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EIGEN MODES OF THE DOUBLE DNA CHAIN HELIX VIBRATIONS

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Different models of two coupled homogeneous DNA chain vibrations are proposed in the literature. By using as the basic approach to the DNA mathematical modelling published by N. Kovaleva, L. Manevich in 2005 and 2007, we consider a linearized model to obtain main chain subsystems of the double DNA helix. Analytical expressions of the circular eigen frequencies for the homogeneous model of the double DNA chain helix are obtained. The corresponding vibration eigen modes and possibilities of the appearance of resonant regimes as well as dynamical absorption under external excitations are considered. Two sets of normal eigen coordinates of the double DNA chain helix for separation of the system into two uncoupled chains are identified. This may correspond to the base pair order in complementary chains of the DNA double helix in a living cell.

Key words: DNA, eigen main chains, eigen circular frequency, vibration modes

1. Introduction

DNA is a biological polymer which can exist in different forms (A, B, Z, E, ...) but only B form can be found in live organisms. Chemically, DNA consists of two long polymers of simple units called nucleotides, with backbones made of sugars and phosphate groups joined by ester bonds. To each sugar one of four types of molecules called bases is attached. Two bases on opposite strands are linked via hydrogen bonds holding the two strands of DNA together. It is the sequence of these four bases along the backbone that encodes information the mechanical properties of DNA are closely related to its molecular structure

and sequence, particularly the weakness of hydrogen bonds and electronic interactions that hold the strands of DNA together compared to the strength of bonds within each strand. Every process which binds or reads DNA is able to use or modify the mechanical properties of DNA for purposes of recognition, packaging and modification. It is important to note that, the DNA found in many cells can be macroscopic in length – a few centimeters long for each human chromosome. Consequently, cells must compact or "package" DNA to carry it within them (Bryant *et al.*, 2003; Gore *et al.*, 2006; Volkenstein, 1975).

Knowledge of the elastic properties of DNA is required to understand the structural dynamics of cellular processes such as replication and transcription.

Binding of proteins and other ligands induces a strong deformation of the DNA structure.

The aim of our work was to model the DNA dynamics (vibrations of DNA chains) as a biological system in specific boundary conditions that are possible to occur in a life system during regular function of a DNA molecule.

2. Mechanical properties of DNA determined experimentally

Experimental evidence suggests that DNA mechanical properties, in particular intrinsic curvature and flexibility, have a role in many relevant biological processes.

For small distortions, DNA overwinds under tension (Gore *et al.*, 2006). Lowering of the temperature does increase the DNA curvature. Curved DNA sequences migrate more slowly on polyacrylamide gels than their non-curved counterparts possessing the same length. The anomaly in gel mobility is related to the extent of DNA curvature (Tsai and Luo, 2000). The DNA double helix is much more resistant to twisting deformations than bending deformations, almost all of the supercoiling pressure is normally relieved by writhing (Arsuaga *et al.*, 2002). The twist angle of the helix has been shown to depend on sequence when the molecule is in solution, both by the effects on supercoiling parameters when short segments of the known sequence are inserted into closed circular DNA (Peck and Wang, 1981; Tung and Harvey, 1984) and by the nuclease digestion patterns of DNA adsorbed on surfaces (Behe *et al.*, 1981; Tung and Harvey, 1984).

As a biomolecule, DNA also has electronic properties. When DNA is placed in vacuum it shares characteristics with semiconductors. In a solution, DNA transfers electrons via a different mechanism (Westerhoff and Merz Jr., 2006). Under low tension, DNA behaves like an isotropic flexible rod. At higher tensions, the behaviour of over- and underwound molecules is different. In each

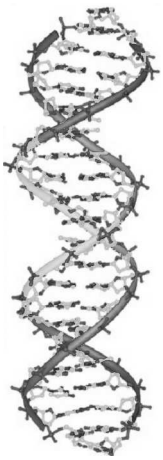

Fig. 1. Model of DNA duble helix from www.wikipedia.org

case, DNA undergoes a structural change before the twist density necessary for buckling is reached (Bryant *et al.*, 2003).

Mg2+ can induce or enhance curvature in DNA fragments and helps stabilize several types of DNA structures (Brukner *et al.*, 1994). The fraction of bent molecules seen by EM or SFM was higher in the presence of cationic metals. DNA length varied in solution with different ionic forces. It is significantly longer in solution with a lower ionic force (Frontali *et al.*, 1979).

3. DNA models by Kovaleva and Manevich

A number of mechanical models of the DNA double helix have been proposed till today. Different models focuse on different aspects of the DNA molecule (biological, physical and chemical processes in which DNA is involved). They show that in a double DNA helix, a localised excitation (breather) can exist, which corresponds to predominant rotation of one chain and small perturbation of the second chain using the coarse-grained model of the DNA double helix. Each nucleotide is represented by three beads with interaction sites corresponding to the phosphate group, group of sugar ring, and the base (Kovaleva *et al.*, 2007).

Kovaleva *et al.* (2007) pointed out that solitons and breathers play a functional role in DNA chains. In the model, the DNA backbone is reduced to a polymeric structure and the base is covalently linked to the center of the sugar ring group, thus a DNA molecule with N nucleotides corresponds to $3N$

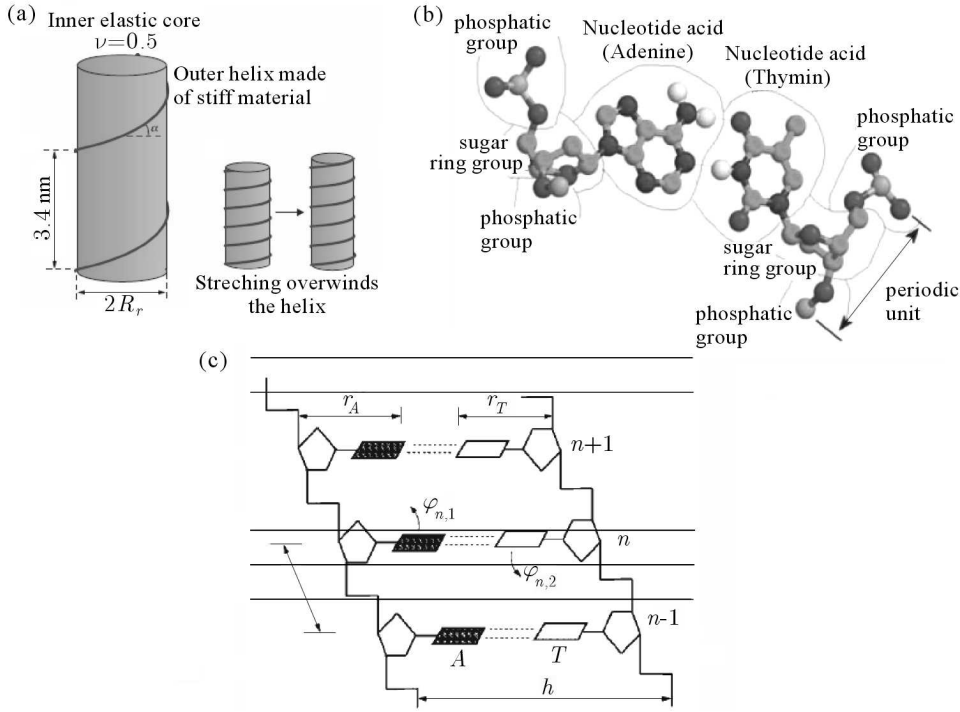

Fig. 2. (a) "Toy mechanical" model of DNA. a, DNA is modeled as an elastic rod (grey) wrapped helically by a stiff wire (red) (Gore *et al.*, 2006); (b) model scheme of a double helix on six coarse-grained particles (Kovaleva *et al.*, 2007); (c) fragment of the DNA double chain consisting of three AT base pairs. Longitudinal pitch of the helix $a = 3.4$ Å, transverse pitch $h = 16.15$ Å (Kovaleva and Manevich, 2005)

interaction centers. Apart from its well-known role as the cellular storehouse of information, DNA is now being used to construct rigid scaffolds in one, two and three dimensions on the nanoscale. This field is termed *Structural DNA Nanotechnology*. It seeks to use the base complementarily design principle of DNA to create ordered superstructures from a set of DNA sequences that selfassemble into regular, well-defined topologies on the nanoscale (Anselmi *et al.*, 2005). Starting from a coarse-grained off-lattice model of DNA and using cylindrical coordinates, the authors derived simplified continuum equations corresponding to vicinities of gap frequencies in the spectrum of linearised equations of motion. It is shown that the obtained nonlinear continuum equations describing modulations of normal modes admit spatially localised solitons which can be identified with breathers. The authors formulated conditions of the breathers existence and estimated their characteristic parameters. The relationship between the derived model and more simple but

widely used models is discussed. The analytical results are compared with the data of numerical study of discrete equations of motion (see Fig. 2b).

Kovaleva and Manevich (2005) presented the simplest model describing opening of the DNA double helix. Corresponding differential equations are solved analytically using multiple-scale expansions after transition to complex variables. The obtained solution corresponds to localised torsional nonlinear excitation – breather. Stability of the breather is also investigated.

In their work, Kovaleva and Manevich (2005) considered B form of the DNA molecule, the fragment of which is presented in Fig. 1b. The lines in the figure correspond to the skeleton of the double helix, black and grey rectangles show the bases in pairs (AT and GC). Let us focus our attention on rotational motions of the bases around the sugar phosphate chains in the plane perpendicular to the helix axis.

The authors deal with the planar DNA model in which the chains of the macromolecule form two parallel straight lines placed at a distance h from each other, and the bases can make only rotary motions around their own chain, being all the time perpendicular to it. The authors accepted as generalized (independent) coordinates $\varphi_{k,1}$ the angular displacement of the k-th base of the first chain, and as generalized (independent) coordinates $\varphi_{k,2}$ the angular displacement of the k-th base of the second chain. Then, by using the accepted generalized coordinates $\varphi_{k,1}$ and $\varphi_{k,2}$ for k-th bases of both chains in the DNA model, the authors derived a system of differential equations describing DNA model vibrations in the following forms

$$\begin{aligned} &J_{k,1}\ddot{\varphi}_{k,1} - \frac{K_{k,1}}{2}[\sin(\varphi_{k+1,1} - \varphi_{k,1}) - \sin(\varphi_{k,1} - \varphi_{k-1,1})] + \\ &\quad + K_{\alpha\beta} r_\alpha (r_\alpha - r_\beta) \sin\varphi_{k,1} + \\ &\quad - K_{\alpha\beta} \frac{1}{4}\Big(1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}}\Big)(r_\alpha - r_\beta)^2 \sin(\varphi_{k,1} - \varphi_{k,2}) = 0 \\ &J_{k,2}\ddot{\varphi}_{k,2} - \frac{K_{k,2}}{2}[\sin(\varphi_{k+1,2} - \varphi_{k,2}) - \sin(\varphi_{k,2} - \varphi_{k-1,2})] + \\ &\quad + K_{\alpha\beta} r_\alpha (r_\alpha - r_\beta) \sin\varphi_{k,2} + \\ &\quad + K_{\alpha\beta} \frac{1}{4}\Big(1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}}\Big)(r_\alpha - r_\beta)^2 \sin(\varphi_{k,1} - \varphi_{k,2}) = 0 \end{aligned} \tag{3.1}$$

where $J_{k,1}$ is the axial mass moment of inertia of the k-th base of the first chain; $J_{k,2}$ is the axial mass moment of mass inertia of the k-th base of the second chain, and the dot denotes differentiation with respect to time t. For the base pair, the axial mass moments of inertia are equal to $J_{k,1} = m_\alpha r_\alpha^2$, $J_{k,12} = m_\beta r_\beta^2$. The base mass m_α, length r_α, and the corresponding axial

mass moment of inertia $J_{k,1} = m_\alpha r_\alpha^2$ for all possible base pairs was assumed as in Zhang *et al.* (1994). The fourth terms in the previous system of equations describe interaction of the neighbouring bases along each of the macromolecule chains. The parameter $K_{k,i}$ $(i = 1, 2)$ characterises the energy of interaction of the k-th base with the $(k+1)$-th one along the i-th chain $i = 1, 2$. There are different estimations of rigidity. For calculations, the most appropriate value is close $K_{k,i} = K = 6 \cdot 10^3$ kJ/mol.

4. Consideration of the basic DNA model – linearised Kovaleva-Manevich's DNA model

Let us investigate an oscillatory model of DNA, considered by Kovaleva and Manevich (2005) and presented in the previous Section by a system of differential equations (3.1) expressed by generalized (independent) coordinates $\varphi_{k,1}$ and $\varphi_{k,2}$ for k-th bases of both chains in the DNA model.

For the beginning, it is necessary to consider the corresponding linearised system of previous differential equations in the following form

$$\begin{aligned} &J_{k,1}\ddot{\varphi}_{k,1} - \frac{K_{k,1}}{2}[(\varphi_{k+1,1} - \varphi_{k,1}) - (\varphi_{k,1} - \varphi_{k-1,1})] + K_{\alpha\beta} r_\alpha (r_\alpha - r_\beta)\varphi_{k,1} + \\ &\quad - K_{\alpha\beta}\frac{1}{4}\Big(1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}}\Big)(r_\alpha - r_\beta)^2(\varphi_{k,1} - \varphi_{k,2}) = 0 \\ &J_{k,2}\ddot{\varphi}_{k,2} - \frac{K_{k,2}}{2}[(\varphi_{k+1,2} - \varphi_{k,2}) - (\varphi_{k,2} - \varphi_{k-1,2})] + K_{\alpha\beta} r_\alpha (r_\alpha - r_\beta)\varphi_{k,2} + \\ &\quad + K_{\alpha\beta}\frac{1}{4}\Big(1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}}\Big)(r_\alpha - r_\beta)^2(\varphi_{k,1} - \varphi_{k,2}) = 0 \end{aligned} \tag{4.1}$$

or in that form

$$\begin{aligned} &\frac{2J_{k,1}}{K_{k,1}}\ddot{\varphi}_{k,1} - [(\varphi_{k+1,1} - \varphi_{k,1}) - (\varphi_{k,1} - \varphi_{k-1,1})] + \frac{2K_{\alpha\beta} r_\alpha (r_\alpha - r_\beta)}{K_{k,1}}\varphi_{k,1} + \\ &\quad - \frac{K_{\alpha\beta}}{2K_{k,1}}\Big(1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}}\Big)(r_\alpha - r_\beta)^2(\varphi_{k,1} - \varphi_{k,2}) = 0 \\ &\frac{2J_{k,2}}{K_{k,2}}\ddot{\varphi}_{k,2} - [(\varphi_{k+1,2} - \varphi_{k,2}) - (\varphi_{k,2} - \varphi_{k-1,2})] + \frac{2K_{\alpha\beta} r_\alpha (r_\alpha - r_\beta)}{K_{k,2}}\varphi_{k,2} + \\ &\quad + \frac{K_{\alpha\beta}}{2K_{k,2}}\Big(1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}}\Big)(r_\alpha - r_\beta)^2(\varphi_{k,1} - \varphi_{k,2}) = 0 \end{aligned} \tag{4.2}$$

For the case of homogeneous systems we can take into consideration that $J_{k,1} = J_{k,2} = J$ and $K_{k,1} = K_{k,2} = K$.

By changing the generalized coordinates $\varphi_{k,1}$ and $\varphi_{k,2}$ for k-th bases of both chains in the DNA model into the following new ones ξ_k and η_k through the relationships

$$\xi_k = \varphi_{k,1} - \varphi_{k,2} \qquad \eta_k = \varphi_{k,1} + \varphi_{k,2} \tag{4.3}$$

The previous system of differential equations (4.2) acquires the following form

$$\begin{aligned} &\frac{2J}{K}\ddot{\xi}_k - \xi_{k+1} + 2\xi_k\Big[1 + \frac{K_{\alpha\beta}r_\alpha(r_\alpha - r_\beta)}{K} - \frac{K_{\alpha\beta}}{2K}\Big(1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}}\Big)(r_\alpha - r_\beta)^2\Big] + \\ &\quad -\xi_{k-1} = 0 \\ &\frac{2J}{K}\ddot{\eta}_k - \eta_{k+1} + 2\eta_k\Big(1 + \frac{K_{\alpha\beta}r_\alpha(r_\alpha - r_\beta)}{K}\Big) - \eta_{k-1} = 0 \end{aligned} \tag{4.4}$$

where $k = 1, 2, \ldots, n$.

The first series of the previous system of equations is decoupled and independent with relations of the second series of the equations. *Then we can conclude that the new coordinates of ξ_k and η_k are main coordinates of DNA chains and that we obtain two fictive decoupled single eigen chains of the DNA liner model. This is the first fundamental conclusion as an important property of the linear model of vibrations into double DNA helix.*

Systems of differential equations (4.2) contain two separate subsystems of differential equations expressed by *the coordinates of ξ_k and η_k* which are main *coordinates of the double DNA chain helix and separate the linear DNA model into two independent chains. Then, it is* possible to apply the trigonometric method (Rašković, 1965, 1985; Hedrih, 2006, 2008a,b) to both series of equations (both subsystems) in the form $(k = 1, 2, \ldots, n)$

$$\begin{aligned} \xi_k &= A_k \cos(\omega t + \alpha) = C \sin k\varphi \cos(\omega t + \alpha) \\ \eta_k &= \widetilde{A}_k \cos(\omega t + \alpha) = D \sin k\vartheta \cos(\omega t + \alpha) \end{aligned} \tag{4.5}$$

where

$$A_k = C \sin k\varphi \qquad \widetilde{A}_k = D \sin k\vartheta \tag{4.6}$$

are amplitudes of separate eigen chains of the model *of the double DNA chain helix, and ω circular eigen frequency of one vibration mode.*

After introducing the proposed solutions into differential equations of previous separate subsystems (4.4), we obtain the following separate subsystems

of algebraic equations with respect to the amplitudes A_k and $\widetilde{A}_k$

$$\begin{aligned}
&-A_{k+1}+2A_k\Big\{\Big[1+\frac{K_{\alpha\beta}r_\alpha(r_\alpha-r_\beta)}{K}-\frac{K_{\alpha\beta}}{2K}\Big(1-\frac{\omega_{\alpha\beta2}}{\omega_{\alpha\beta1}}\Big)(r_\alpha-r_\beta)^2\Big]+\\
&\quad-\frac{J}{K}\omega^2\Big\}-A_{k-1}=0\\
&-\widetilde{A}_{k+1}+2\widetilde{A}_k\Big(1+\frac{K_{\alpha\beta}r_\alpha(r_\alpha-r_\beta)}{K}-\frac{2J}{K}\omega^2\Big)-\widetilde{A}_{k-1}=0
\end{aligned}\tag{4.7}$$

After applying the following denotations

$$\begin{aligned}
&\mu-\kappa=\frac{K_{\alpha\beta}r_\alpha(r_\alpha-r_\beta)}{K}-\frac{K_{\alpha\beta}}{2K}\Big(1-\frac{\omega_{\alpha\beta2}}{\omega_{\alpha\beta1}}\Big)(r_\alpha-r_\beta)^2\\
&\kappa=\frac{K_{\alpha\beta}}{2K}\Big(1-\frac{\omega_{\alpha\beta2}}{\omega_{\alpha\beta1}}\Big)(r_\alpha-r_\beta)^2\\
&\mu=\frac{K_{\alpha\beta}r_\alpha(r_\alpha-r_\beta)}{K}\qquad\qquad u=\frac{J}{K}\omega^2
\end{aligned}\tag{4.8}$$

we obtain the following simple forms of subsystems (4.7)

$$\begin{aligned}
&-A_{k+1}+2A_k(1+\mu-\kappa-u)-A_{k-1}=0\\
&-\widetilde{A}_{k+1}+2\widetilde{A}_k(1+\mu-u)-\widetilde{A}_{k-1}=0
\end{aligned}\tag{4.9}$$

After introducing proposed solutions (4.6), the trigonometric method is applied and we obtain two equations

$$\begin{aligned}
&C\sin k\varphi[-2\cos\varphi+2(1+\mu-\kappa-u)]=0\\
&D\sin k\vartheta[-2\cos\vartheta+2(1+\mu-u)]=0
\end{aligned}\tag{4.10}$$

From the previous system, we obtain the following eigen numbers for both separate eigen chains of the model *of the double DNA chain helix in the following forms*

$$u=2\sin^2\frac{\varphi}{2}+(\mu-\kappa)\qquad\qquad u=2\sin^2\frac{\vartheta}{2}+\mu\tag{4.11}$$

and the corresponding analytical expressions for *circular eigen frequencies of vibration modes of separate chains* ω^2

$$\omega_s^2=\frac{K}{J}\Big[2\sin^2\frac{\varphi_s}{2}+(\mu-\kappa)\Big]\qquad\qquad \omega_s^2=\frac{K}{J}\Big[2\sin^2\frac{\vartheta_s}{2}+\mu\Big]\tag{4.12}$$

5. Boundary conditions of the double DNA chain helix

Now, it is necessary to consider some boundary conditions of the s-th double DNA chain helix in accordance with possible real situations. For that reason, we take into account two cases of the double DNA chain helix, in which the ends of chains are either free or fixed. Then, we can write the following boundary conditions for the double DNA chain helix:
— first case: both ends of the double DNA chain helix are free. In that situation the first and n-th equations from the subsystems are in the form

$$A_1(1+\mu-\kappa-2u)-A_2=0 \qquad -A_{n-1}+A_n(1+\mu-\kappa-2u)=0 \tag{5.1}$$

and

$$\widetilde{A}_1(1+\mu-\kappa-2u)-\widetilde{A}_2=0 \qquad -\widetilde{A}_{n-1}+\widetilde{A}_n(1+\mu-2u)=0 \tag{5.2}$$

and after applying proposed solutions (4.6) we obtain that

$$\varphi_s=\frac{s\pi}{n} \qquad \vartheta_s=\frac{s\pi}{n} \qquad s=1,2,\ldots,n \tag{5.3}$$

— second case: both ends of the double DNA chain helix are fixed

$$\begin{aligned} &A_k=C\sin k\varphi && A_0=A_{n+1}=0 && A_{m+1}=C\sin(n+1)\varphi=0\\ &\widetilde{A}_k=D\sin k\vartheta && \widetilde{A}_0=\widetilde{A}_{n+1}=0 && \widetilde{A}_{m+1}=D\sin(n+1)\vartheta=0\\ &\varphi_s=\frac{s\pi}{n+1} && \vartheta_s=\frac{s\pi}{n+1} && s=1,2,\ldots,n \end{aligned} \tag{5.4}$$

Then the analytical expressions for ω_s^2 – *circular eigen frequencies of the vibration modes of separate chains in* the double DNA chain helix are

$$\begin{aligned} \omega_s^2&=\frac{K}{J}\Big[2\sin^2\frac{\varphi_s}{2}+\frac{K_{\alpha\beta}r_\alpha(r_\alpha-r_\beta)}{K}-\frac{K_{\alpha\beta}}{2K}\Big(1-\frac{\omega_{\alpha\beta2}}{\omega_{\alpha\beta1}}\Big)(r_\alpha-r_\beta)^2\Big]\\ \omega_s^2&=\frac{K}{J}\Big[2\sin^2\frac{\vartheta_s}{2}+\frac{K_{\alpha\beta}r_\alpha(r_\alpha-r_\beta)}{K}\Big] \end{aligned} \tag{5.5}$$

— first case: both ends of the double DNA chain helix are free (see Fig. 3)

$$\begin{aligned} \omega_s^2&=\frac{K}{J}\Big[2\sin^2\frac{s\pi}{2n}+\frac{K_{\alpha\beta}r_\alpha(r_\alpha-r_\beta)}{K}-\frac{K_{\alpha\beta}}{2K}\Big(1-\frac{\omega_{\alpha\beta2}}{\omega_{\alpha\beta1}}\Big)(r_\alpha-r_\beta)^2\Big]\\ \omega_s^2&=\frac{K}{J}\Big[2\sin^2\frac{s\pi}{2n}+\frac{K_{\alpha\beta}r_\alpha(r_\alpha-r_\beta)}{K}\Big] \end{aligned} \tag{5.6}$$

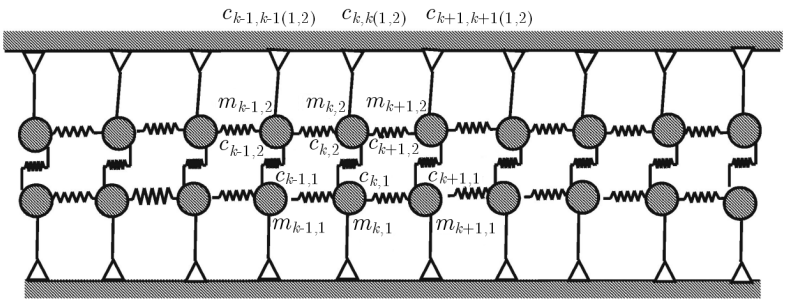

Fig. 3. Double DNA chain helix in form of a multipendulum model with free ends

— second case: both ends of the double DNA chain helix are fixed (see Fig. 4)

$$\omega_s^2 = \frac{K}{J}\Big[2\sin^2\frac{s\pi}{2(n+1)} + \frac{K_{\alpha\beta}r_\alpha(r_\alpha - r_\beta)}{K} - \frac{K_{\alpha\beta}}{2K}\Big(1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}}\Big)(r_\alpha - r_\beta)^2\Big]$$
$$\omega_s^2 = \frac{K}{J}\Big[2\sin^2\frac{s\pi}{2(n+1)} + \frac{K_{\alpha\beta}r_\alpha(r_\alpha - r_\beta)}{K}\Big] \tag{5.7}$$

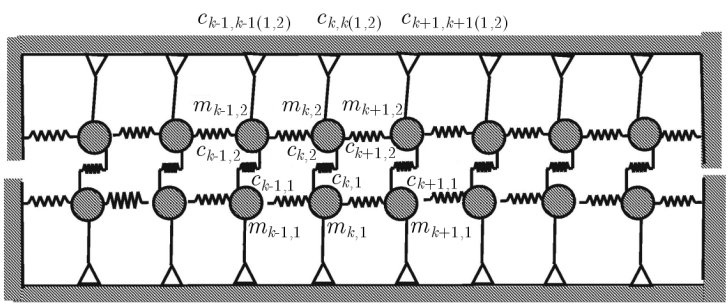

Fig. 4. Double DNA chain helix in form of a multipendulum system with fixed ends

6. Concluding remarks

At the end, we can conclude that the new coordinates of ξ_k and η_k composed by generalized coordinates in as $\xi_k = \varphi_{k,1} - \varphi_{k,2}$ and $\eta_k = \varphi_{k,1} + \varphi_{k,2}$ are main coordinates of the double DNA chain helix and that it is possible to obtain two fictive decoupled and separated single eigen chains of the double DNA chain helix linear model. This is the first fundamental conclusion as an important property of the linear model of vibrations in the double DNA helix. Considered

as a linear mechanical system, a DNA molecule as a double helix has its circular eigen frequencies and that is its characteristic. Mathematically, it is possible to decuple it into two chains with their own circular eigen frequencies which are different. This may correspond to different chemical structure (the order of base pairs) of the complementary chains of DNA. We are free to propose that every specific set of the base pair order has its circular eigen frequencies, and it changes when DNA chains are coupled in the system of double helix. DNA as a double helix in a living cell can be considered as a nonlinear system, but under certain conditions its behaviour can be described by linear dynamics.

Additionally, analytical expressions for the quadrate of ω_s – circular eigen frequencies of the vibration modes of separate chains of the homogeneous double DNA chain helix are obtained. By using these results, it is easy to consider these values as a series of resonant frequencies under external multi-frequency excitations, and also as the reason for the appearance of dynamical absorbtion phenomena as well as some explanation of real processes in the homogeneous double DNA chain helix. Next considerations will be focused on small nonlinearity in the double DNA chain helix vibrations and rare nonlinear phenomena such as resonant jumps and energy interactions between nonlinear modes.

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Postacie własne drgań podwójnego łańcucha helisy DNA

Streszczenie

W literaturze można spotkać opis różnych modeli sprzężonych drgań jednorodnego łańcucha DNA. W prezentowanej pracy rozważania oparto na zlinearyzowanym modelu Kovalevej i Manevicha (2005, 2007) do wydzielenia głównych podukładów łańcuchowych podwójnej helisy DNA. Uzyskano analityczne wyrażenia na częstości własne jednorodnego modelu helisy i odpowiadające im postacie własne oraz potwierdzono możliwość wystąpienia rezonansów i dynamicznej absorpcji drgań przy obecności wymuszeń zewnętrznym polem sił. Zidentyfikowano dwa zbiory współrzędnych normalnych helisy DNA potrzebnych do separacji układu na dwa rozprzężone łańcuchy. Niewykluczone, że mogą one odpowiadać rzędowi podstawowych komplementarnych podwójnych łańcuchów DNA w żywej komórce.

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