12

New Conceptions about Structure Formation of Biopolymers

Shabalkin I.P. and Shabalkin P.I.
Cancer Research Center of RAMS,
Laboratory of Molecular Biological Investigation Methods,
Russia

1. Introduction

The primary structure of protein (L.Pauling) and DNA (J.Watson and F.Crick) was elucidated more than 50 years ago. According to Pauling's model the backbone of the polypeptide chain consists of monomers, each of which includes amino and carboxylic group residues. In Watson-Crick model (Watson a. Crick, 1953) each DNA chain backbone structure consists of monomers composed from saccharide - deoxyribose and phosphoric acid residue - phosphatic group (PO_4). A common feature of these models is that protein and nucleic acid monomers should follow strictly one after another in the same position set by model in the polymer chain backbones. It is one of the essential drawbacks of both models. In particular, processes involving transpositions of repeated units in the polymer chain backbone are not considered in the given models though it is known that transposition (rearrangement) is a typical phenomenon for the majority of polymeric compounds.

So, if we designate iminogroup (-NH-) in the peptide bond (CO - NH) of the protein as "I", and double bond C=O as "D" then dimers having 4 different types of transpositions in the primary structure of the protein chain backbone are possible: [(I-D) + (D-I)], [(I-D) + (I-D)], [(D-I) + (D-I)], [(D-I) + (I-D)]. Accordingly, it is possible to conclude that during polymerization of such biopolymers as DNA, RNA and proteins transpositions should exist in their backbone, i.e. given process is a universal phenomenon. And monomer units transpositions should meet the requirement of optimum compactization of molecular structure in the limited space.

Let's consider as an example what properties DNA molecule should possess to correspond to the compactization principle existing in the nature. It is known, that the total length of DNA macromolecule in cell can be as large as 2 metres. In this case DNA in cell nucleus (with average size of 5-7 microns) should be packed so that its length has decreased not less than 10000 times (Zbarskii, 1988). In other words, there should be some means for DNA compactization in nucleus at minimum energy cost either on the compactization or on information signal transfer.

2. Primary DNA structure

One of mechanisms of DNA linear size contraction is a possibility of existence of bend deformation of short segments in DNA chain. However according to Watson-Crick model of

DNA B-form is a rigid rod with the limited macroscopic flexibility. Curling of such a long molecule demands extremely major energy expenditures. By common measure of the macromolecule flexibility, defined in the length of a geometrical segment A («Kuhn's segment»), calculations show that for DNA A=900 - 1000 Å (angstrom). Big length of Kuhn's segment means that monomer rotation is severely hindered in the DNA macromolecule.
Regarding aforesaid we have assumed that in the backbone of each DNA molecule chains [considering that monomer consists of saccharide ("s") and phosphate («p»)] monomers transpositions can occur (Polymer Encyclopedia, 1977), i.e. dimers of different types can be present:

1. (p-s) + (s-p);
2. (p-s) + (p-s);
3. (s-p) + (s-p);
4. (s-p) + (p-s).

Different interaction modes between monomers in the backbone of DNA polymer chains allow us to mark out dimers with different bonding strength between monomers. It means that in DNA:

1. there are dimers with phosphodiesther bond P-O-C, [(s-p) + (s-p)]; [(p-s) + (p-s)];
2. there are dimers with phosphatic bonds P-O-P, [(s-p) + (p-s)];
3. there are sections with glycosidic bonds C-O-C, [(p-s) + (s-p)].

As phosphodiesther bond P-O-S includes units of both P-O and C-O bonds then differences in the bond characteristics between different heteroatoms are reduced in our case to an assessment of properties of P-O and C-O bonds (table №1) actually.

Ionic part in bonding (%)		Bond energy (kJ/mol)		Effectiveness of hydrolytic cleavage (%)	
P-O	C-O	P-O	C-O	P-O	C-O
39	22	342	332	10	90

Table 1. P-O and C-O bonds characteristics according to the data published in literature (Allcook, 1967; Ingold, 1973).

From table №1 follows that C-O bond is weaker than P-O one.
Presence of dimers with different extent of bonding strength between monomers in the DNA chain promotes augmentation of molecular flexibility. It dilates DNA molecule compactization possibilities in cell nucleus as short segments of the chain can be packed in the limited space in the most dense way. However there is an open question whether DNA primary structure formation taking into account different types of dimers in the course of chemical evolution occurred by chance or due to some law.
On the basis of statements that «a chance is the form of unknown law», and that harmony of the world is reduced to the harmony of numbers (Shevelev, 1990) we have assumed that polymerization of DNA chain in nature goes according to the mathematical law known as a Fibonacci numerical series. Fibonacci numbers are units of a numerical recursive sequence 1; 1; 2; 3; 5; 8; 13; 21... (Fibonacci series) in which each succedent, since the third, is equal to the sum of two previous (Renji, 1980). Considering possibility of existence of inverted monomers let's examine process of formation of primary structure of single-stranded DNA, assuming that the first term of the series in the numerical sequence (we will note it as $1^{а}$) is a monomer in which phosphate is on the first place and saccharide is on the second place: (p-s). Then the second term of Fibonacci series ($1^{в}$) is an inverted monomer: (s-p).

Considering this condition, each term of Fibonacci number series consisting of certain number of segments of DNA chain accordingly, looks like the following:

$1^{а}$ = (p-s);

$1^{в}$ = (s-p);

$2=1^{в} + 1^{а}$ = [(s-p) + (p-s)];

$3=2+1^{в}$ = [(s-p) + (p-s) + (s-p)];

5=3+2 = [(s-p) + (p-s) + (s-p) + (s-p) + (p-s)] etc.

As a result of consecutive addition of each succedent of Fibonacci number sequence to previous ($1^{а}+1^{в}$+2+3+5+8 +...) we have a segment of DNA molecule primary structure:

(p-s) + (s-p) + [(s-p) + (p-s)] + [(s-p) + (p-s) + (s-p)] + [(s-p) + (p-s) + (s-p) + (s-p) + (p-s)] + [(s-p) + (p-s) + (s-p) + (s-p) + (p-s) + (s-p) + (p-s) + (s-p)] + [(s-p) +... etc.

Having observed principles of segment's primary structure organization of one strand (we will name it "lagging" for convenience) of DNA molecule, it is necessary to discuss structural features of second strand ("leading"). For a "leading" strand of DNA the first term of Fibonacci series ($1^{а}$) is (s-p), and second ($1^{в}$) - (p-s). Accordingly:

$1^{а}$ = (s-p); $1^{в}$ = (p-s);

$2=1^{в}+1^{а}$ = [(p-s) + (s-p)];

$3=2+1^{в}$ = (p-s) + (s-p) + (p-s)];

5=3+2 = [(p-s) + (s-p) + (p-s) + (p-s) + (s-p)] etc.

As a result we have a segment of primary structure of "leading" strand of DNA molecule consisting of 21 monomers:

(s-p) + (p-s) + [(p-s) + (s-p)] + [(p-s) + (s-p) + (p-s)] + [(p-s) + (s-p) + (p-s) + (p-s) + (s-p)] + [(p-s) + (s-p) + (p-s) + (p-s) + (s-p) + (p-s) + (s-p) + (p-s)] + [(p-s) +...

Thus, a special feature of DNA structural organization model that we offer is possibility of existence of monomers transpositions in the molecule backbone. And as a result of transpositions in DNA there are dimers with different values of bend angles in three-dimensional space.

According to literary data in dimer [(p-s) + (s-p)] angle between monomers equals 60^{o} (Finean, 1967), in dimer [(s-p) + (p-s)] bend angle is 90^{o} (Wiser a. Kleiton, 1965), in dimers [(s-p) + (s-p)], [(p-s) + (p-s)] bend deformation correspond to an angle of 120^{o} (Smith et al., 1976). Different angles in dimers promote selective arrangement of side groups (nitrogen bases) in primary structure of a biopolymer.

Aforesaid process is based on the principle of maximum compactization of molecule in limited space that is allocation of side groups in the interior space of dimer depends on their molecular mass. Considering that the principle of maximum structure compactization acts at all levels of polymeric compound organizations, we admit that nitrogen bases guanine and adenine should be placed where the dimers having an angle of 120^{o} are formed as they have the greatest size among other nitrogen bases. Then cytosine should be linked with dimers having an angle of 60^{o} and thymine should be linked with dimers having an angle of 90^{o} as thymine occupies more space than cytosine because of the presence of CH_3-group in this base.

At once another question arises. Is it possible to establish what nitrogen base corresponds to the first monomer in a dimer and what to the second? Positive answer can be obtained if we proceed from the conception that value of bend angle during dimer formation depends on a position occupied by every second monomer in relation to the first. For clearness let's observe a trimer of the strand consisting of monomers №1-3:

1 2 3 1 2
[(p-s) + (s-p) + (s-p)]. According to our hypothesis, in dimer [(p-s) + (s-p)] angular deformation equals 60°, that assumes cytosine addition to monomer №2.

2 3
Dimer [(s-p) + (s-p)] has bend angle of 120°. In this case nitrogen base for monomer №3 should be purine (A or G) for purines as the bulkiest nitrogen bases the easiest way to be placed is to be in space of the dimer having a bend angle 120°.

In case of dimer [(s-p) + (p-s)] where the bend angle equals 90° the second monomer has thymine as a side group. If we proceed our analysis of nitrogen bases allocation in monomers of DNA chain backbone depending on the role of the second monomer in each dimer one should admit that **biopolymer chain structure actually can be established completely**. At the same time we have not yet solved the next problem: whether nitrogen bases should be placed outside or inside each chain?

There are three possible options.

The first option: all nitrogen bases are located inside backbone composed from two chains of DNA. Watson-Crick model of DNA corresponds to this alternative (Watson a. Crick, 1953).

The second option is Pauling-Corey model of DNA. Nitrogen bases are located outside molecule's backbone (Pauling a. Corey, 1953).

The third option is offered in this paper. It is supposed in this variant that part of nitrogen bases lies outside from polymer backbone.

Why are we not satisfied by the first two options and in particular by the first one?

At first, in this variant the hierarchical principle of the DNA macromolecular organization is violated as on high levels of compactization of such giant polymeric compound as DNA complementarity principle is absent because of bases hidden in the lowest level of DNA structural organization have no opportunity to form complementary pairs between the fragments belonging to higher supramolecular levels of DNA structural organization. Secondly, lack of bases outside of backbone of DNA molecule does not allow cellular systems to control processes of growth, development and organism functioning because «signal molecules» are absent on subunits surfaces belonging to various levels of the structural organization of molecule. These "signal molecules" are "coded" nitrogen bases which switch on or off various biochemical processes in the cell as DNA is the carrier of genetical information of organism life.

The second model of DNA does not meet the requirements for DNA structure for two reasons:

1. it does not have complementarity of bases in DNA chains at all that reduces stabilization of DNA molecule;
2. DNA represents the structure composed from three chains.

The third option takes account of advantages and drawbacks of the first two variants and therefore corresponds as it seems to us optimal structure of DNA. In this variant allocation of nitrogen bases in each chain goes in turn. In other words, in a dimer of each chain one nitrogen base is outside concerning other nitrogen base which is a part of this dimer.

Such order of bases distribution in each chain is stipulated by the fact during dimer formation the bend angle of one monomer concerning another does not allow disposing both bases (which are parts of this dimer) in interior space of dimer. Thus in dimers [(s-p) + (p-s)], [(p-s) + (s-p)] saccharide of one monomer can be in other position concerning saccharide of adjacent monomer like alteration of saccharide position during pre-mRNA capping (Patrushev, 2000).

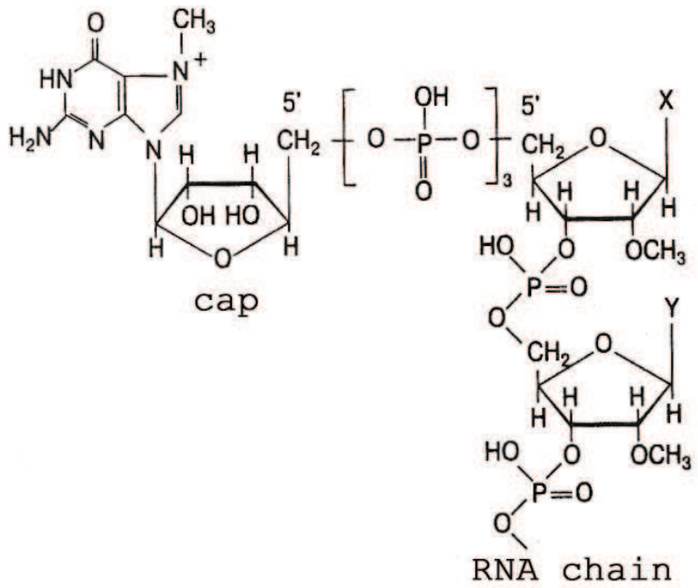


Fig. 1. Cap mRNA. (Patrushev, 2000).

On fig. 2 the fragment of DNA molecule including 2 chains (left and right) is presented. Each chain is composed of 4 monomers.

The backbone of left chain includes monomers:

1 2 3 4 1 2 3 4

(s-p) + (p-s) + (p-s) + (s-p); backbone of right is (p-s) + (s-p) + (s-p) + (p-s).

We consider the left chain as "leading" because it starts with the most ancient nucleotide - deoxyadenylic acids (Shabalkin et al. 2003). The right chain called "lagging" is biased on one nucleotide concerning the left chain. It allows "lagging" chain to form the first complementary pair of DNA molecule: T+A. That process became possible because it has already been determined in the first dimer of "leading" chain as we have shown what nitrogen base should be the second monomer of dimer [(s-p) + (p-s)].

It is necessary to note, that nitrogen base of the first monomer of "leading" chain - adenine (A) - should be outside the chain for it has a function of the first signal molecule which starts DNA structure formation. Pattern of nitrogen bases located partially outside the backbone of chains allows stabilization of fragments of supramolecular structures at various levels of DNA molecular organization by means of complementary pairs formation. All aforesaid means that the model of DNA structural organization introduced in this paper better corresponds the role that DNA plays in the life of an organism than the first two models mentioned above.

So, what is the advantage of our model in comparison with already existing models of biopolymers?

At first, in existing models the processes of monomers transposition in polymer chain backbone haven't been taken into account in spite of the fact that monomers' rearrangements allow to have mini-segments in a chain with different extent of bonding strength between monomers. Secondly, difference in bonding between monomers specifies the existence of relatively weakly bonded segments promoting augmentation of chain flexibility that dilates possibilities of compactization of molecule in space and of identification of sites of preferable location and coordination binding of ligands. Thereby

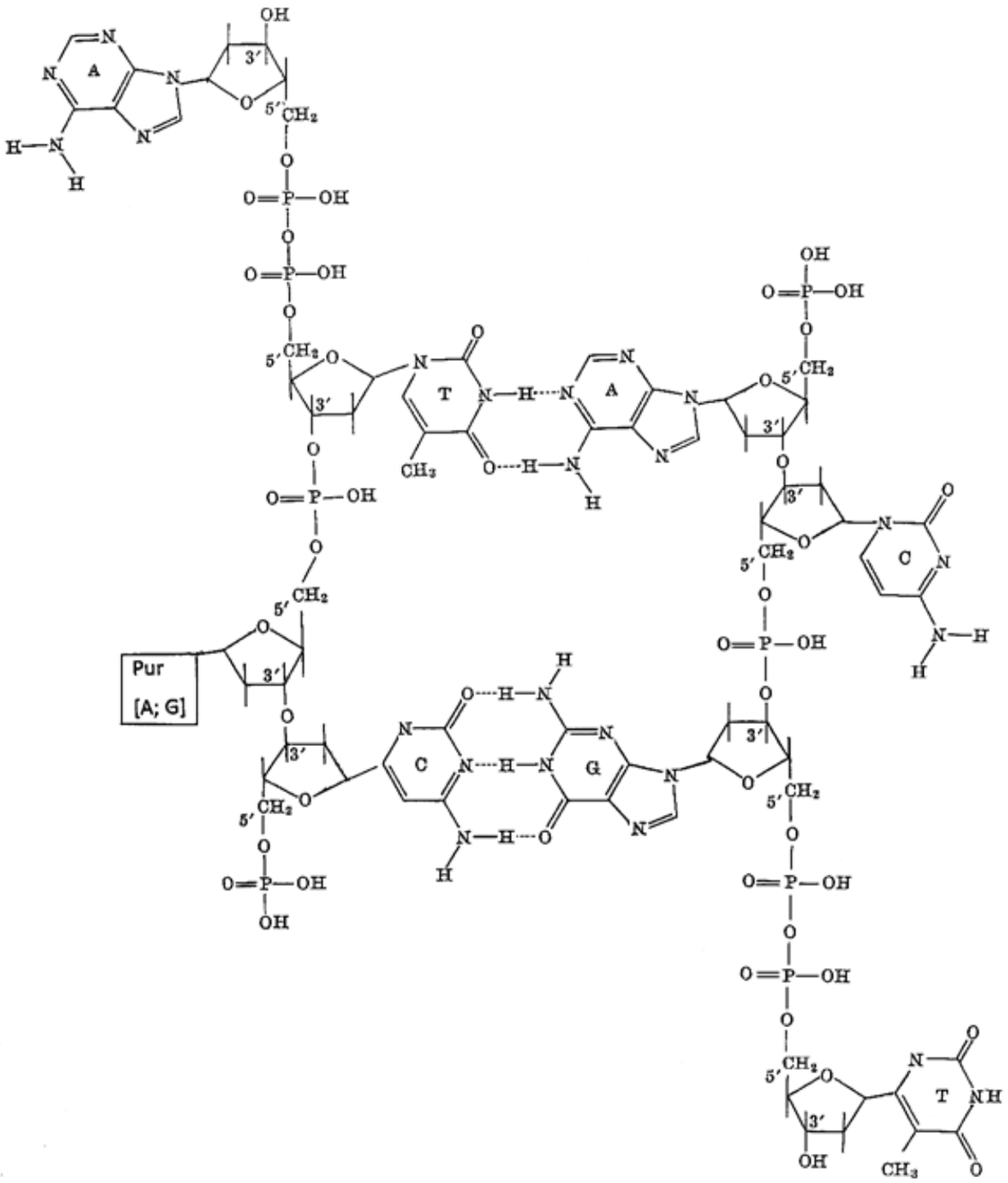


Fig. 2. A fragment of DNA double helix where the part of nitrogen bases of each DNA chain lies outside polymeric backbone.

transpositions of monomers in polymer chain suppose creation of the brand new molecular biosystems meeting the requirements of maximum compactization of molecule in limited space and of augmentation of biopolymer structure informational capacity owing to existence of different variants of monomers' compactization. And these processes are carried out not in a random way but obey to mathematical laws. In the third, proceeding from the assumption that polymerization of biopolymer chain in nature goes according to the

mathematical law known as Fibonacci numerical series we have found **the order** of formation of the backbone of polymeric chain primary structure, that is possibility of synthesis of molecular systems with **predicted** disposition of separate fragments of chain in space is established. Thus, if we take into account that transcription is a process of synthesis of informational RNA (mRNA) which carries the information containing on the dubbed section of DNA, and mRNA is used as a template in the course of translation defining sequence of amino acids in the growing protein polymer chain, then actually backbones of mRNA chains as well as protein molecules repeat the order and method of alternation of monomers described in the backbone of DNA chain.

3. Supramolecular DNA structure

During the study of the primary DNA structure, a question arose about the size of a minimum fragment of single DNA strand that can be a moiety participating in the formation of a supramolecular structure of the molecule. To this end, we analyzed division of a linear segment into two parts according to the golden proportion rule. The golden section principle is based on the fundamental property: the ratio of the greater part to the total segment is equal to the ratio of the smaller part to the greater part (Renji, 1980). In numerical terms, the equality of these two ratios (golden proportion) is expressed by an irrational number ≈0.618…, i.e. m/M=M/T (where m and M are the smaller and greater parts and T is the total). Since the backbone of the primary structure of DNA molecule is a linear structure consisting of monomer moieties of the same length, we can select a mini-fragment that is the first building block of DNA molecule. Imagine that we divide a singlestrand DNA fragment consisting of 144 monomers. The given segment (so called «the nucleosome core») – a unit of supramolecular DNA structure, which virtually does not duffer from the data of other authors (Chentsov, 2004; Zbarskii, 1988), who consider that the nucleosome core contains 140-147 monomers. let us assume that the first fragment of the DNA chain primary structure (144 monomers long, according to the new model of DNA structure (Shabalkin I., Shabalkin P., 2006)) looks as follows:

1 2 3 4 5 6 7 8 9 10
(P–S)+(S–P)+[(S–P)+(P–S)]+[(S–P)+(P–S)+(S–P)]+[(S–P)+(P–S)+(S–P)+
11 12 13 14 15 16 17 18 19 20
(S–P)+(P–S)]+[(S–P)+(P–S)+(S–P)+(S–P)+(P–S)+(S–P)+(P–S)+(S–P)]+
21 22 23 24 25 26 27 28 29 30
[(S–P)+(P–S)+(S–P)+(S–P)+(P–S)+(S–P)+(P–S)+(S–P)+(S–P)+(P–S)+
31 32 33 34 35 36 37 38 39 40
(S–P)+(S–P)+(P–S)]+[(S–P)+(P–S)+(S–P)+(S–P)+(P–S)+(S–P)+(P–S)+
41 42 43 44 45 46 47 48 49 50
(S–P)+(S–P)+(P–S)+(S–P)+(S–P)+(P–S)+(S–P)+(P–S)+(S–P)+(S–P)+
51 52 53 54 55 56 57 58 59 60
(P–S)+(S–P)+(P–S)+(S–P)]+[(S–P)+(P–S)+(S–P)+(S–P)+(P–S)+(S–P)+
61 62 63 64 65 66 67 68 69 70
(P–S)+(S–P)+(S–P)+(P–S)+(S–P)+(S–P)+(P–S)+(S–P)+(P–S)+(S–P)+
71 72 73 74 75 76 77 78 79 80
(S–P)+(P–S)+(S–P)+(P–S)+(S–P)+(S–P)+(P–S)+(S–P)+(S–P)+(P–S)+
81 82 83 84 85 86 87 88 89 90
(S–P)+(P–S)+(S–P)+(S–P)+(P–S)+(S–P)+(S–P)+(P–S)]+[(S–P)+(P–S)+
91 92 93 94 95 96 97 98 99 100
(S–P)+(S–P)+(P–S)+(S–P)+(P–S)+(S–P)+(S–P)+(P–S)+(S–P)+(S–P)+

101 102 103 104 105 106 107 108 109 110
(P–S)+(S–P)+(P–S)+(S–P)+(S–P)+(P–S)+(S–P)+(P–S)+(S–P)+(S–P)+
111 112 113 114 115 116 117 118 119 120
(P–S)+(S–P)+(S–P)+(P–S)+(S–P)+(P–S)+(S–P)+(S–P)+(P–S)+(S–P)+
121 122 123 124 125 126 127 128 129 130
(S–P)+(P–S)+(S–P)+(P–S)+(S–P)+(S–P)+(P–S)+(S–P)+(P–S)+(S–P)+
131 132 133 134 135 136 137 138 139 140
(S–P)+(P–S)+(S–P)+(S–P)+(P–S)+(S–P)+(P–S)+(S–P)+(S–P)+(P–S)+
141 142 143 144
(S–P)+(P–S)+(S–P)]+[(S–P)+…

The process of division of a DNA chain fragment 144 monomers long can be described by stages of this fragment division on condition that each of the two different (by length) parts of the initial fragment (let us call them segments) are fragments (shorter than the initial one!) also capable of dividing in accordance with the golden ratio rule until the equality of two proportions remains valid (Fig. 3). Hence, at stage I the fragment (total) divides in point 0 into two segments, one of them consisting of 89 monomers (longer segment) and the other has 55 monomers (shorter one). According to the golden ratio, we have two equal proportions: 55/89=89/144 or 55/89≈0.617...; 89/144≈0.618... The two proportions remain equal (0.62) after this division of the initial fragment into two parts. This equality (0.62) is retained at other stages of the initial fragment division:

34/55=55/89 or 34/55≈0.618; 55/89≈0.618;
21/34=34/55 or 21/34≈0.618; 34/55≈0.618;
13/21=21/34 or 13/21≈0.619; 21/34≈0/618;
8/13=13/21 or 8/13≈0.615; 13/21≈0.619.

The process of the initial fragment division is over at stage VI (Fig. 3) by the formation of one minifragment consisting of 13 monomers. It consists of two mini-segments of different length: large (8 monomers) and small (5 monomers): 5/8=8/13 or 5/8≈0.625; 8/13≈0.615. The next stages of fragmentation of the minifragments consisting of 8 or 5 monomers each do not correspond to the golden ratio rule, as the equality of the two proportions is violated: 3/5≠5/8 or 0.6≠0.625; 2/3≠3/5 or 0.67≠0.6. Hence, the results of analysis indicate that the last mini-fragment, which determines the number of monomers, components of the unit participating in the nucleosome core formation; the unit is to have 5 or 8 monomers.

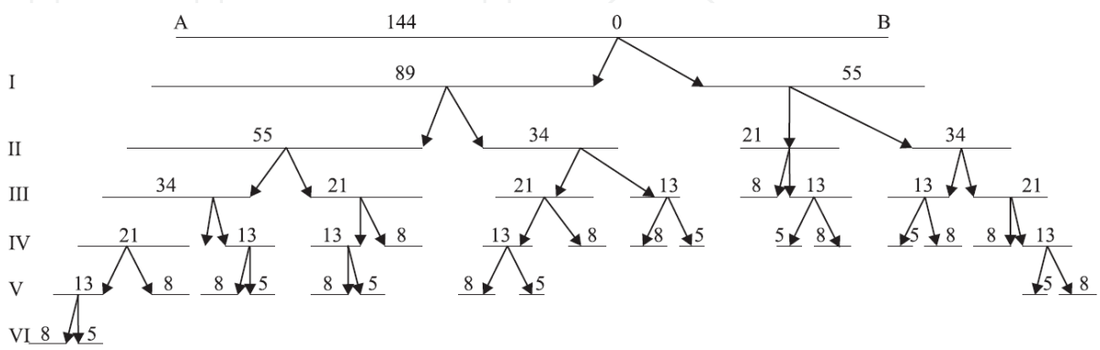


Fig. 3. Scheme of division of one DNA strand fragment (144 monomers long) into two segments according to the "golden ratio" rule. I-VI: stages of the initial fragment division to the minimum size, meeting the golden ratio requirement. Arabic figures show the number of monomers.

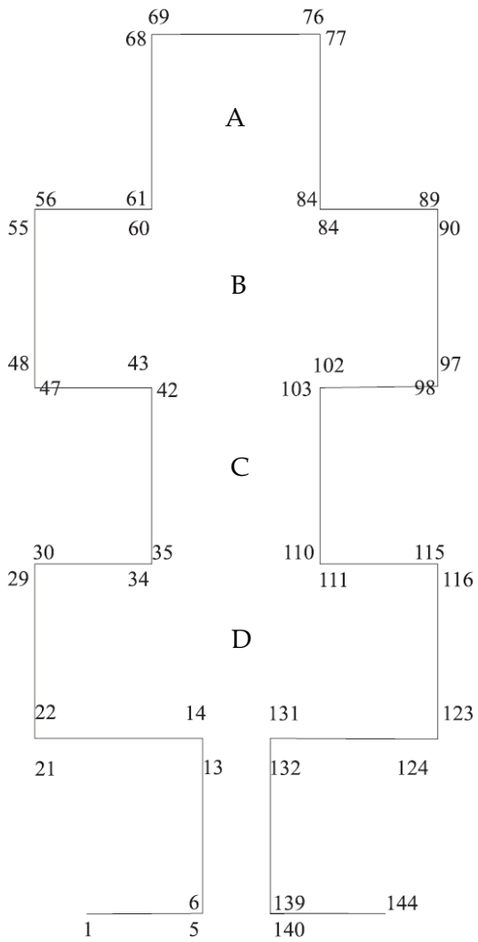


Fig. 4. Scheme of DNA strand nucleosomal loop formation in a twodimensional space. Arabic figures: orderly numbers of monomers.

The structure assembled by stages (in opposite order; Fig. 3) from these mini-segments is geometrically similar to a plus (Fig. 4). In this case the chain curvature is realized at the interface of two segments in points having dimers [(S–P)+(P–S)].

The figure of a cross (fig. 4) represents itself an example of creation of braiding structures during the nucleosome crust forming. The segments №1-5 and №140-144 are the basis of a such loop. Besides the ordering of such a loop is put into effect in 6 stages. During stage I, a small loop is formed consisting of two fragments: one of them includes 8 monomers and the other contains 5 monomers. During stage II, a loop consisting of 73 monomers is formed. It includes 13 monomers forming a loop during stage I of nucleosome assembly and 60 additional monomers. During stage III, 63 monomers are added to the preexisting 73 monomers constituting the macro-loop structure. The assembly process during which new monomers are added to preexisting complex of monomers is completed at stage IV, when the last 8 monomers are added to 136 preexisting monomers. Stages V and VI consist in the formation of the two-dimentional macronucleosome into three-dimentional structure-nucleosome.

Why the Nature has chosen the loop for compactization of the DNA strand? First, appearance of lateral segments (loops), distant from the main chain, leads to shortening of

the linear length of DNA chain. Second, it promotes cooperation of the loops (Polymer Encyclopedia, 1977) due to local orientation ordering of the segments which became closer to each other in space during condensation of the main chain (Khokholov, 1988). The segments brought closer to each other stabilize the chain carcass at the expense of the formation of extra bonds. Third, transition of a chain site from linear to annular form (loop) is more advantageous energetically and for compactization of DNA structure. This closed circular structure can fold into a more complex structure to three-dimensional one, *e.g.* by dividing the loop in the horizontal plane into 4 blocks (a-d) followed by bending of each block by 90° relative to the other one (fig.4). Generally, the three-dimensional structure of the nucleosome can be presented by a hollow rectangular structure, which is formed by certain kinds of histones, which take part into the process of blocks joining.

In this model of macronucleosome loop we only demonstrated the role of [(S–P)+(P–S)] dimers in compaction of the loop, but did not take into account the peculiarities of compaction of the structure including other types of dimers [(S–P)+(S–P)] and [(P–S)+(S–P)]. The participation of the latter should considerably modify the structure of nucleosome loop, because of different strength of bonds between the monomers in different types of dimers. Taking into account this fact and different angles between the monomers in these three types of dimers (60°, 90°, 120°) and bearing in mind that the process of structure compaction obeys the principle of least surface at the same volume we conclude that DNA should include geometrical forms that are presented by regular polygons. Moreover, DNA is a liquid crystal and combines the properties of a fluid and a solid, therefore it should include the elements of regular 3D crystalline lattice consisting of regular tetrahedrons and octahedrons. We believe that these are the geometrical figures that participate in loop formation. The first mini-segment of the loop including four monomers consists of regular tetrahedron and octahedron, the moieties of regular crystalline lattice (Fig. 5), because crystalline lattice cannot be constricted with only one type of geometrical figure (Varga, 1978). For illustration let us trace the formation of the first least structural unit, participating in the construction of the nucleosome core, in mini-segment consisting of 5 first monomers (fig. 5):

1 2 3 4 5
(P–S)+(S–P)+(S–P)+(P–S)+(S–P)+…

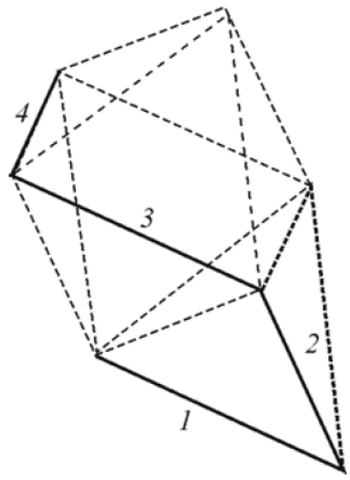


Fig. 5. Minimum crystalline lattice unit consisting of regular tetrahedron and octahedron. 1-4: fragment chain including monomers:

1 2 3 4
[(P–S)+(S–P)+(S–P)+(P–S)]

The order of the monomers location in the analyzed segment indicates the formation of dimers of all three possible types. In the first dimer [(P–S)+(S–P)] monomers *1* and *2* form an angle of 60°. The second dimer [(S–P)+(P–S)] is a result of monomers *3* and *4* binding at an angle of 90°. The third dimer [(S–P)+(S–P)] forms as a result of monomers *2* and *3* binding at an angle of 120°. It is involved as a binding component in the formation of the first and second dimers into one structural unit.

In fact, the mechanism of the nucleosome core fragment assembly is a process repeating (in a certain sequence) all 3 types of dimers, which suggests the formation of a compact structure, that is, the short fragments of the chain with different shape of bending deformation can be packed most compactly. The minisegment of DNA chain carcass including 5 monomers little resembles the unit of a correct crystal lattice constituted (as we have mentioned above) from correct tetrahedron and octahedron. It is more likely a fragment of a broken line assembled from similar components bending at different angles. However, this structure is a unit of a correct crystal lattice, as the monomers constituting it form dimers with angles corresponding to the angles of polygonal geometrical figures of this unit. The fact that it has "vacant" spaces indicates that initially it was similar to a common broken line, but later (in the course of biochemical evolution) all these spaces were presumably filled, and the structural unit of the crystal lattice was fully realized. The "vacant" spaces are most likely the zones in which the DNA repeats are located, serving for improving the stability of the biological system, as the more repeats a system contains, the more reliable it is.

So we can say, that a nucleosome – is a three-dimentional hollow structure. Its segments consist of 5 or 8 monomers and besides they have structures similar to a regular tetrahedron or octahedron. The last is a unit of a regular crystalline array. The existence of such structures is explained by the fact that a biopolymer is in need of them not only for realizing of functions of a storage of information, but for transferring of information too. This structure corresponds to chain fragments where acoustic signals propagate without energy loss.

The types of transformations described by us for the formation of nucleosomic moiety of one DNA chain are completely valid for the other DNA chain with consideration for rearrangement of monomers in its primary structure. Bearing in mind that DNA molecule consists of two strands starting from either (S–P), or inverted (P–S) monomer, we assume that two types of nucleosomic moieties correspond them in different strands. These two moieties are the monomers similar to monomers of the primary DNA structure and participate in the formation of the structure of each of two supramolecular DNA strands. However, it remains unknown where nucleosomes are arranged along the DNA chain according to certain regularity or this is a random process. If the primary structure of biopolymers obeys certain mathematical regularities, the assembly of supramolecular structural moieties corresponding to different levels of biopolymer organization should comply the regularities characteristic of its primary structure. Let us assume that we assemble individual nucleosomes into a chain corresponding to a higher level of structural organization of DNA. To this end, it is reasonable to use the principle of primary structure based on permutation of (P–S) monomers in the chain backbone according to Fibonacci number sequence. Let the monomer corresponding to the first member in the Fibonacci sequence (1^a) be a nucleosome , which begins with a segment (so called "Head") and ends with another segment ("Tail") is defined as a monomer ("H-T"). Then, another nucleosome will become similar to a monomer of the second rank of Fibonuchi (1^b), and during the process of segments' rearrangement will correspond to a monomer "Tail-Head" ("T-H"). So

using the rearrangement we can devide nucleosomes into 2 types, which help to organize one chain from of a sum of Fibonacci numbers: $1^a+1^b+2+3+5+\ldots$*etc.*
This chain can be presented as a "primary" structure and transformed into a 3D structure according to the golden proportion principle. Since supramolecular structure of DNA molecule is organized by the hierarchical principle, the formation of multicomplexes of nucleosomes should basically repeat the stages of assembly of a single nucleosome.

4. Features of DNA synthesis

In is interesting to consider the mechanism of functioning of DNA polymerases, because these processes include break and transfer of DNA chain to another active center. It is known that the chain can be broken due to interaction of the growing active center with introduced second monomer increasing chain rigidity. Chain transfer is a transfer of active center of the molecule to another molecule initiating the growth of a new chain (Polymer Encyclopedia. 1977) These processes directly depends on [(S–P)+(P–S)] dimers. The point is that enzymes catalyzing the growth of polynucleotide chain (*e.g*. DNA polymerase) do not work in this case, because they normally attach the next monomer only to the 3′-hydroxyl group of the sugar in the end monomer, which should not be phosphorylated at the stage of chain elongation. When DNA polymerase approach the dimer [(S–P)+(P–S)], the chain is broken. In order to continue the process of chain elongation, the enzyme should find the transition point. Let us discuss these processes in more detail on the basis of matrix (template) backbone monomer synthesis of the "leading" and "lagging" chains also presented by their monomers (Fig. 6). Eukaryotes have several types of DNA polymerases (Patrushev, 2000); let the first type of DNA polymerase start working and transcribe the "leading" chain, where the first monomer is (S-P). After synthesis of the first daughter domain (P–S) complimentary to the first monomer in the "leading" chain matrix, transcription of this chain is terminated, because the second monomer in the chain starts from the phosphate group. The synthesis of the daughter DNA chain is paused (!) for a while. Several processes take place in the cell during this pause. Break hydrogen bond between the nitrogenous bases of the second monomer of the "leading" chain and the first monomer of the "lagging" chain leads to outside displacement of the sugar and nitrogenous base (adenine) of the first monomer in the "lagging" chain. This phenomenon was observed by investigators using a magnetic forceps for untwisting of the B-DNA (Allemand et al., 1998). The first nucleotide of the "lagging" chain in the new position becomes available to other DNA polymerase, which can use single-strand structures starting from (P–S) monomers as the template. After synthesis of the first daughter monomer (S–P) in the "lagging" chain, this DNA polymerase cannot work on the same template, because monomers are unavailable, because they are shield by type I DNA polymerase. When type I DNA polymerase finds a new matrix, in particular the second monomer of the "lagging" chain and moves to this new active center, type II DNA polymerase jumps from the "lagging" chain to the "leading" one and starts DNA synthesis using the second and third monomers of this chain as the template. Generally, during replication the synthesis of the daughter fragment on one template DNA chain is broken and the catalyzing enzyme moves to a new active center, *i.e.* to the second template DNA chain. This is a cyclic process associated with changes of active center. During replication, the "leading" chain is by one nucleotide ahead to the "lagging" chain. Every time the pause occurs between termination and activation of DNA synthesis in new active center, when no DNA is synthesized; hence, DNA synthesis has a successively interrupted nature.

It should be noted that the hypothesis on the interrupted nature of DNA synthesis was put forward by some authorities (Cornberg, 1974; Eigen a. Schster, 1982; Finean, 1967; Shabalkin, 1977), and was even experimentally proven (Shabalkin, 1976). According to Shabalkin's hypothesis (Shabalkin, 1976) synthesis of a DNA daughter strand fragment occurs in a limited region of only one DNA matrix strand. There is no DNA synthesis in complementary region of the second matrix strand at this moment. On completion of the replication in the DNA first matrix strand the DNA synthesis is over. After a pause the replication proceeds in a limited region of the DNA second matrix strand. Thus, we can conclude that the process of biochemical evolution of biopolymers led to the appearance of mechanisms based on the principle of maximum structural compaction in a limited space. This was associated with selective distribution of nitrogenous bases or R-groups of proteins in biopolymer macromolecules to certain locations determined by bending deformations of dimers in the biopolymer backbone.

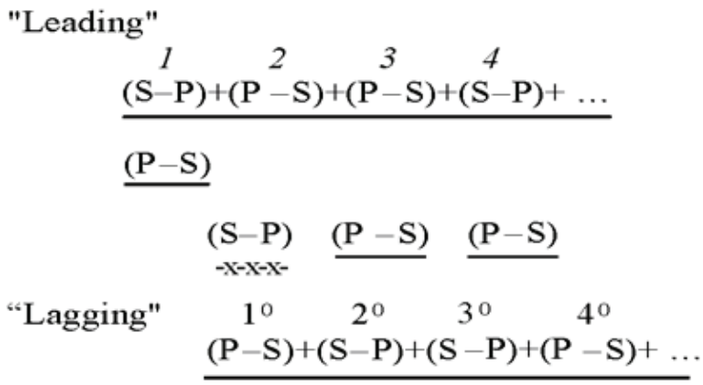


Fig. 6. Scheme of functioning of DNA polymerases involving break and transfer of DNA chain to another active center.

1
(S–P): the first monomer of the “leading” DNA chain;
1º
(P–S): the first monomer of the “lagging” DNA chain.

5. Conclusion

To make the conclusion, we may say: the main feature of biopolymers’ structure is a rearrangement if its monomers. Besides the order of monomers in this chain is presupposed by mathematic regularity, known as numerals of Fibonuchi. As a result of this rearrangement new dimmers appear with new bends in space.

Different bends of dimmers promote a proper arrangement of side groups in the biopolymer’s structure. Besides in a dimer’s chain there is one group is situated on the outside of the other one. So outside groups stabilize structures of biopolymers and have a function of “signal” molecules in biological process.

The next feature of our model is forming of a supramolecular structure of a biopolymer with the help of fragments of the initial structure, which are formed by a mathematic regularity “gold proportion”. So according to this proportion, the initial mini-fragment of this chain includes two mini-segments: a large one containing 8 monomers and a smaller one containing 5 monomers. So the forming structure of the elements of supramolecular

structure should correspond to the "principle of solidness", which is presupposed to take into account economy of space but not volume. The given condition could be fulfilled if the biopolymer's structure have elements of proper forms: tetrahedron and octahedron, formed by monomers of a proper chain.

Together proper tetrahedron and octahedron is a unit of a regular crystalline array, which is the most favorable conformation, where short parts of its chain of different forms can be combined tightly.

The fact that this system consists of structural elements presented by regular geometric figures creates prerequisites for assignment of biology and medicine to exact sciences at the modern level of nanotechnology development. For instance, deciphering of information encoded by biopolymers provides the possibility for the synthesis of drugs strictly identical by their stereo structure to biological targets in cells and for the creation of artificial compounds regulating functional activity of biopolymer.

6. References

Allcook H. R. (1967). Heteroatom ring system and polymers. N-Y., Lon.

Allemand J.F. Bensimon D., Lavery R., and Croqette V. (1998). Proc. Natl. Acad. Sci. Vol. 95, № 24, pp, 14152-14157.

Chentsov Yu. S. (2004). Introduction in cell biology. (in Russian), Moscow.

Cornberg A. , (1974). DNA synthesis. San Francisco.

Eigen M. a. Schuster P. (1982). A principle of natural self-organization. (in Russian), Moscow.

Finean J.B. (1967). Biological ultrastructure. N.-Y., Lon.

Ingold C. (1973). Teoreticheskie of an organic chemistry bottom. (in Russian), Moscow, pp. 979-983.

Khokhlov A. R. (1988). Liquid crystal polymers. (in Russian), Moscow, pp. 32-38.

Patrushev L.I. (2000). Expression of genes. (in Russian), Moscow.

Pauling L., Corey R.B. (1953). Proc. Natl. Acad. Sci. USA. Vol. 39. pp. 84-97.

Polymer encyclopedia. (1977), Vol. 2. (in Russian), Moscow, pp. 101-102, pp. 383-384, pp. 405-406, p. 959, p. 580.

Renji A. (1980) Trilogija about the mathematics. (in Russian), Moscow.

Shabalkin I.P. (1976). Arkh. Anat. Vol. 71., № 9, pp. 29-35.

Shabalkin I.P. (1977). Thilologia. Vol. 19., № 5, pp. 474-477.

Shabalkin I.P., Shabalkin P. I, Jagubov A.S. (2003). The Log of evolutionary biological chemistry and physiology. Vol. 49, №5, pp. 488-495.

Shabalkin I.P. a. Shabalkin P.I. (2006). Akt. Probl. Sovr. Nauki. (in Russian), Moscow, №3, pp. 269-271.

Shevelev I.S. (1990). The Golden section. (in Russian), Moscow.

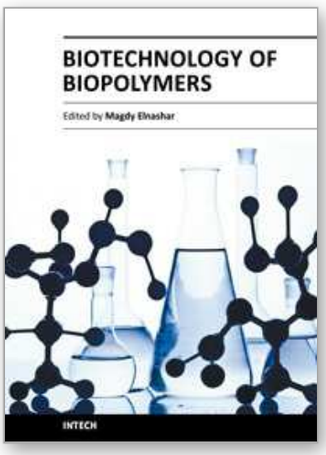
Smith I., Smith M.J., Dore C.F. (1976). "Model for macromolecules: nucleic acids and proteins". In "Chromatographic and Electrophoretic Techniques". Vol. 2., chapter 16. pp. 409-453.

Varga T. (1978). Mathematics. (in Russian), Moscow.

Watson J.D., Crick F.H.C. (1953). Nature. Vol. 171, pp.737-738.

Weser D.V. and Kleiton F.K. (1965). Macromolecule on the basis of phosphorus. In the book "Inorganic polymers". (in Russian), Moscow, pp. 31-83.

Zbarsky I.B. (1988). Organization of a cell nucleus. (in Russian), Moscow.



Biotechnology of Biopolymers

Edited by Prof. Magdy Elnashar

ISBN 978-953-307-179-4
Hard cover, 364 pages
Publisher InTech
Published online 24, June, 2011
Published in print edition June, 2011

The book "Biotechnology of Biopolymers" comprises 17 chapters covering occurrence, synthesis, isolation and production, properties and applications, biodegradation and modification, the relevant analysis methods to reveal the structures and properties of biopolymers and a special section on the theoretical, experimental and mathematical models of biopolymers. This book will hopefully be supportive to many scientists, physicians, pharmaceutics, engineers and other experts in a wide variety of different disciplines, in academia and in industry. It may not only support research and development but may be also suitable for teaching. Publishing of this book was achieved by choosing authors of the individual chapters for their recognized expertise and for their excellent contributions to the various fields of research.

INTECH
open science | open minds

InTech Europe
University Campus STeP Ri
Slavka Krautzeka 83/A
51000 Rijeka, Croatia
Phone: +385 (51) 770 447
Fax: +385 (51) 686 166
www.intechopen.com

InTech China
Unit 405, Office Block, Hotel Equatorial Shanghai
No.65, Yan An Road (West), Shanghai, 200040, China
中国上海市延安西路65号上海国际贵都大饭店办公楼405单元
Phone: +86-21-62489820
Fax: +86-21-62489821

IntechOpen