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Collective Excitations in DNA

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Abstract

In this contribution, a simple two-dimensional model of the DNA is presented. In this model the two polynucleotide strands are linked together through the hydrogen bonds which are described by the Morse potential. The longitudinal links between base pairs are described by anharmonic potential. The model predicts that an open state of the molecular chain in the form of nonlinear structure named cuspon, arise under certain conditions. We suggest that anharmonicity may play an important role in DNA denaturation.

1. Introduction

The dynamics of DNA transcription is one of the most fascinating problems of modern Molecular Biology because it is at the basis of life. However, it is also a very difficult problem due to the complex roles played by RNA polymerases in the process. It is now well established [1] that a local denaturation of DNA is involved in this process, so it is interesting to investigate the dynamics of the double helix as a preliminary step for understanding the transcription.

The possibility that nonlinear effects might concentrate vibrational energy in DNA into localized soliton like objects, was first developed by Krumhansl and his co-workers [2–4], who suggested a theory of soliton excitations as an explanation of the open states of DNA. Related studies of solitons in DNA have also been presented by Yomosa [5], who proposed a soliton theory using a plane base-rotor model. This model was further refined by Takeno and Homma, [6] who

allowed discreteness effects to be taken into account, and by Zhang, [7] who improved the model for base coupling. M. Peyrard and A.R. Bishop [8] investigated the statistical mechanics of a simple lattice model for the denaturation of the DNA double helix. Recently, in the work [9], we have found new effects that they called reversible and irreversible denaturation of solitons in a non stationary harmonic potential. We suggest an application of this discovery to the denaturation of the DNA.

In this paper we investigate the open states and denaturation of the DNA by means of an extension of the Peyrard model, but taking into account anharmonic interactions between successive base pairs.

2. The Model

For each base pair, the model includes two degrees

of freedom u_n and v_n which correspond to the displacements of the bases from their equilibrium positions along the direction of the hydrogen bonds that connect the two bases into a pair. Following previous investigations on DNA [8], the potential for the hydrogen bonds is approximated by a Morse potential. A harmonic coupling due to the staking is assumed between neighboring bases so that the Hamiltonian for the model is:

$$H = \sum_n \frac{1}{2} m (\dot{u}_n^2 + \dot{v}_n^2) + \frac{1}{2} k [(u_n - u_{n-1})^2 + (v_n - v_{n-1})^2] + V(u_n - v_n) \quad (1)$$

with

$$V(u_n - v_n) = D \{ \exp[-a(u_n - v_n)] - 1 \}^2.$$

For simplicity, this is an homogeneous model, so we use a common mass m for the bases and the same coupling constant k along the chain. The Morse potential represents the two or three bonds which connect the two bases in a pair.

With these assumptions, motions of the two strands can be described in terms of the variables

$$x_n = (u_n + v_n) / \sqrt{2}, \quad y_n = (u_n - v_n) / \sqrt{2},$$

which represent the in-phase and out-of-phase motions, respectively. Only the out-of-phase displacements y_n stretch the hydrogen bonds. The Hamiltonian (1) becomes

$$H = H(x) + H(y) = \sum_n \left\{ \frac{p_n^2}{2m} + \frac{1}{2} k (x_n - x_{n-1})^2 \right\} + \sum_n \left\{ \frac{q_n^2}{2m} + \frac{1}{2} k (y_n - y_{n-1})^2 + D \left\{ \exp[-a\sqrt{2}y_n] - 1 \right\}^2 \right\}. \quad (2)$$

To explore the process of the open states and denaturation, it is interesting to relate the model with the parameters that involve nonlinear excitations. Since the nonlinearities appear in terms of the variable y , we consider

$$H(y) = \sum_n \frac{m}{2} \left(\frac{dy_n}{dt} \right)^2 + W(y_n, y_{n-1}) + V(y_n) \quad (3)$$

where

$$W(y_n, y_{n-1}) \quad (4)$$

is the potential between adjacent base pairs, and

$$V(y_n) = D \left\{ \exp[-a\sqrt{2}y_n] - 1 \right\}^2 \quad (5)$$

is the Morse potential. In the harmonic approximation, the equation of motion arising from (3) is:

$$m \frac{d^2 y_n}{dt^2} - k(y_{n-1} + y_{n+1} - 2y_n) - 2\sqrt{2} a e^{-\sqrt{2} a y_n} (e^{-\sqrt{2} a y_n} - 1) = 0. \quad (6)$$

2.1. Domain Wall Between Open and Closed Regions

Although actual units are important to compare the results with experiments, for theoretical calculations, it is very useful to express the problem in terms of dimensionless quantities. It is natural to introduce the dimensionless stretching of the base pairs as $Y = ay$. If we measure the energy in units of the depth D of the Morse potential, the dimensionless Hamiltonian is $H' = H/D$, and defining the dimensionless quantity $S = k/(Da^2)$, and dimensionless time $\tau = \sqrt{Da^2/mt}$, we obtain the Hamiltonian H' only in terms of dimensionless quantities in the form

$$H' = \sum_n \frac{1}{2} P_n^2 + \frac{1}{2} S (Y_n - Y_{n-1})^2 + (e^{-Y_n} - 1)^2 \quad (7)$$

with

$$P_n = \frac{dY_n}{d\tau}$$

from which one can derive dimensionless equations of motion, that depend on a single parameter S which is equal to $S = 0.0987$ with our potential parameters. In the continuum limit, the dynamical equation resulting from Hamiltonian (3) takes the form

$$\frac{\partial^2 Y}{\partial t^2} - S \frac{\partial^2 Y}{\partial x^2} + \frac{\partial V(Y)}{\partial Y} = 0 \quad (8)$$

with

$$V(Y) = (e^{-Y} - 1)^2$$

has an exact static solution, which has a meaning for the physics of DNA.

Looking for a solution that does not depend on time, one obtains

$$-S \frac{d^2 Y}{dx^2} + \frac{\partial V(Y)}{\partial Y} = 0, \quad (9)$$

which is easily solved by quadrature. Therefore, equation (9) gives the following solution

$$Y(x) = \ln \left[1 + e^{\sqrt{2/S}(x-x_0)} \right], \quad (10)$$

where x_0 is an integration constant that determines the position of the solution.

This solution (10) describes a configuration where one part of the molecule ($x < x_0$) is closed, while for ($x \gg x_0$) the base pair separation grows linearly with space and the molecule is fully denaturated. It

corresponds to a domain wall between two states of the DNA molecule.

Let us evaluate the energy of this solution for a finite chain of N base pairs. Sites with an index smaller than x_0 are such that $Y \simeq 0$. The Morse potential and the coupling energy between adjacent sites vanish. For sites with an index larger than x_0 , $Y \gg 1$ and the Morse potential takes the value $+1$ while $dY/dx \simeq \sqrt{2/S}$ corresponds to a coupling energy $0.5S \left(\sqrt{2/S}\right)^2 = 1$. Therefore, each site with an index larger than x_0 contributes to the energy by $e = 2$. As a result, the energy of the domain wall is

$$E_P^+ = 2(N - x_0) + O(N^0),$$

where the term $O(N^0)$ corresponds to the core of the wall ($x \simeq x_0$) where Y evolves smoothly from the bottom of the Morse potential towards the plateau. In the limit $N \rightarrow \infty$ the energy of the domain wall becomes infinite.

For finite N , one can note that the energy of the wall gets smaller if x_0 increases, i.e. if the closed region of the molecule extends. Solution (10) is thus unstable. It tends to move in the direction that closes the base pairs.

3. Anharmonic Potential Between Pair of Bases

In order to improve the description of the staking interaction, i.e. the interaction between adjacent base pairs let us introduce anharmonic interaction between pair of bases. As it is well known the harmonic expression $U(y_n, y_{n-1}) = k(y_n - y_{n-1})^2/2$ resulted from an expansion of the interaction potential around its minimum. But in DNA one base pair can be open while its neighbors are not [11], which implies large values of the difference $(y_n - y_{n-1})$. Therefore, a small amplitude expansion is too rough. To derive a more appropriate potential one has to take into account its physical origin. A large contribution to the staking interaction comes from the overlap of the π electrons of the base plateaux [11]. When a base moves out of the stack, the overlap decreases and its interaction with neighboring bases weakens. The redistribution of the π electrons which occurs when hydrogen bonds are broken also contributes to this effect. The specificity of the staking interaction can be described by an improved potential which has been used in other fields of physics [12–14] and we propose here the anharmonic potential for the Eq. (4).

The Hamiltonian for this case takes the form

$$H = \sum_n \left\{ \frac{m}{2} \left(\frac{dy_n}{dt} \right)^2 + \frac{k_1}{2} (y_n - y_{n-1})^2 \right.$$

$$\left. + \frac{C_{nl}}{4} (y_{n+1} - y_n)^4 + D \left\{ e^{[-a\sqrt{2}y_n]} - 1 \right\}^2 \right\} \quad (11)$$

where we have introduced the expression for the interaction potential of the form

$$U(y_{n+1} - y_n) = \frac{C_l}{2} (y_{n+1} - y_n)^2 + \frac{C_{nl}}{4} (y_{n+1} - y_n)^4 \quad (12)$$

where

$$C_l \equiv (k_1/m)d^2 \quad (13)$$

and C_{nl} denote the strength of the linear and nonlinear coupling respectively.

The equation of motion for the n th base pair becomes

$$\begin{aligned} \frac{d^2 y_n}{dt^2} &= C_l (y_{n-1} + y_{n+1} - 2y_n) \\ &+ C_{nl} \left[(y_{n+1} - y_n)^3 - (y_n - y_{n-1})^3 \right] + \\ &+ 2\sqrt{2}aDe^{-\sqrt{2}ay_n} \left(e^{-\sqrt{2}ay_n} \right) \end{aligned} \quad (14)$$

where y_n varies slowly from one site to another, and one can use the standard continuum approximation $y_n(t) \rightarrow y(x, t)$, and expand $y_{n\pm 1}$. Under these conditions, setting $X = x/d$ (that is, measuring the distance x in units of lattice spacing d), Eq. (14) reduces to

$$\begin{aligned} \frac{\partial^2 y}{\partial t^2} &- \left[C_l + 3C_{nl} \left(\frac{\partial y}{\partial X} \right)^2 \right] \frac{\partial^2 y}{\partial X^2} \\ &- 2\sqrt{2}De^{-\sqrt{2}ay} \left(e^{-\sqrt{2}ay} \right). \end{aligned} \quad (15)$$

We then look for localized waves of permanent profile of the form $y(s) = y(X - vt)$, where $s \equiv X - vt$ is a single independent variable depending on v which is an arbitrary velocity of propagation.

Integrating Eq. (15) and taking account of these conditions, we obtain

$$\begin{aligned} 2(v^2 - C_l)y_{ss} - 3C_{nl}y_{ss}y_s^2 \\ - 2D\alpha e^{-\alpha y} (e^{-\alpha y} - 1) = 0 \end{aligned} \quad (16)$$

where $\alpha \equiv \sqrt{2}a$.

Next we define $\varphi \equiv e^{-\alpha y}$,

$$y = -\frac{1}{\alpha} \log \varphi, \quad y_s = -\frac{1}{\alpha} \frac{\varphi_s}{\varphi}$$

and substitute these values in Eq. (16) we get

$$A\varphi_s^4 - B\varphi_s^2\varphi^2 - D\varphi^5(\varphi - 2) - C\varphi^4 = 0 \quad (17)$$

with $B = \frac{2(v^2 - C_l)}{2} \frac{1}{\alpha^2}$, $A = \frac{3}{4} C_{nl} \frac{1}{\alpha^4}$,

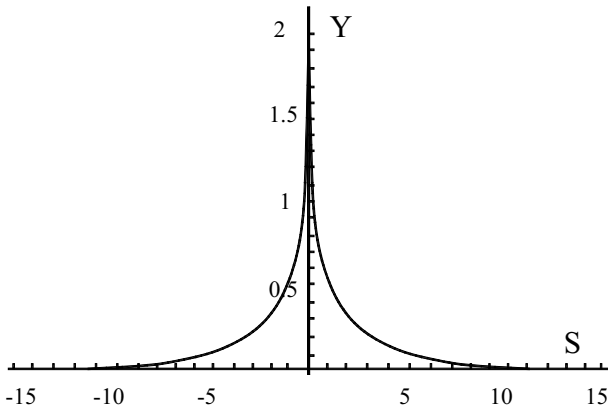


Fig. 1. Typical soliton like structure that resembles the well known peak solution. The x- axe represents the base pair number and y-axis indicates the stretching of the hydrogen bond.

4. Solutions

We now analyze the Eq. (17) and try to characterize the solitonic patterns if they exist. In order to do this we begin with a primary constriction: the essential features of physically available solutions are determined by imposing the boundary condition. Traveling wave solutions $y(s) = y(x - vt)$ with constant velocity v can also be obtained when the boundary conditions are determined by the expressions

$$y \rightarrow y_0, s \rightarrow \pm\infty, \varphi \rightarrow \varphi_0, \varphi_s \rightarrow 0. \tag{18}$$

As a result of the application of the boundary condition (18) from Eq. (17) we obtain

$$D\varphi_0^5(\varphi_0 - 2) + C\varphi_0^4 = 0 \tag{19}$$

solving for φ_0 one obtains $\varphi_0 = 1 \pm \sqrt{1 - C/D}$. From which, if $C = 0$, then we have two values $\varphi_0 = 2$, and $\varphi_0 = 0$.

In order to solve the differential equation (17), it seems natural to introduce the following ansatz. Soliton like structures are available if the parameters of the model satisfy the following relation:

$$v^2 = C_l + \sqrt{3C_{nl}D}. \tag{20}$$

After some algebra the solutions can be found analytically and, several cases can be considered from the physical point of view. The first case is done when we have the following field $\varphi_0 = 2$. In this case the solution can be represented as

$$\varphi = 2 \text{Tanh}^2 \left(\frac{1}{2} \sqrt{B/A} (s - s_0) \right)$$

that finally one obtains the non-analytic solution named *cuspon* (see figure 1)

$$y + y_0 = -\frac{1}{\alpha} \text{Log} \left[\text{Tanh}^2 \left(\frac{1}{2} \sqrt{B/A} (s - s_0) \right) \right]. \tag{21}$$

with

$$y_0 = -\frac{1}{\alpha} \text{Log} [2].$$

5. Numerical Values in the Process of Denaturation of DNA

The parameters we use have been calibrated by comparison with experiments, in particular the thermal denaturation. The parameters for $V(y)$ are: $D = 0.03 \text{ eV}$, which is slightly above $k_B T$ at room temperature. (k_B being the Boltzmann constant) and $a = 4.5 \text{ \AA}^{-1}$. The chosen value for k_l is $k_l = 0.06 \text{ eV/\AA}^2$ see Eq. (13), which corresponds to a weak coupling between the bases and $C_{nl} = 0.026 \text{ eV/\AA}^4$. The average masses of bases is $m = 230 \text{ amu}$. The distance d between adjacent bases is $d = 3.4 \text{ \AA}$.

The values have been given with a system of units adapted to the scales of the problem: length unit: 1 *Angstrom*; mass unit: 1 *amu*; energy unit: 1 *eV*; this defines a time unit t_0 by means of the relation $e = ml^2 t_0^{-2}$ that gives a value for the time

$$t_0 = 1.018 \cdot 10^{-14} \text{ s} \tag{22}$$

whose inverse is

$$v = 9.8 \cdot 10^{13} \text{ Hz} \tag{23}$$

which is inside the Infra Red region of the electromagnetic spectrum.

From Eq. (21) we can obtain the pulse length, and after substituting the corresponding values we obtain

$$L \approx 24 \text{ bp (base pairs)} \tag{24}$$

when compared with experimental data [2], $L = 10 \text{ bp}$, we notice that there is a slight difference, however it is important to notice that as shown in figure (1), there is a little region inside the pulse which overcomes the needed energy to break the hydrogen bond and this region would be $L \approx 10 \text{ bp}$, which we consider as the open state of the DNA.

From the continuum approximation of Eq. (11) using Eqs. (5) and (12), one can calculate the total (kinetic and potential) energy localized in the traveling pulse:

$$E = 0.0618 \text{ eV}. \tag{25}$$

When we compare this energy with experimental results [15,16], $E = 0.26 \text{ eV}$ we notice some differences, however we must take into account that our model is homogeneous, i.e., it considers only one kind of base pair. When heterogeneity is taken into account, the energy may change since it depends on

the sequence of base pair [17]. Finally, from Eq. (20), we can calculate the pulse velocity to obtain:

$$v = 4 \text{ bp/ps.} \quad (26)$$

The experimental data available indicate the velocity of a “bubble” as 1 pb/ns^2 . Here is important to notice that this value depends strongly on the parameter k_1 , i.e, the coupling constant in the molecule, which has not been exactly determined. Therefore the value we have obtained could be improved once k_1 has been determined experimentally by means of Infra Red or Raman spectroscopy.

6. Conclusions

In this paper, a simple two-dimensional model for the DNA has been presented. Particular attention has been devoted to longitudinal wave propagation from an anharmonic perspective. We have compared the harmonic with anharmonic approximation and results indicate that the anharmonic interaction could play a role in the process of open state of the DNA which are the precursors for the denaturation of the molecule. Thus, anharmonicity may play an important role in the dynamical process of the DNA allowing the appearance of nonlinear structures named cusps that model the behavior of hydrogen bonds.

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