Considering Vibrations of the Double DNA Main Chains Via a Model with Hereditary Properties

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Abstract: Using a basic approach to DNA mathematical models published by N. Kovaleva, L. Manevich in 2005 and 2007, and investigated by authors, a corresponding linearized model, we consider the double DNA (dDNA) as a system with elements with hereditary properties to obtain main chain subsystems of the double DNA. Analytical expressions of the eigen circular frequencies for the homogeneous linearized model of the dDNA chain helix are used to obtain corresponding eigen hereditary properties vibration modes. We identified two sets of eigen normal coordinates of the DNA hereditary properties chain helix for separation of the system into two uncoupled hereditary properties chains. The results open possibilities for different approach to explaining the behavior of the double DNA chain helix and of transfer of oscillatory signals trough the chains. Under certain sequences it is possible that oscillatory signal is transferred only through one main eigen chain. This may correspond to base pair order and translation process in complementary hereditary properties chains of DNA double helix in a living cell. Corresponding integral-differential equations are obtained and analyzed.

Keywords: DNA, double chain system, eigen main chains, eigen modes, hereditary vibration modes, DNA models by N. Kovaleva and L. Manevich, visco-elastic properties, creep properties..

1. INTRODUCTION

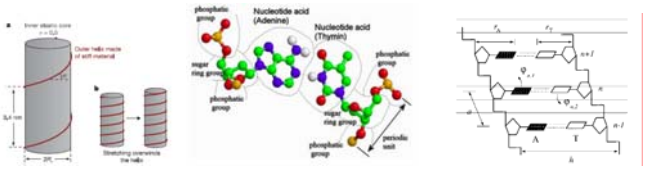
DNA is a biological polymer that chemically consists of two long polymers of simple units called nucleotides, with backbone made of sugars and phosphate groups joined by ester bonds. One of four types of molecules called bases is attached to each sugar. Two bases on opposite strands are linked via hydrogen bonds holding the two strands of DNA together. It is the sequence of these four bases along the backbone that encodes information. The basic function of DNA in the cell is to encode the genetic material. For using that information to make proteins, DNA molecule has to interact with other molecules in the cell nucleus. DNA molecules can be considered to be a mechanical structure on the nano level. There are different approaches to studding the mechanical properties of the DNA molecule (experimental, theoretical modeling). 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 strands of DNA together compared to the strength of bonds within each strand.

In the papers by Hedrih (Stevanović) K. and Hedrih A. (2008, 2009, 2009a, 2009b and 2009c) using a basic approach to DNA mathematical models published by N. Kovaleva, L. Manevich (2005 and 2007), and investigated corresponding linearized model, we consider the double DNA (dDNA) as a system with elastics elements and with a fractional order elements as well as a analogous system with hereditary properties of elements to obtain main chain subsystems of the double DNA. Analytical expressions of the eigen circular frequencies for the homogeneous linearized model of the dDNA chain helix are used to obtain corresponding eigen fractional order creep vibration modes. We identified two sets of eigen normal coordinates of the DNA fractional order chain helix for separation of the system into two uncoupled fractional order chains. The visualization of the eigen fractional order creep vibration modes of the double DNA fractional order chain helix is presented.

The results open possibilities for different approach to explaining the behavior of the double DNA chain helis and of transfer of oscillatory signals trough the chains. Under certain sequences it is possible that half number multi frequency oscillatory signals are transferred only through one eigen main chain. This may correspond to base pair order and translation process in complementary fractional order chains of DNA double helix in a living cell. Expressions for the kinetic and potential energy as well as energy interaction between chains in the double DNA chain helix are obtained and analyzed for a linearized model. Also, for the eigen main chains of the double DNA chain helix are defined and corresponding expressions of the kinetic and potential energies of these uncoupled main chains. By obtained expressions we concluded that no energy interaction between

eigen main chains of the double DNA chain helix. Time expressions of the main coordinates of the two eigen main chains are expressed by time, and eigen circular frequencies. Also generalized coordinates of the double DNA chain helix are expressed by time and eigen circular frequencies.

A number of mechanical models of the DNA double helix have been proposed till today (see Fig. 1 and Refs. Arsuaga, J. and Other.(2002), Behe M.,and Other. (1981), Brukner and Other. (1994), Bryant and Other (2003), Frontali and Other (1979), Gore and Other (2006), Lu Tsai and Liaofu Luo, (2000), Lu Tsai and Liaofu Luo, (2000), Lance M. Westerhoff, Kenneth M. Merz Jr., (2006), Peck and Other (1981), Tung and Harvey (1984), Westerhoff and Merz (2006)). Different models are focusing on different aspects of the DNA molecule (biological, physical and chemical processes in which DNA is involved). In a double DNA helix a localized excitation (breather) can exist which corresponds to predominant rotation of one chain and small perturbation of second chain using coarse-grained model of DNA double helix. In this model, each nucleotide is represented by three beads with interaction sites corresponding to a phosphate group, the group of sugar ring, and the base (see Ref. Kovaleva N., Manevich L., (2005)). N. Kovaleva and L. Manevich (2007) point out that solitons and breathers play a functional role in DNA chains.



a* **b*** **c***

Figure 1. a* "Toy mechanical" model of DNA by Jeff Gore, Zev Bryant, Marcelo (2006) **b*** The model scheme of a double helix on six coarse-grained particles (Torvik and Other (1984)); **c*** Fragment of the DNA double chain consisting of three AT base pairs (Kovaleva and Manevich L., (2005)).

In a model, the DNA backbone is reduced to the polymeric structure and the base is covalently linked to the center of sugar ring group, thus a DNA molecule with N nucleotides corresponds to 3N interaction centers. Starting from a coarse-grained off-lattice model of DNA and using cylindrical coordinates, authors derive simplified continuum equations corresponding to vicinities of gap frequencies in the spectrum of linearized equations of motion. It is shown that obtained nonlinear continuum equations describing modulations of normal modes, admit spatially localized solitons, which can be identified with breathers. Authors formulated conditions of the breathers existence and estimate their characteristic parameters. The relationship between derived model and more simple and widely used models is discussed. The analytical results are compared with the data of a numerical study of discrete equations of motion (See Figure 1.b*).

2. LINEARIZED MODEL AND SET OF THE DOUBLE DNA XHAIN HELIX OF THE EIGEN MAIN CHAINS

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 rotation motions around their own chain, being all the time perpendicular to it. Authors accepted as generalized (independent) coordinates $\varphi_{k,1}$ that are the angular displacement of the k-th base of the first chain, and as generalized (independent) coordinates $\varphi_{k,2}$ is the angular displacement of the k-the base of the second chain. Here $\mathbf{J}_{\mathbf{k},1}$ is the axial moment of mass inertia of the k-th base of the first chain; $\mathbf{J}_{\mathbf{k},2}$ is the axial moment of mass inertia of the k-th base of the second chains (for the detail see Ref. Kovaleva and Manevich, 2005).

Parameter $K_{k,i}$, $i=1,2$ characterizes the potential energy of interaction of the k-th base with the $(k+1)$-th one along the i-th chain. There are different estimations of rigidity. For the calculation we use the most appropriate value that is close to $K_{k,i}=K=6\times10^3[kJ/mol]$. By using the following notations (see Refs. [12-14]):

$$\kappa=\frac{K_{\alpha\beta}}{2K}\left(1-\frac{\omega_{\alpha\beta2}}{\omega_{\alpha\beta1}}\right)\left(r_\alpha-r_\beta\right)^2,\ \mu=\frac{K_{\alpha\beta}r_\alpha\left(r_\alpha-r_\beta\right)}{K},\ u=\frac{\mathbf{J}}{K}\omega^2 \qquad (1)$$

the corresponding analytical expressions of the square of ω - eigen circular frequencies of vibration modes of separate main chains of linearized double DNA chain helix model, obtained by trigonometric method (see Refs. Rasković (1965) and Hedrih (Stevanović) (2006)) are:

$$\omega^2_{\xi,s}=\frac{K}{J}\left[2\sin^2\frac{\varphi_s}{2}+(\mu-\kappa)\right]\ \text{ and }\ \omega^2_{\eta,r}=\frac{K}{J}\left[2\sin^2\frac{\vartheta_r}{2}+\mu\right] \qquad (2)$$

where φ_s and $\vartheta_r, s, r=1,2,3,....,n$ depend of the boundary chain conditions.

3. STANDARD LIGHT HEREDITARY ELEMENT

Light standard coupling element of negligible mass in the form of axially stressed rod without bending, and which has the ability to resist deformation under static and dynamic conditions. *Light standard hereditary element* for which the constitutive stress-strain relation for the restitution force as the function of element elongation is given by integral member in the form

$$P(t)=-c_0\left[x(t)-\int_0^t R(t-\tau)x(\tau)d\tau\right]=-c_0\left[x(t)-I\ [x(t)]\right] \qquad (3)$$

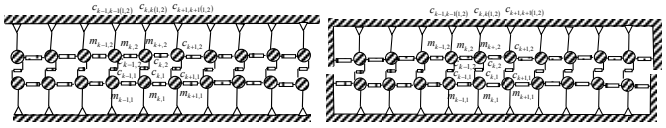
where $R(t-\tau)=\frac{c_\sigma-c_0}{nc_\sigma}e^{-\frac{1}{n}(t-\tau)}$ is relaxation kernel, n, c and $\widetilde{c}$ are coefficients of the rigidity, momentaneous and prologues one and tome relaxation , $\beta=\frac{1}{n}$ is coefficient of the element relaxation (for detail see Monograph Goroško and Hedrih (Stevanović) (2001) and Ref. Hedrih (Stevanović) (2006) and

$$I\ [x(t)]=\left[\int_0^t R(t-\tau)x(\tau)d\tau\right]=\left(\int_0^t R(t-\tau)\bullet(\tau)d\tau\right)x(t) \qquad (4)$$

integral operator.

4. THE DOUBLE DNA HEREDITARY CHAIN HELIX MODEL ON THE BASIS OF KOVALEVA-MANEVICH'S DNA MODEL

For the double DNA hereditary chain model on the basis of the linearized Kovaleva-Manevich's DNA model (see Refs. Kovaleva-Manevich (2005) and (2007)), we accept the two chains as they are presented in Figure 2. in the form of the double chain system containing two coupled multi pendulum subsystem, in with corresponding material particles of the corresponding multi-pendulum chains are each two inter coupled by one standard light hereditary element (see Refs. Gorosko and Hedrih (Stevanović) (2001)).



a* b*

Figure 2. Double DNK fractional order (or/and hereditary) chain helix in the form of multi-pendulum model with free (a*) and fixed (b*) ends.

Then we can use a system of coupled linear differential equations (see Refs. [16], [12], [13], [14]) extended by members containing integral operators in the form (5)-(6). Then we can write a corresponding system of coupled integral-differential equations for the homogeneous double DNA hereditary chain helix in the form:

$$\frac{2\mathbf{J}}{K}\ddot{\varphi}_{\mathbf{k},\mathbf{1}}-\left[\left(\varphi_{\mathbf{k}+1,\mathbf{1}}-\varphi_{\mathbf{k},\mathbf{1}}\right)-\left(\varphi_{\mathbf{k},\mathbf{1}}-\varphi_{\mathbf{k}-1,\mathbf{1}}\right)\right]-I\left[\left(\varphi_{\mathbf{k}+1,\mathbf{1}}-\varphi_{\mathbf{k},\mathbf{1}}\right)-\left(\varphi_{\mathbf{k},\mathbf{1}}-\varphi_{\mathbf{k}-1,\mathbf{1}}\right)\right]+$$
$$+2\mu\varphi_{\mathbf{k},\mathbf{1}}-\kappa\left(\varphi_{\mathbf{k},\mathbf{1}}-\varphi_{\mathbf{k},2}\right)-\kappa I\left[\left(\varphi_{\mathbf{k},\mathbf{1}}-\varphi_{\mathbf{k},2}\right)\right]=0 \tag{5}$$

$$\frac{2\mathbf{J}_{\mathbf{k},2}}{K_{\mathbf{k},2}}\ddot{\varphi}_{\mathbf{k},2}-\left[\left(\varphi_{\mathbf{k}+1,2}-\varphi_{\mathbf{k},2}\right)-\left(\varphi_{\mathbf{k},2}-\varphi_{\mathbf{k}-1,2}\right)\right]-I\left[\left(\varphi_{\mathbf{k}+1,2}-\varphi_{\mathbf{k},2}\right)-\left(\varphi_{\mathbf{k},2}-\varphi_{\mathbf{k}-1,2}\right)\right]+$$
$$+2\mu\varphi_{\mathbf{k},2}+\kappa\left(\varphi_{\mathbf{k},\mathbf{1}}-\varphi_{\mathbf{k},2}\right)+\kappa I\left[\left(\varphi_{\mathbf{k},\mathbf{1}}-\varphi_{\mathbf{k},2}\right)\right]=0$$

as our intention is to use previous double DNA hereditary chain model for the case of the homogeneous system parameters we take into account that: $K_{\mathbf{k},\mathbf{1},\sigma}=K_{\mathbf{k},2,\sigma}$=K. By using change of the generalized coordinates $\varphi_{k,1}$ and $\varphi_{k,2}$ for k-th bases of both chains in the DNA model into following new ξ_k and η_k by the following dependence: $\xi_k=\varphi_{k,1}-\varphi_{k,2}$ and $\eta_k=\varphi_{k,1}+\varphi_{k,2}$, previous system of differential equations (6) obtains the following form:

$$\frac{2\mathbf{J}}{K}\ddot{\xi}_{\mathbf{k}}-\xi_{k-1}+2\xi_k-\xi_{k+1}+I\left[-\xi_{k-1,}+2\xi_k-\xi_{k+1}\right]+2\mu\xi_{\mathbf{k}}-2\kappa\xi_{\mathbf{k}}-2\kappa I\left[\xi_{\mathbf{k}}\right]=0 \tag{6}$$

$$\frac{2\mathbf{J}}{K}\ddot{\eta}_{\mathbf{k}}-\eta_{k-1,}+2\eta_k-\eta_{k+1}+I\left[-\eta_{k-1,}+2\eta_k-\eta_{k+1}\right]+2\mu\eta_{\mathbf{k}}=0,$$
$$k=1,2,3,.....,n \tag{7}$$

First series (6) of the previous system of integral-differential equations is decoupled and independent in relation to the second series (11) of integral-differential equations. *Then we can conclude that new coordinates of* ξ_k *and* η_k *are main coordinates of double DNA hereditary chains and that we obtain two fictive decoupled eigen* hereditary, different, *chains of the double DNA hereditary chain helix model. This is the second fundamental conclusion as an important property of the hereditary order homogeneous model of vibrations in a* double DNA hereditary homogeneous helix.

Systems of integral-differential equations (10)-(11) contain two separate subsystems of integral-differential equations expressed by *coordinates of* ξ_k *and* η_k which are main *coordinates of eigen main chains of a double DNA fractional order chain helix and separate DNA hereditary model into two independent hereditary chains*. We can see that there are full mathematical analogy and phenomenological mapping between two models: a double DNA fractional order chain helix model and a double DNA hereditary chain helix.

5. THE MAIN PARTIAL HEREDITARY OSCILLATOR OF THE DOUBLE DNA HEREDITARY CHAIN HELIX MODEL

By using system the (6)-(7) of uncoupled integral-differential equations and as corresponding subsystems of eigen main chains of the corresponding model of double DNA hereditary chain helix vibrations we can obtain corresponding main coordinates $\zeta_{\varsigma,s}$ and $\zeta_{\eta,r}, r,s=1,2,3,...,n$ and corresponding double subsystems of the main partial hereditary oscillators described by the following uncoupled integral-differential equations containing each only one normal coordinate from the two subsets $\zeta_{\varsigma,s}$ and $\zeta_{\eta,r}$:

$$\ddot{\zeta}_{\varsigma,s}+\omega_{\xi,s}^2\zeta_{\varsigma,s}+\omega_{\xi,s}^2 I\left[\zeta_{\varsigma,s}\right]=0,\ s=1,2,3,4,...,n \tag{8}$$

$$\ddot{\zeta}_{\eta,r}+\omega_{\eta,r}^2\zeta_{\eta,r}+\omega_{\eta,r}^2 I\left[\zeta_{\eta,r}\right]=0,\ r=1,2,3,..,n \tag{9}$$

In the previous systems (8)-(9) square of the eigen frequencies, $\omega_{\xi,s}^2$ and $\omega_{\eta,r}^2$ of the linearized systems are defined by expression (2).

6. SOLUTION OF THE MAIN PARTIAL HEREDITARY OSCILLATOR

For to obtain solutions of the previous derived integral-differential equations (8) and (9), all equal mathematical type:

$$\ddot{y}(t)+\omega_0^2\left[y(t)-\int_{-\infty}^{t}R(t-\tau)y(\tau)d\tau\right]=\tilde{F}(t) \tag{10}$$

To determine by unique way a solution of the previous integral-differential equation it is necessary to define the initial condition. Initial condition is possible to express by following:

$$y(0)=y_0\quad \dot{y}(0)=\dot{y}_0 \tag{11}$$

In these cases initial conditions are defined in classical way by initial position $y(0)$ and initial velocity $\dot{y}(0)$ of the material particle.

History of the rheological standard hereditary element loading in these integral-differential equations is taken into account by integral members in the period of integration $(-\infty,0)$ For solving differential equation (11) in every case, initial conditions are defined by three initial conditions $y(0), \dot{y}(0)$ and $\ddot{y}(0)$. In these cases initial conditions are defined by initial position $y(0)$, initial velocity $\dot{y}(0)$ and initial acceleration $\ddot{y}(0)$ of the material particle. Last initial condition initial acceleration $\ddot{y}(0)$ of the material particle is

directly defined from stress-strain state of the standard hereditary (rheological) element on the basis of element loading history. Particular examples to obtain or to define the third initial condition in accordance of the different loaded element history are presented in the Refs. Goroško and Hedrih (Stevanović) K., (2001) and (2008). In these cited Refs. a detailed schema for to obtain initial conditions of the hereditary oscillator in the case of the impulse external excitations is presented.

6.1. Estimations of the frequency, decrement and coefficient of the rheology of the hereditary oscillator.

Characteristic equations for differential equation (10) of oscillations of the partial hereditary oscillator have the following form (see Refs, Goroško and Hedrih (Stevanović) K., (2001) and (2008)):

$$n\lambda^3+\lambda^2+n\omega_0^2\lambda+\omega_0^2 k=0\,,\ k=\frac{\widetilde{c}}{c} \tag{11}$$

Lets present the roots of the previous equation in the complex form

$$\lambda_0=-\delta_0\ ,\ \ \lambda_{1,2}=-\delta\pm i\omega \tag{12}$$

and after their introduction in the characteristic equation (11) we obtain:

$$(\lambda+\delta_0)(\lambda+\delta+i\omega)(\lambda+\delta-i\omega)=0 \tag{13}$$

After compurgation between corresponding coefficients of the corresponding exponents of equations (11) and (13), we obtain relations between kinetic parameters of the hereditary oscillator in the following forms:

$$\frac{\delta_0(\omega^2+\delta^2)}{(\omega^2+\delta^2+2\delta\delta_0)}=\omega_0^2 k\,,\ \delta_0+2\delta=\frac{1}{n}\,,\ \ (\omega^2+\delta^2+2\delta\delta_0)=\omega_0^2 \tag{14}$$

from which follow:

$$\delta_0=\frac{k}{n}\left(1+\frac{2\delta\delta_0}{\omega^2+\delta_0^2}\right) \tag{15}$$

$$\delta=\frac{1}{2n}-\frac{\delta_0}{2}=\frac{c-\widetilde{c}}{2nc}-\frac{\widetilde{c}}{nc}\frac{\delta\delta_0}{\omega^2+\delta_0^2}=\frac{1-k}{2n}-\frac{k}{n}\frac{\delta\delta_0}{\omega^2+\delta_0^2} \tag{16}$$

$$\omega^2=\omega_0^2\left[1-\frac{\delta(\delta+2\delta_0)}{\omega^2}\right] \tag{17}$$

In the first approximation, taking into account that ratio $(\delta/\omega)^2$ is small, the kinetic parameters δ_0,δ,ω of the hereditary oscillator in the first approximation are obtained in the forms:

$$\delta_0=\frac{k}{n}\,,\ \delta=\frac{1-k}{2n}\,,\ \ \omega^2=\omega_0^2 \tag{18}$$

By using expressions (18) of the first approximation and put them in the expressions (15)-(17), the kinetic parameters δ_0,δ,ω of the hereditary oscillator in the second approximation are obtained in the forms:

$$\delta_0=\frac{k}{n}\left[1+\frac{(1-k)k}{n^2\omega_0^2}\right] \tag{19}$$

$$\delta=\frac{1-k}{2n}\left[1-k^2\frac{1}{n^2\omega_0^2}\right] \tag{20}$$

$$\omega^2=\omega_0^2\left[1-(1-k)\frac{1+3k}{4}\frac{1}{4n^2\omega_0^2}\right] \tag{21}$$

By this way, values of hereditary oscillator coefficients δ_0,δ and circular frequency ω are defined by expressions (19)-(21) with high degree of precision.

By using previous considerations and approximation of the standard hereditary oscillator coefficients δ_0,δ and circular frequency ω defined by expressions (19)-(21), the solution of the equation (10) for the standard hereditary oscillator we can write in the following form:

$$y(t)=f_s\left[\frac{1}{k}+\left(\frac{k-1}{k}\right)e^{-\delta_0 t}-e^{-\delta t}\cos\omega t-\frac{3}{2}\frac{1-k}{n^2\omega^2}\sin\omega t\right] \tag{22}$$

for initial conditions $y(0)=0$, $\dot{y}(0)=0$, $\ddot{y}(0)+\widetilde{P}(0)=f_s\omega_0^2$, where $\widetilde{P}(0)=\omega_0^2 y(0)$, corresponding to applied heavy material particle with force (weight) $mg=cf_s$ and with zero initial velocity of the hereditary oscillator material particle correspond to the unstressed and non-deformed natural state of the hereditary element in the hereditary oscillator.

7. KINETIC PARAMETERS OF THE EIGEN MAIN HEREDITARY OSCILLATORS OF DOUBLE DNA HEREDITARY CAIN HELIX VIBRATIONS

By using expressions (19)-(21), two subsets of the kinetic parameters corresponding to first eigen main chain $\delta_{0(\xi,s)},\delta_{(\xi,s)},\omega_{(\xi,s)}$ and to second eigen main chain $\delta_{0(\eta,s)},\delta_{(\eta,s)},\omega_{(\eta,s)}$ of the eigen main hereditary oscillators (8)-(9) of double DNA hereditary chain helix vibrations in the second approximation are obtained in the following forms:

A* first subset:

$$\delta_{0(\xi,s)}=\frac{k}{n}\left[1+\frac{(1-k)k}{n^2\omega_{\xi,s}^2}\right]\qquad s=1,2,3,4...,n \tag{23}$$

$$\delta_{(\xi,s)}=\frac{1-k}{2n}\left[1-k^2\frac{1}{n^2\omega_{\xi,s}^2}\right] \tag{24}$$

$$\widetilde{\omega}_{(\xi,s)}^2=\omega_{\xi,s}^2\left[1-(1-k)\frac{1+3k}{4}\frac{1}{4n^2\omega_{\xi,s}^2}\right] \tag{25}$$

B* Second subset:

$$\delta_{0(\eta,r)}=\frac{k}{n}\left[1+\frac{(1-k)k}{n^2\omega_{\eta,r}^2}\right]\qquad r=1,2,3,4...,n \tag{30}$$

$$\delta_{(\eta,r)}=\frac{1-k}{2n}\left[1-k^2\frac{1}{n^2\omega_{\eta,r}^2}\right] \tag{31}$$

$$\widetilde{\omega}_{(\eta,r)}^2=\omega_{\eta,r}^2\left[1-(1-k)\frac{1+3k}{4}\frac{1}{4n^2\omega_{\eta,r}^2}\right] \tag{32}$$

8. CONCLUDING REMARKS

In the end, we can conclude that new coordinates of ξ_k and η_k composed by generalized coordinates vy the way $\xi_k=\varphi_{k,1}-\varphi_{k,2}$ and $\eta_k=\varphi_{k,1}+\varphi_{k,2}$ are main coordinates of the eigen main chains of the double DNA hereditary chain helix

and that it is possible to obtain two fictive decoupled and separated eigen single hereditary chains as two subsystems of the double DNA hereditary homogeneous chain helix model. This is the first fundamental conclusion and an important property of the hereditary model of vibrations in a double DNA hereditary helix. Considered as a hereditary mechanical system, DNA molecule as a double hereditary helix has its eigen hereditary vibration modes and that is its characteristic. Mathematically, it is possible to decuple it into two chains with their eigen modes closest to the eigen modes of the linearized models of main chains with corresponding sets of the circular 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 base pair order has its eigen circular 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 nonlinear system but under certain condition its behavior can be describe by linear dynamics.

Then, analytical expressions of the square of $\omega_{\xi,s}^2$ and $\omega_{\eta,r}^2$ - *eigen circular frequencies of the vibration modes of the separate chains* of the homogeneous double DNA chain helix are obtained. By using these results it is easy to consider these values of the system $\omega_{\xi,s}^2$ and $\omega_{\eta,r}^2$ - *eigen circular frequencies of free vibrations as series of resonant frequencies under external multi frequencies excitations, and also possibilities for the appearance of dynamical absorption phenomena and find explanation with real processes in the* homogeneous double DNA ideal-elastic/fractional order/ hereditary chain helix. Next consideration is focused on the small nonlinearity in the double DNA chain helix vibrations and rare nonlinear phenomena such as resonant jumps and energy interactions between nonlinear modes.

The analysis showed that there is no transfer of energy between main chains of the double DNA chain helix considered as a hereditary chain helix, and that transfer of energy appears only between material particles in the corresponding subset of the corresponding main chain. These results may be important for future application in theoretical and experimental medical investigations. As we take into account a hereditary no conservative model of the double DNA chain helix, then it is possible to conclude that main chains oscillate with no constant total mechanical energy and, also, with different initial main chain total energy values, as well as with different set of the eigen frequencies. Under the external one frequency excitation, in only in one main chain is possible that resonance regime appear, but also there are possibilities for dynamical absorption existence.

Transcription process of DNA is well described at biochemical level. During transcription part of double DNA is unzipped, and only one chain helix is used as a matrix for transcription. For better understanding DNA and its function it is necessary to consider its behaviour through bioelectrical and mechanical point of view. If we know what is happened to DNA at biomechanical, bioelectrical and biochemical level during transcription our understanding of its function will be more complete. This may open a wide array of possibilities of using DNA as an essential structure in technical devices.

Also, by use modification of the linearized model by introducing standard light elements with constitutive relation on the coupled fields with thermo modifications is possible to introduce a hybrid model of the double DNA chain helix with analysis of the more complex process of the transfer energy and corresponding analogy this model with real DNA system.

Acknowledgement. Part of this research was supported by the Ministry of Sciences and Technology of Republic of Serbia through Mathematical Institute SANU Belgrade Grant ON144002 "Theoretical and Applied Mechanics of Rigid and Solid Body. Mechanics of Materials" and Faculty of Mechanical Engineering University of Niš.

Part of this research was supported by the Ministry of Sciences and Technology of Republic of Serbia through Faculty of Technology, Belgrade, Grant ON142075.

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APPENDIX - NOMENCLATURE

DNA – Deoxyribonucleic acid (DNA)

$\varphi_{k,1}$ and $\varphi_{k,2}$ $[rad]$ - generalized coordinate – angles of the k -th base of the first and second chain of the double DNA chain helix;

$\mathbf{J}_{\mathbf{k},\mathbf{1}}$ and $\mathbf{J}_{\mathbf{k},2}$ $[kgm^2]$- is the axial moment of mass inertia of the k -th base of the first and second chain of the double DNA chain helix;

$\dot{\varphi}_{k,1}$ [rads^{-1}] - angular velocity of the k -th base of the first chain of the he double DNA chain helix;

$\mathbf{J}_{\mathbf{k},\mathbf{1}} = m_\alpha r_\alpha^2$, $\mathbf{J}_{\mathbf{k},\mathbf{12}} = m_\beta r_\beta^2$ $[kgm^2]$ - the base pair the axial moments of mass inertia ;

m_α $[kg]$- the value of the base mass , r_α $[m]$ - the length

$K_{k,i}$, $i = 1,2$ [KJmol^{-1}]- parameters characterize the energy of interaction of the k -th base with the $(k+1)$-th one along the i -th chain $i = 1,2$.

$K_{k,i} = K = 6 \times 10^3 [\text{KJmol} - 1]$ - for the calculation that the most appropriate value is close /

ξ_k, η_k $[rad]$, $k = 1,2,3,.....,n$ - main orthogonal coordinates of the eigen main chains of the double DNA chain helix;

$\xi_k = \varphi_{k,1} - \varphi_{k,2}$ and $\eta_k = \varphi_{k,1} + \varphi_{k,2}$, $k = 1,2,3,.....,n$

$\omega_{\alpha\beta 2}$ and $\omega_{\alpha\beta 1}$ $[\sec^{-1}]$ - are frequencies of rotational motions of the bases, in similar and opposite directions accordingly, of the k -th base of the first chain of the double DNA chain helix;

$K_{k,1} = K_{k,2} = K$ - for the case of homogeneous double DNA chain helix;

$\omega_{\xi,s}^2$ and $\omega_{\eta,r}^2$ $[\sec^{-2}]$, $s,r = 1,2,3,4...,n$ - set of the n eigen circular frequencies of the first and second eigen main chain of the homogeneous linear double DNA chain helix;

$\tilde{\omega}_{(\xi,s)}^2$ and $\tilde{\omega}_{(\eta,r)}^2$, $s,r = 1,2,3,4...,n$ -two subsets of the set of the homogeneous double DNA chain helix frequencies in the second approximation;

$\delta_{0(\xi,s)}, \delta_{(\xi,s)}, \tilde{\omega}_{(\xi,s)}$ and $\delta_{0(\eta,s)}, \delta_{(\eta,s)}, \tilde{\omega}_{(\eta,s)}$ - kinetic parameters corresponding to first eigen main chain and to second eigen main chain of the corresponding two subset s of the eigen main hereditary oscillators of the homogeneous double DNA chain helix in the second approximation.