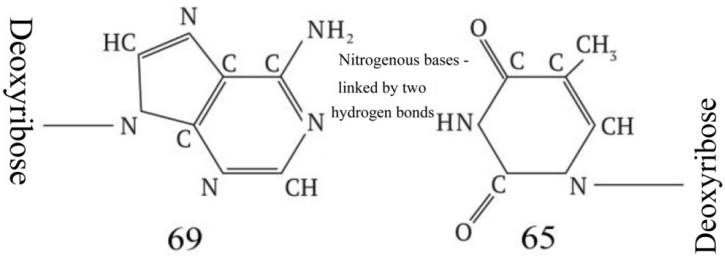
An interesting feature of DNA has recently been discovered. This is "number RM". How is it related to energy?

To do this, consider the scheme of the structure of DNA.

Scheme of arrangement of complementary nitrogenous bases in DNA.

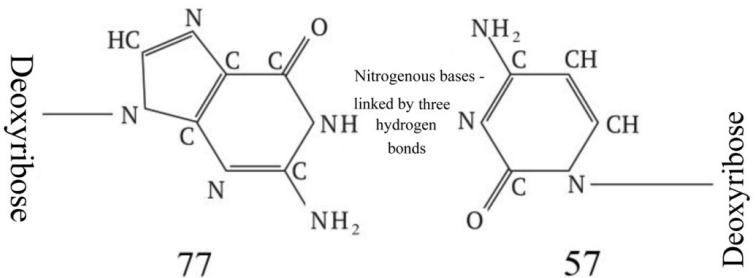
Adenine

Thymine



Guanine

Cytosine



You can see some numbers on the scheme. These numbers

show the sum of the electrons of each nitrogenous base included in the DNA. In adenine, the total number of electrons is 69, in thymine – 65, in the other pair guanine contains 77 electrons, cytosine – 57.

Complementary pairs:

$$\text{Adenine} + \text{Thymine} = 69 + 65 = 134$$

$$\text{Guanine} + \text{Cytosine} = 77 + 57 = 134$$

The number 134 is the number RM.

The number RM is the total number of electrons in complementary pairs of nitrogenous bases in DNA and is equal to 134.

What does this number give?

Based on the data obtained, it can be concluded that equal electrostatic repulsive forces act between complementary pairs of nitrogenous bases in the DNA molecule. Therefore, the complementarity of nitrogenous bases in DNA is also determined by the total number of electrons in the planes – the number RM.

Now back to the “junk” DNA.

It is known that in the non-coding part of the molecule, so called CpG islands are found, as well as complementary pairs of nitrogenous bases: C -G.

CpG islands are regions of DNA where the cytosine nucleotide follows the guanine nucleotide in a linear sequence. CpG islands are often located near structural genes that contain regulatory sequences characteristic of promoters. CpG islands are present in these regions in approximately 60% of genes.

So we came to the main point. What is the unknown function of “junk” DNA?

This function is the formation of energy, which is released in the form of heat during the unwinding of DNA in the process of demethylation.

But first, let's recall what DNA methylation is.

DNA methylation is the addition of a methyl group ($-\text{CH}_3$) to cytosine from the S-adenosylmethionine acceptor and is catalyzed by an enzyme.

In this case, a stronger twisting of DNA occurs as a result of an increase in the electrostatic repulsive forces between neighboring complementary pairs of nitrogenous bases.

Methylated cytosine in subsequent reactions is oxidized by other enzymes and passes back into cytosine:

Cytosine \rightarrow 5-methylcytosine \rightarrow 5-hydroxymethylcytosine \rightarrow 5-formylcytosine \rightarrow 5-carboxycytosine \rightarrow Cytosine

An important merit in the study of the stages of demethylation belongs to a group of researchers led by Professor Yi

Zhang. They discovered intermediate nitrogenous bases of demethylation.

At the initial stages, the DNA is uniformly twisted along its entire length or only a section of it. This is due to an increase in the number of electrons, which leads to stronger twisting and tension in chemical bonds.

During the transition to “pure” cytosine, the DNA is unwound along the entire length or again only its portion depends on what is demethylated.

Then energy is generated in the form of heat, which is necessary for further biochemical processes and such complex as DNA replication.

Therefore, this once again confirms that in nature there is nothing superfluous, “non-functional”.

When DNA is demethylated along its entire length, it is this part of it that plays the leading role.

The more pairs of G—C in non-coding DNA the part, the faster the DNA will unwind.

It turns out that cytosine methylation is an activator of processes, and the main epigenetic changes in DNA are nothing

more than the stages of demethylation.

Thus, DNA is not only a carrier of hereditary information, but performs another function – energy.

Therefore, DNA can rightfully be considered the main molecule of life.

Sources

Кнорре Д.Г., Мызина С.Д. Биологическая химия. – 3. – Москва: Высшая школа, 2000. – 479 с.

Альбертс Б., Брей Д., Льюис Дж. и др. Молекулярная биология клетки в 3-х томах, М.: Мир.

Tet proteins can convert 5-methylcytosine to 5-formylcytosine and 5-carboxylcytosine. Ito S, Shen L, Dai Q, Wu SC, Collins LB, Swenberg JA, He C, Zhang Y. Science. 2011 Sep 2; 333(6047):1300-3. doi: 10.1126/ science.1210597. Epub 2011 Jul 21.

Черкес Ф. К., Богоявленская Л. Б., Бельская Н. А. Микробиология / Под редакцией Ф.К. Черкес. Москва: Медицина, 1987.

Байгужина Закия. ДНК раскрывает свою тайну. Издатель-

ские решения, 2019. ISBN 978-5-0050-8006-6

Wikipedia. Non-coding DNA.

Википедия. Правила Чаргаффа.

Википедия. Чаргафф, Эрвин.

Википедия. Комплементарность (биология).

Википедия. Крик, Фрэнсис.

Википедия. Уотсон, Джеймс.

Википедия. Франклин, Розалинд.

Википедия. Уилкинс, Морис.

Википедия. Дезоксирибонуклеиновая кислота.

Википедия. S-Аденозилметионин.

Википедия. ДНК-метилтрансфераза.

Википедия. Метилирование ДНК.

Википедия. Мусорная ДНК.

Википедия. 5-Гидроксиметилцитозин.

Wikipedia. 5-Hydroxymethylcytosine.

Википедия. Макроэргические соединения.

Wikipedia. Yi Zhang (biochemist).

Википедия. Проект «Геном человека»