

# Is DNA a nonlinear dynamical system where solitary conformational waves are possible?

LUDMILA V YAKUSHEVICH

*Institute of Cell Biophysics, Russian Academy of Sciences, Pushchino, Moscow Region, 142290 Russia*

*(Fax, 0967-790509; Email, yakushev@icb.psn.ru)*

DNA is considered as a nonlinear dynamical system in which solitary conformational waves can be excited. The history of the approach, the main results, and arguments in favour and against are presented. Perspectives are discussed pertaining to studies of DNA's nonlinear properties.

## 1. Introduction

In recent years, many investigators dealing with large-amplitude internal motions in DNA have come to the conclusion that the molecule can be considered as a nonlinear dynamical system where solitary conformational waves can be excited. Do these waves really exist in DNA? Or is this only an example of an incorrect "invasion" of physicists into biology (Frank-Kamenetskii 1987b)? The final answer has not yet been obtained although many authors have tried.

Firstly, the question was formulated twenty years ago in the paper of Englander *et al* (1980), which was titled "Nature of the open state in long polynucleotide double helices: possibility of soliton excitations". In the paper the first nonlinear hamiltonian of DNA was presented and this result gave a powerful impulse for investigations of the nonlinear DNA dynamics by physicists-theoreticians. A large group of authors, including Krumhansl and Alexander (1983), Takeno and Homma (1983), Yomosa (1983, 1984), Homma and Takeno (1984), Fedyanin and Yakushevich (1984), Krumhansl *et al* (1985), Fedyanin *et al* (1986), Fedyanin and Lisy (1986), Yakushevich (1987, 1989a, 1991), Zhang (1987), Muto *et al* (1988, 1989, 1990), Prohofsky (1988), van Zandt (1989), Peyrard and Bishop (1989), Gaeta (1990, 1992, 1999), Dauxois (1991), Salerno (1991), Zhou and Zhang (1991), Dauxois *et al* (1992), Bogolubskaya and Bogolubsky (1994), Gonzalez and Martin-Landrove (1994), Hai (1994), Barbi *et al* (1999), Campa and Giansanti (1999) and Homma (1999) made contributions to the development of theoretical

studies of the problem by improving the model hamiltonian, suggesting new models, investigating corresponding nonlinear differential equations and their soliton-like solutions, consideration of statistics of DNA solitons and calculations of corresponding correlation functions. At the same time period several brave attempts to explain different experimental data in the frameworks of the nonlinear conceptions were made in spite of the hot discussion in scientific literature (Frank-Kamenetskii 1987a). Interpretations of experimental data on hydrogen-tritium exchange (Englander *et al* 1980), on resonant microwave absorption (Webb and Booth 1969; Swicord and Davis 1982, 1983; Edwards *et al* 1984) (interpretations were made by Muto *et al* 1988 and Zhang 1989) and on neutron scattering by DNA (Baverstock and Cundal 1989; Yakushevich 1999) were among them. Moreover some of the investigators tried to use the nonlinear approach to explain the dynamical mechanisms of the DNA functioning. The works devoted to dynamical mechanisms of transitions between different DNA forms (Sobel 1984; Khan *et al* 1985; Zhang and Olson 1987), long-range effects (Yakushevich 1989b, 1992; Volkov 1990), regulation of transcription (Polozov and Yakushevich 1988), DNA denaturation (Peyrard and Bishop 1989), protein synthesis (namely, insulin production) (Balanovskii and Beaconsfield 1985), carcinogenesis (Ladik *et al* 1978) were only some of the examples. We should add, however, that most of the measured data admit alternative interpretations. And may be only the work published by Selvin *et al* (1992), where the torsional rigidity of positively and negatively supercoiled DNA was measured, gave a rather reliable evidence

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that the DNA molecule can exhibit nonlinear properties. It was a romantic period of the studies of nonlinear DNA dynamics, described completely in the reviews (Scott 1985; Zhou and Zhang 1991; Yakushevich 1993; Gaeta *et al* 1994) and books (Peyrard 1995; Yakushevich 1998).

What can we say now about the possibility of solitary waves in DNA? Are the results of soliton physics dealing with nonliving systems, applicable to biology, which deals with living systems? And can we state in general that physical principles are as much universal as mathematical ones, which penetrate everywhere without any limits? Or may be there is a boundary beyond which only biology remains?

In this paper we consider a remarkable example of penetration of physical ideas to biology: nonlinear solitary waves, which are well known in physics as interesting phenomena observed in many media and studied in mathematics as particular solutions of the nonlinear differential equations, are considered here in connection with DNA. We describe shortly new arguments in favour of the approach, which are based on the analysis of the internal motions of DNA and on the general principles of mathematical modelling of the motions. We present a general description of the DNA internal dynamics and discuss when and why the dynamics exhibits the nonlinear behaviour. Then we construct mathematical model of the internal DNA mobility, and show that corresponding dynamical equations do admit solitary wave solutions.

## 2. General picture of the internal DNA mobility

From the point of view of a physicist the DNA molecule is nothing but a system consisting of many interacting atoms organized in a special way in space. It was shown by Franklin and Gosling (1953), Watson and Crick (1953), Wilkins *et al* (1953) and Crick and Watson (1954) that: (i) under usual external conditions (temperature, pH, humidity, etc) the molecule has the form of double helix, and (ii) the helix is not a static structure. On the contrary, the DNA molecule is a very flexible molecule. One of the reasons of this is the thermal bath where the DNA molecule is usually immersed. Collisions with the molecules of the solution which surrounds DNA, local interactions with proteins, drugs or with some other ligands also lead to internal mobility. As a result, different structural elements of the DNA molecule such as individual atoms, groups of atoms (bases, sugar rings, phosphates), fragments of the double chain including several base pairs are in constant motion. More or less complete descriptions of internal motions occurred in DNA and their main dynamical characteristics such as characteristic times, amplitudes, energies of activation, were listed in the works of Fritzsche (1982), Keepers and James (1982), McClure (1985), McCommon and Harvey (1987), Yakushevich (1989b,

1993) and Yakushevich and Komarov (1998). Some examples of the internal motions are shown schematically in figure 1. At least two important conclusions can be made from the analysis of these lists:

- (i) First of all we can state that the general picture of the internal DNA mobility is very complex: many types of internal motions with different characteristic times, amplitudes and energies of activation. In practice, however, investigators deal with limited groups of the motions with characteristics close to corresponding parameters of the biological processes considered.
- (ii) The motions can be divided into two main groups: the first one includes small-amplitude internal motions and the other one includes large-amplitude motions. To describe mathematically small-amplitude internal motions, it is enough to use the so-called harmonic (or linear) approximation. But to describe the large-amplitude motions, we need to use anharmonic (or nonlinear) approach because linear approximation becomes incorrect when the amplitudes of the motions are not small.

Two examples of the large-amplitudes internal motions are shown in figure 1. Local unwinding of the double helix is the first example (figure 1e). Some authors name this motion “the formation of open state”. It is widely accepted that this motion plays an important role in DNA functioning. Indeed, the process of DNA-protein recognition includes the formation of open state to have a possibility to “recognize” the sequence of bases. Local unwinding is an important element of binding RNA polymerase with promoter regions at the beginning of transcription. Formation of unwound regions is known also as an important part of the process of DNA melting.

Transitions between different conformation states shown in figure 1f, are the second example. These motions also play an important role in DNA functioning. Indeed, it is well known that the changing of the conformation of a fragment of DNA leads to the changing of the coefficient of the binding of this fragment with protein molecules and ligands. And this in turn can lead to the crucial changing in the cell biological activity.

## 3. The main approximate models of the DNA structure and dynamics

To describe mathematically the internal DNA mobility different approximate models are used. In table 1 some of the models, arranged in the order of increasing their complexity, are presented.

In the first line of the table 1 the simplest models of DNA, namely, the model of elastic thread and its discrete version, are shown. To describe mathematically the internal dynamics of elastic rod it is enough to write three cou-

pled differential equations: one for longitudinal motions, one for torsional motions and one for transverse motions. To describe the discrete version we need to write  $3N$  equations.

In the second line of the table 1 a little more complex models of the internal DNA dynamics are shown. They take into account that the DNA molecule consists of two polynucleotide chains. The first of the models consists of two elastic threads weakly interacting with one another and being wound around each other to produce the double helix. The discrete version of the model is nearby. The next two models in the line are simplified versions of the previous two models. In these models the helicity of the DNA structure is neglected. To describe mathematically the model consisting of two weakly interacting elastic threads, we need to write six coupled differential equations: two equations for longitudinal motions, two equations for torsional motions and two equations for transverse motions in both threads. Mathematical description of the discrete versions consists of  $6N$  coupled equations.

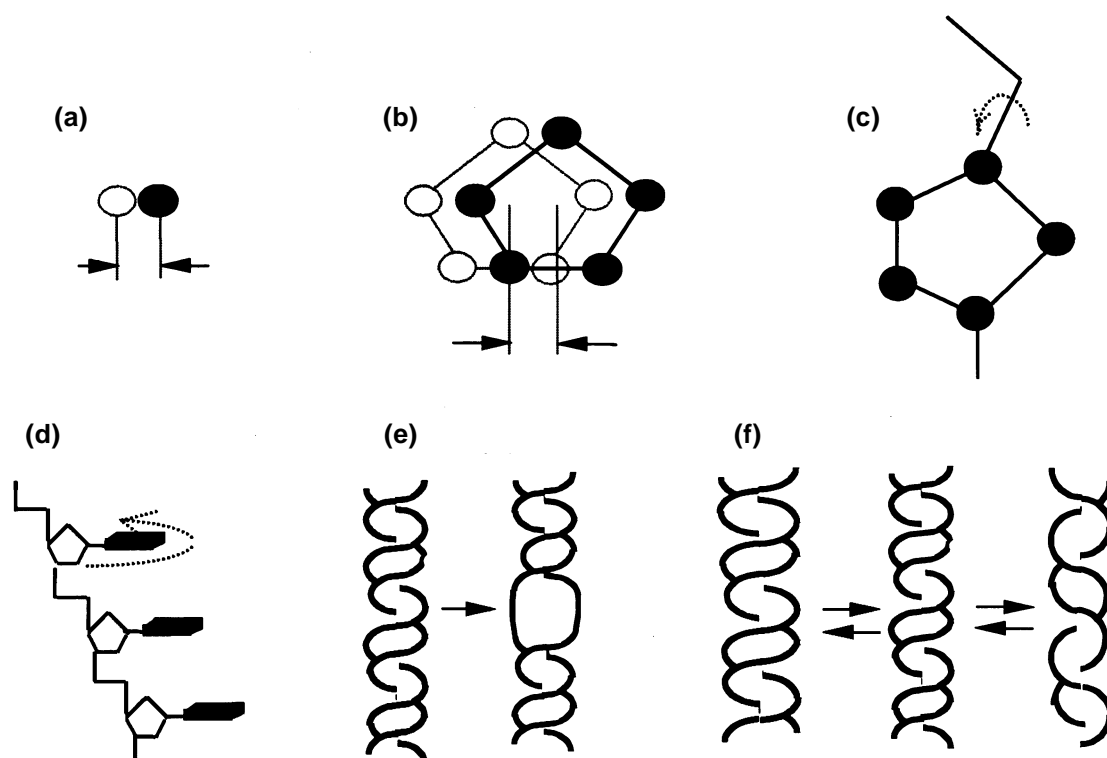
In the third line a more complex model of the DNA internal dynamics is shown. It takes into account that each of the polynucleotide chains consists of three types of atomic groups (bases, sugar rings, phosphates). In the table 1 different groups are shown schematically by dif-

ferent geometrical forms, and for simplicity the helicity of the structure is omitted. The number of equations required to describe mathematically internal motions is substantially increased in this case.

The list of approximate models can be continued and new lines with more and more complex models of DNA structure and dynamics can be added till the most accurate model which takes into account all atoms, motions and interactions, is reached.

#### 4. Mathematical description of the internal DNA dynamics: model hamiltonian and dynamical equations

To describe internal DNA dynamics mathematically let us begin with choosing appropriate approximate model. Usually the choice of the model depends on the problem considered and on the required accuracy of mathematical description. Let us consider as an example the problem of local unwinding of the DNA double helix. As it follows from the table 1, the models of the second line are the simplest models which can be used. To obtain the analytical form of corresponding six coupled differential equations, let us use the method developed recently in our



**Figure 1.** Some examples of the internal motions possible in DNA. Displacements of individual atoms from their equilibrium positions (a), displacements of atomic groups (b), rotations of atomic groups around single bonds (c), rotations of bases around sugar-phosphate chain (d), local unwinding of the double helix (e), and transitions between different DNA forms (f).

previous work (Yakushevich 2000) and write corresponding hamiltonian in the vector form

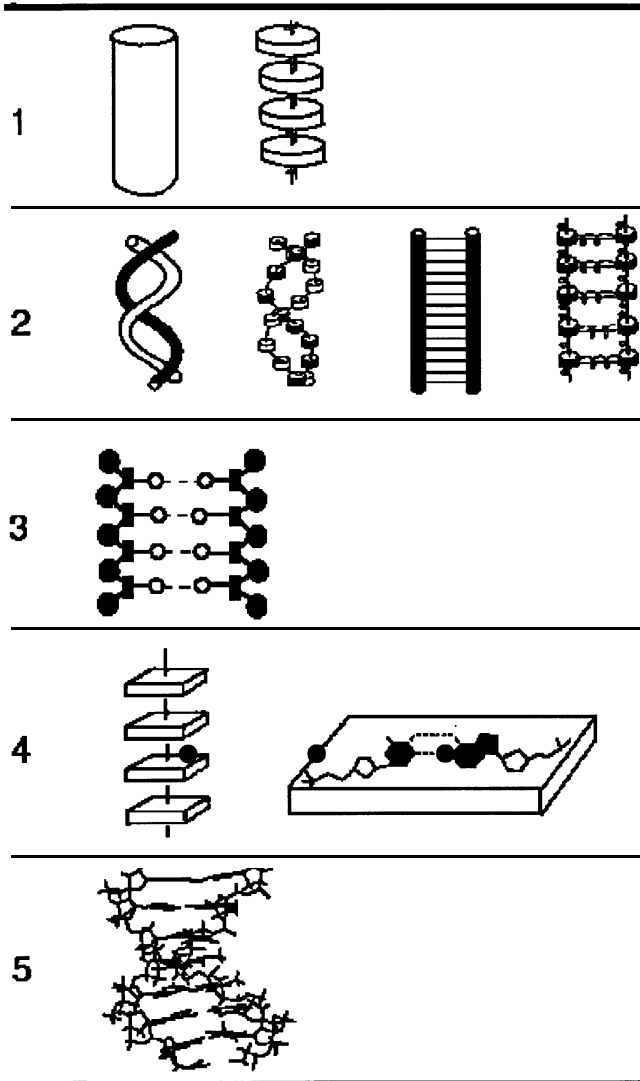
$$H_{\text{general}} = \sum_n [m(dU_{n,1}/dt)^2 + m(dU_{n,2}/dt)^2]/2 + \sum_n K[|U_{n,1} - U_{n-1,1}|^2/2 + |U_{n,2} - U_{n-1,2}|^2/2] + \sum_n V(|U_{n,1} - U_{n,2}|), \quad (1)$$

where  $U_{n,i}(t)$  is the vector which describes torsional, transverse and longitudinal displacements

$$U_{n,1} = \{R_0(1 - \cos \Theta_{n,1}) + u_{n,1} \cos \Theta_{n,1}; -R_0 \sin \Theta_{n,1} + u_{n,1} \sin \Theta_{n,1}; z_{n,1}\}; \quad (2)$$

$$U_{n,2} = \{-R_0(1 - \cos \Theta_{n,2}) + u_{n,2} \cos \Theta_{n,2}; R_0 \sin \Theta_{n,2} + u_{n,2} \sin \Theta_{n,2}; z_{n,2}\},$$

**Table 1.** Approximate models of DNA structure and dynamics.



where  $\Theta_1$  and  $\Theta_2$  are the angles of rotations of bases around the sugar-phosphate chains;  $u_{n,1}$  and  $u_{n,2}$  are the transverse displacements of nucleotides;  $z_{n,1}$  and  $z_{n,2}$  are the longitudinal displacements;  $m$  is a common mass of nucleotides;  $K$  is the coupling constant along each strand;  $R_0$  is the radius of DNA;  $a$  is the distance between bases along the chains; and  $V$  is the potential function describing interaction between bases in pairs. Hamiltonian (1) can be considered as a generalization of two well known particular nonlinear models of the DNA internal dynamics: the model of Peyrard and Bishop (1989), which describes transverse DNA dynamics, and the model of Yomosa (1983), which describes torsional DNA dynamics.

To obtain the explicit form of the model hamiltonian, let us insert now formula (2) into (1). To simplify calculations, let us suggest a simple form for potential function

$$V(|U_{n,1} - U_{n,2}|) = \sum_n k |U_{n,1} - U_{n,2}|^2/2, \quad (3)$$

and omit the terms describing the helicity of the DNA structure which can be taken into account at the final stage of the calculations (Yakushevich 1984; Gaeta 1990, 1992). As a result of calculations we obtain the discrete version of the model hamiltonian

$$H = (m/2)\sum_n \{[(du_{n,1}/dt)^2 + (R_0 - u_{n,1})^2(d\Theta_{n,1}/dt)^2 + m(dz_{n,1}/dt)^2] + [(du_{n,2}/dt)^2 + (R_0 + u_{n,2})^2(d\Theta_{n,2}/dt)^2 + m(dz_{n,2}/dt)^2]\} + (K/2)\sum_n \{[2R_0^2[1 - \cos(\Theta_{n,1} - \Theta_{n-1,1})] + u_{n,1}^2 + u_{n-1,1}^2 - 2u_{n,1}u_{n-1,1} \cos(\Theta_{n,1} - \Theta_{n-1,1}) - 2R_0 u_{n,1}[1 - \cos(\Theta_{n,1} - \Theta_{n-1,1})] - 2R_0 u_{n-1,1}[1 - \cos(\Theta_{n,1} - \Theta_{n-1,1})] + |z_{n,1} - z_{n-1,1}|^2 + |z_{n,2} - z_{n-1,2}|^2 + [2R_0^2[1 - \cos(\Theta_{n,2} - \Theta_{n-1,2})] + u_{n,2}^2 + u_{n-1,2}^2 - 2u_{n,2}u_{n-1,2} \cos(\Theta_{n,2} - \Theta_{n-1,2}) + 2R_0 u_{n,2}[1 - \cos(\Theta_{n,2} - \Theta_{n-1,2})] + 2R_0 u_{n-1,2}[1 - \cos(\Theta_{n,2} - \Theta_{n-1,2})]]\} + (k/2)\sum_n \{[2R_0^2 \{(1 - 2\cos \Theta_{n,1}) + (1 - 2\cos \Theta_{n,2}) + [1 + \cos(\Theta_{n,1} - \Theta_{n,2})]\} - 2R_0 u_{n,1}(1 - 2\cos \Theta_{n,1}) + 2R_0 u_{n,2}(1 - 2\cos \Theta_{n,2}) + u_{n,1}^2 + u_{n,2}^2 - 2u_{n,1}u_{n,2} \cos(\Theta_{n,1} - \Theta_{n,2}) - 2R_0 u_{n,1} \cos(\Theta_{n,1} - \Theta_{n,2}) + 2R_0 u_{n,2} \cos(\Theta_{n,1} - \Theta_{n,2})] + k |z_{n,1} - z_{n,2}|^2\}, \quad (4)$$

which can be written in a more convenient form

$$H = H(f) + H(\Psi) + H(g) + H(\text{interact.}). \quad (5)$$

Where hamiltonians

$$H(f) = (mR_0^2/2)\sum_n (df_{n,1}/dt)^2 + (mR_0^2/2)\sum_n (df_{n,2}/dt)^2 + (KR_0^2/2)\sum_n (f_{n,1} - f_{n-1,1})^2 + (KR_0^2/2)\sum_n (f_{n,2} - f_{n-1,2})^2 + (kR_0^2/2)\sum_n (f_{n,1} + f_{n,2})^2, \quad (6)$$

$$H(\Psi) = (mR_0^2/2)\sum_n (d\Psi_{n,1}/dt)^2 + (mR_0^2/2)\sum_n (d\Psi_{n,2}/dt)^2 + (KR_0^2/2)\sum_n [1 - \cos(\Psi_{n,1} - \Psi_{n-1,1})] + (KR_0^2/2)$$

$$\Sigma_n[1 - \cos(\Psi_{n,2} - \Psi_{n-1,2})] + (kR_0^2)\Sigma_n\{2(1 - \cos \Psi_{n,1}) + 2(1 - \cos \Psi_{n,2}) - [1 - \cos(\Psi_{n,1} + \Psi_{n,2})]\}, \quad (7)$$

$$H(g) = (mR_0^2/2)\Sigma_n(dg_{n,1}/dt)^2 + (mR_0^2/2)\Sigma_n(dg_{n,2}/dt)^2 + (KR_0^2/2)\Sigma_n(g_{n,1} - g_{n-1,1})^2 + (KR_0^2/2)\Sigma_n(g_{n,2} - g_{n-1,2})^2 + (kR_0^2/2)\Sigma_n(g_{n,1} + g_{n,2})^2, \quad (8)$$

$$H(\text{interact.}) = (mR_0^2/2)\Sigma_n(-2f_{n,1} + f_{n,1}^2)(d\Psi_{n,1}/dt)^2 + (mR_0^2/2)\Sigma_n(-2f_{n,2} + f_{n,2}^2)(d\Psi_{n,2}/dt)^2 + (KR_0^2)\Sigma_n[1 - \cos(\Psi_{n,1} - \Psi_{n-1,1})][f_{n,1}f_{n-1,1} - f_{n-1,1} - f_{n,1}] + (KR_0^2)\Sigma_n[1 - \cos(\Psi_{n,2} - \Psi_{n-1,2})][f_{n,2}f_{n-1,2} - f_{n-1,2} - f_{n,2}] - (2kR_0^2)\Sigma_n(f_{n,1})(1 - \cos \Psi_{n,1}) - (2kR_0^2)\Sigma_n(f_{n,2})(1 - \cos \Psi_{n,2}) + (kR_0^2)\Sigma_n(-f_{n,1}f_{n,2} + f_{n,1} + f_{n,2})[1 - \cos(\Psi_{n,1} + \Psi_{n,2})], \quad (9)$$

and new variables

$$f_{n,1} = u_{n,1}/R_0; f_{n,2} = -u_{n,2}/R_0; \Psi_{n,1} = \Theta_{n,1}; \Psi_{n,2} = -\Theta_{n,2}, \quad (10)$$

$$g_{n,1} = z_{n,1}/R_0; g_{n,2} = -z_{n,2}/R_0$$

are used. Here  $H(f)$  is a part of the model hamiltonian which describes transverse motions;  $H(\Psi)$  is a part of the model hamiltonian which describes torsional motions;  $H(g)$  is a part of the model hamiltonian which describes longitudinal motions;  $H(\text{interact.})$  is a part of the model hamiltonian which describes interactions between the motions.

If we are interested in the solutions which are rather smooth functions (or in other words, if the functions  $f_1, f_2, g_1, g_2, \Psi_1, \Psi_2$  change substantially only at the distances which are much more than the distance between neighbouring base pairs), we can use continuous approximation. Then the model hamiltonian takes the form

$$H_{\text{cont.}} = (\mathbf{r}_m R_0^2/2) \int dz [(\partial_1/\partial t)^2 + (\partial_2/\partial t)^2] + (Y R_0^2/2) \int dz [(\partial_1/\partial z)^2 + (\partial_2/\partial z)^2] + (Y R_0^2/2) \int dz (f_1 + f_2)^2 + (\mathbf{r}_m R_0^2/2) \int dz [(\partial g_1/\partial t)^2 + (\partial g_2/\partial t)^2] + (Y R_0^2/2) \int dz [(\partial g_1/\partial z)^2 + (\partial g_2/\partial z)^2] + (Y R_0^2/2) \int dz (g_1 + g_2)^2 + (\rho_m R_0^2/2) \int dz [(1 - f_1)^2 (\partial \Psi_1/\partial t)^2 + (1 - f_2)^2 (\partial \Psi_2/\partial t)^2] + (Y R_0^2/2) \int dz [(1 - f_1)^2 (\partial \Psi_1/\partial z)^2 + (1 - f_2)^2 (\partial \Psi_2/\partial z)^2] + (Y R_0^2) \int dz \{2(1 - f_1)(1 - \cos \Psi_1) + 2(1 - f_2)(1 - \cos \Psi_2) + (-f_1 f_2 + f_1 + f_2 - 1)[1 - \cos(\Psi_1 + \Psi_2)]\}, \quad (11)$$

where  $m/a = \mathbf{r}_m$ ;  $Ka = Y$ ;  $k/a = y$ . And the dynamical equations which correspond to the model hamiltonian (11) can be easily obtained from the general theory of hamiltonian systems

$$\mathbf{r}_m(d^2 f_1/dt^2) + \mathbf{r}_m(1 - f_1)(d\Psi_1/dt)^2 = Y \partial^2 f_1/\partial z^2$$

$$+ Y(\partial \Psi_1/\partial z)^2(1 - f_1) - y(f_1 + f_2) + 2y(1 - \cos \Psi_1) - y(1 - f_1)[1 - \cos(\Psi_1 + \Psi_2)], \quad (12)$$

$$\mathbf{r}_m(d^2 f_2/dt^2) + \mathbf{r}_m(1 - f_2)(d\Psi_2/dt)^2 = Y \partial^2 f_2/\partial z^2 + Y(\partial \Psi_2/\partial z)^2(1 - f_2) - y(f_1 + f_2) + 2y(1 - \cos \Psi_2) - y(1 - f_2)[1 - \cos(\Psi_1 + \Psi_2)], \quad (13)$$

$$\mathbf{r}_m(1 - f_1)(d^2 \Psi_1/dt^2) - 2\mathbf{r}_m(df_1/dt)(d\Psi_1/dt) = Y(\partial^2 \Psi_1/\partial z^2)(1 - f_1) - 2Y(\partial \Psi_1/\partial z)[\partial f_1/\partial z] - 2y[(\sin \Psi_1)] + y(1 - f_1)[\sin(\Psi_1 + \Psi_2)], \quad (14)$$

$$\mathbf{r}_m(1 - f_2)(d^2 \Psi_2/dt^2) - 2\mathbf{r}_m(df_2/dt)(d\Psi_2/dt) = Y(\partial^2 \Psi_2/\partial z^2)(1 - f_2) - 2Y(\partial \Psi_2/\partial z)[\partial f_2/\partial z] - 2y[(\sin \Psi_2)] + y(1 - f_1)[\sin(\Psi_1 + \Psi_2)]. \quad (15)$$

$$\mathbf{r}_m(d^2 g_1/dt^2) = Y \partial^2 g_1/\partial z^2 - y(g_1 + g_2), \quad (16)$$

$$\mathbf{r}_m(d^2 g_2/dt^2) = Y \partial^2 g_2/\partial z^2 - y(g_1 + g_2). \quad (17)$$

And this is the sought mathematical description of the internal DNA dynamics, which we obtained in the frameworks of the model consisting of two weakly interacting elastic threads. To prove that conformational solitary waves are possible, it is enough to show that the model equations (12)–(17) have soliton-like solutions.

## 5. Soliton-like solutions and their interpretation

Let us note that the system of equations (12)–(17) can be divided into two independent subsystems. The first one consists of equations (12)–(15) and it describes transverse and torsional internal motions in DNA. Second one consists of equations (16)–(17), and it describes longitudinal motions. Such a division becomes possible because we chose simplified form [see formula (3)] for potential function  $V(|U_{n,1} - U_{n,2}|)$ . In the general case when the formula for potential function is

$$V = D\{\exp[-A(|U_{n,1} - U_{n,2}|)] - 1\}^2, \quad (18)$$

the division into two independent subsystems is not possible. But here, in this paper, we limited ourselves by simplified formula (3), which can be considered as a first term in the expansion

$$V(|U_{n,1} - U_{n,2}|) = D\{\exp[-A|U_{n,1} - U_{n,2}|] - 1\}^2 = 2DA^2|U_{n,1} - U_{n,2}|^2/2 + \dots \quad (19)$$

In this approximation, longitudinal motions can be considered independently. In the next section we describe shortly solutions of equations (16)–(17) which describe longitudinal DNA dynamics.

### 5.1 Longitudinal DNA dynamics

Equations (16)–(17) are well known linear partial differential equations having the solutions in the form of usual plane waves

$$\begin{aligned} g_1(z, t) &= g_{01} \exp[i(qz - w^{\text{long}} t)]; \quad g_2(z, t) \\ &= g_{02} \exp[i(qz - w^{\text{long}} t)], \end{aligned} \quad (20)$$

where  $g_{01}, g_{02}$  are the amplitudes of the waves and  $q$  is the wave vector which lies in the first Brillouin zone. Inserting (20) into (16)–(17) we can easily find the frequencies of longitudinal waves in DNA

$$w_1^{\text{long}} = [(Y/\mathbf{r}_m)q^2 + 2(y/\mathbf{r}_m)]^{1/2}; \quad w_2^{\text{long}} = [(Y/\mathbf{r}_m)]^{1/2}q. \quad (21)$$

As follows from (21), the spectrum of longitudinal oscillations of DNA consists of two branches: one optical branch  $[w_1^{\text{long}}(q)]$  and one acoustic branch  $[w_2^{\text{long}}(q)]$ .

### 5.2 Transverse DNA dynamics

Let us pass now to the other subsystem of the system of dynamical equations (12)–(17). It consists of four equations (12)–(15) which describes transverse and torsional motions. If we assume, however, that transverse motions (variables  $f_1$  and  $f_2$ ) are much faster than the torsional motions (variables  $\Psi_1$  and  $\Psi_2$ ), adiabatic approximation can be applied, and the subsystem of equations (12)–(15) can be divided into two independent parts. The first part will describe torsional DNA dynamics and the second part will describe transverse DNA dynamics. Let us begin with equations (12)–(13) describing transverse dynamics and suggest that the slow variables  $\Psi_1$  and  $\Psi_2$  are constants ( $C_1$  and  $C_2$ , relatively). Then the dynamical equations take the form

$$\begin{aligned} \mathbf{r}_m(d^2 f_1/dt^2) &= Y \partial^2 f_1/\partial z^2 - y(f_1 + f_2) \\ &+ 2y(1 - \cos C_1) - y(1 - f_1)[1 - \cos(C_1 + C_2)], \end{aligned} \quad (22)$$

$$\begin{aligned} \mathbf{r}_m(d^2 f_2/dt^2) &= Y \partial^2 f_2/\partial z^2 - y(f_1 + f_2) \\ &+ 2y(1 - \cos C_2) - y(1 - f_2)[1 - \cos(C_1 + C_2)], \end{aligned} \quad (23)$$

and corresponding model hamiltonian is

$$\begin{aligned} H_{\text{adiab.}}(f) &= (\mathbf{r}_m R_0^2/2) \int dz [(\partial f_1/\partial t)^2 + (\partial f_2/\partial t)^2] \\ &+ (Y R_0^2/2) \int dz [(\partial f_1/\partial z)^2 + (\partial f_2/\partial z)^2] + (y R_0^2/2) \int dz \\ &(f_1 + f_2)^2 + (y R_0^2) \int dz \{2(1 - f_1)(1 - \cos C_1) \\ &+ 2(1 - f_2)(1 - \cos C_2) + (-f_1 f_2 + f_1 + f_2 - 1) \\ &[1 - \cos(C_1 + C_2)]\}. \end{aligned} \quad (24)$$

If we suggest boundary conditions in the form

$$\begin{aligned} \cos \Psi_1 &\rightarrow 1, \text{ when } z \rightarrow \pm \infty; \text{ and } \cos \Psi_2 \rightarrow 1, \\ \text{when } z &\rightarrow \pm \infty, \end{aligned} \quad (25)$$

then the following relations are valid

$$(1 - \cos C_1) = (1 - \cos C_2) = [1 - \cos(C_1 + C_2)] = 0, \quad (26)$$

and the final formula for hamiltonian describing transverse subsystem takes the form

$$\begin{aligned} H_{\text{adiab.}}(f) &= (\mathbf{r}_m R_0^2/2) \int dz [(\partial f_1/\partial t)^2 + (\partial f_2/\partial t)^2] \\ &+ (Y R_0^2/2) \int dz [(\partial f_1/\partial z)^2 + (\partial f_2/\partial z)^2] + (y R_0^2/2) \int dz \\ &(f_1 + f_2)^2. \end{aligned} \quad (27)$$

So, we can conclude that in the adiabatic approximation and for simple model of potential function (3) and boundary conditions (25) any influence of torsional subsystem on transverse subsystem is absent. Equations (22)–(23) take then the form

$$\mathbf{r}_m(d^2 f_1/dt^2) = Y \partial^2 f_1/\partial z^2 - y(f_1 + f_2), \quad (28)$$

$$\mathbf{r}_m(d^2 f_2/dt^2) = Y \partial^2 f_2/\partial z^2 - y(f_1 + f_2), \quad (29)$$

and their solutions are

$$\begin{aligned} f_1(z, t) &= f_{01} \exp[i(qz - w^{\text{tr}} t)]; \\ f_2(z, t) &= f_{02} \exp[i(qz - w^{\text{tr}} t)], \end{aligned} \quad (30)$$

where  $f_{01}, f_{02}$  are the amplitudes of the waves and  $q$  is the wave vector which lies in the first Brillouin zone. Inserting (30) into (28)–(29) we find the frequencies of transverse oscillations in DNA

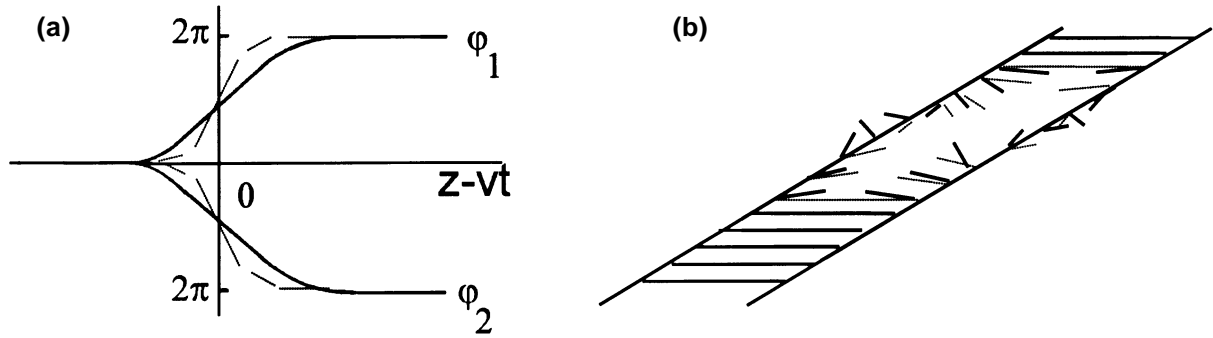
$$w_1^{\text{tr}} = [(Y/\mathbf{r}_m)q^2 + 2(y/\mathbf{r}_m)]^{1/2}; \quad w_2^{\text{tr}} = [(Y/\mathbf{r}_m)]^{1/2}q. \quad (31)$$

So, the spectrum of transverse oscillations of DNA also consists of two branches: one optical branch  $[w_1^{\text{tr}}(q)]$  and one acoustic branch  $[w_2^{\text{tr}}(q)]$ .

### 5.3 Torsional DNA dynamics

To finish the analysis of the system of dynamical equations (12)–(17) it remains only to consider equations (14)–(15) describing torsional DNA dynamics. In accordance with adiabatic approximation, let us write the terms of hamiltonian (11) which contains variables  $\Psi_1, \Psi_2$  and average the values depending on the variables  $f_1$  and  $f_2$ . As a result, we obtain the hamiltonian describing torsional motions written in the adiabatic approximation

$$\begin{aligned} H_{\text{adiab.}}(\Psi) &= E_0 + [\mathbf{r}_m \langle (1 - f_1)^2 \rangle R_0^2/2] \int dz (\partial \Psi_1/\partial t)^2 \\ &+ [\mathbf{r}_m \langle (1 - f_2)^2 \rangle R_0^2/2] \int dz (\partial \Psi_2/\partial t)^2 + [Y \langle (1 - f_1)^2 \rangle \\ &> R_0^2/2] \int dz (\partial \Psi_1/\partial z)^2 + [Y \langle (1 - f_2)^2 \rangle R_0^2/2] \int dz \\ &(\partial \Psi_2/\partial z)^2 + [y \langle (1 - f_1) \rangle R_0^2] \int dz [2(1 - \cos \Psi_1)] \\ &+ [y \langle (1 - f_2) \rangle R_0^2] \int dz [2(1 - \cos \Psi_2)] \end{aligned}$$



**Figure 2.** Kink-like solution (a), and its interpretation as an open state in the double strand DNA (b). Dotted lines correspond to the case when interactions between different types of internal motions (transverse, longitudinal, and torsional) were not taken into account.

$$+ [y <(-f_1 f_2 + f_1 + f_2 - 1) > R_0^2] \int dz [1 - \cos(\Psi_1 + \Psi_2)]. \quad (32)$$

Here  $E_0$  is an average energy of transverse oscillations and  $\langle \dots \rangle$  means averaging over the states of oscillating transverse subsystem.

From the general view of formula (32) we can conclude that in the framework of adiabatic approximation the influence of the transverse subsystem on the torsional is reduced to a simple renormalization of the coefficients of the torsional hamiltonian, and the form of the hamiltonian does not changed. This gives us a possibility to use our previous results on the solutions of the system of coupled nonlinear partial differential equations describing torsional DNA dynamics (Yakushevich 1995).

Indeed let us write dynamical equations corresponding to hamiltonian (32)

$$\mathbf{r}_m \langle (1 - f_1)^2 \rangle (d^2 \Psi_1 / dt^2) = Y \langle (1 - f_1)^2 \rangle (\partial^2 \Psi_1 / \partial z^2) + y [2 \sin \Psi_1 - \sin(\Psi_1 + \Psi_2)], \quad (33)$$

$$\mathbf{r}_m \langle (1 - f_2)^2 \rangle (d^2 \Psi_2 / dt^2) = Y \langle (1 - f_2)^2 \rangle (\partial^2 \Psi_2 / \partial z^2) + y [2 \sin \Psi_2 - \sin(\Psi_1 + \Psi_2)]. \quad (34)$$

As we showed earlier, equations of that type have among others the soliton-like solution

$$\Psi_1(z - vt) = -\Psi_2(z - vt) = 4 \arctan\{\exp[\mathbf{g}(\mathbf{x} - \mathbf{x}_0)/d]\}, \quad (35)$$

where  $\mathbf{g} = [1 - (\mathbf{r}_m/Y)v^2]^{-1/2}$ ;  $\mathbf{x} = z - vt$ ; and  $v$  is the velocity of propagation of the soliton. The values of mass ( $M$ ), energy ( $E$ ) and size ( $d$ ) of the soliton are a little increased in comparison with corresponding values obtained for torsional dynamical system where interactions with transverse and longitudinal motions are not taken into account

$$E = 8 \{2Yy\}^{1/2} \{\langle (1 - f)^2 \rangle\}^{1/2}, \quad (36)$$

$$M = 8 \mathbf{r}_m \{2y/Y\}^{1/2} \{\langle (1 - f)^2 \rangle\}^{1/2}, \quad (37)$$

$$d = Y \langle (1 - f_1)^2 \rangle / 2y. \quad (38)$$

Graphic representation of the solution is shown in figure 2a, and qualitative picture, which corresponds to this solution, is shown schematically in figure 2b. So, the solitary wave solution can be really interpreted as that describing unwound region (or open state).

## 6. Conclusions

In this paper a possibility of nonlinear conformational waves in DNA is considered. We described shortly the history of the problem, the main results, and new arguments which are based on the analysis of the internal motions of DNA and on the general principles of mathematical modelling of the motions. We gave a general description of the DNA internal dynamics and showed when the nonlinear behaviour is exhibited. We illustrated the statement by detailed consideration of one of the examples of large-amplitude internal motions occurred in DNA, namely, by consideration of local unwinding of the double helix. We constructed an appropriate mathematical model, and showed that corresponding dynamical equations admit solitary wave solutions interpreted as unwound regions. This result gives one more argument in favour of the approach where DNA molecule is considered as a nonlinear dynamical system where solitary waves can be excited.

It is necessary to say, however, a few words about limitations of the mathematical proof presented above. First of all we should note, that all calculations were made for simplified mathematical model of DNA which did not take into account inhomogeneity of the DNA structure, existence of dissipation and interactions with surrounding. In the paper we discussed a possibility of excitation of

only a single conformational solitary wave and the problem of assemble of the waves and their statistics were out of our investigation. Consideration of all these aspects could give a more reliable answer to the question formulated in the title of the paper.

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