Materials and Devices
An International Scientific Journal
OPEN ACCESS Freely Accessible Scientific Papers.
CA-IP
Managed by scientists for Science - http://co-ac.com

Article type: A-Regular research paper

Investigation of DNA denaturation from generalized Morse potential

R. El Kinani (1), H. Kaidi (2), M. Benhamou (3)
(1) Physics Department, Faculty of Sciences P.O. Box 11201, Moulay Ismail University, Meknes, Morocco, radouane_kin@yahoo.fr
(2) CRMEF, P.O. Box 255, Meknes, Morocco, hamidkaidi@gmail.com
(3) Physics Department, Faculty of Sciences P.O. Box 11201, Moulay Ismail University, Meknes, Morocco, benhamou.mabrouk@gmail.com

Correspondingauthor: *radouane_kin@yahoo.fr*

RECEIVED: 18 january 2018 / RECEIVED IN FINAL FORM: 30 june 2018 / ACCEPTED: 02 july 2018

Abstract: In this paper, we present a non-linear model for the study of DNA denaturation transition. To this end, we assume that the double-strands DNA interact via a realistic generalized *Morse potential* that reproduces well the features of the real interaction. Using the *Transfer Matrix Method*, based on the resolution of a Schrödinger equation, we first determine *exactly* their solution, which are found to be *bound states*. Second, from an exact expression of the ground state, we compute the denaturation temperature and the free energy density, in terms of the parameters of the potential. Then, we calculate the contact probability, which is the probability to find the double-strands at a (finite) distance apart, from which we determine the behaviour of the mean-distance between DNA-strands. The main conclusion is that, the present analytical study reveals that the generalized Morse potential is a good candidate for the study of DNA denaturation.

Keywords : DNA, INTERACTIONS, GENERALIZED MORSE POTENTIAL, DENATURATION TRANSITION, FREE ENERGY.

Introduction

Deoxyribonucleic acid, more commonly known as DNA, is a complex molecule that contains all of the information necessary to build and maintain an organism. All living things have DNA within their cells. In fact, nearly every cell in a multicellular organism possesses the full set of DNA required for that organism. However, the dynamics of DNA transcription is among the most fascinating problems of modern biophysics, because it is at the basis of life. It is also a very difficult problem due to the complex role played by RNA polymerases in the process. It is now well established (Freifelder, 1987) that the local denaturation of DNA is involved, so that it is interesting to investigate the thermal denaturation of the double-helix as a preliminary step to the understanding of the transcription (Fig. 1).

DNA denaturation is a process that refers to the melting of the double-stranded DNA into two single strands. In fact, such a phenomenon originates from the breaking of hydrogen bonds between the bases in the duplex. Thermodynamically speaking, the major contribution to DNA helix stability is the stacking of the bases on top of one another. Hence, in order to denature DNA, the main obstacle to overcome is the stacking energies providing cohesion between adjacent base pairs.

Moreover, studies of molecular dynamics and structure of nucleic acids are of general importance for the understanding of their functions. As such they have been subject of several theoretical and experimental investigations. Because of the importance of the functions played by DNA denaturation in replication, transcription and recombination processes, many theoretical and experimental techniques have been developed to study melting or strand separation of DNA.

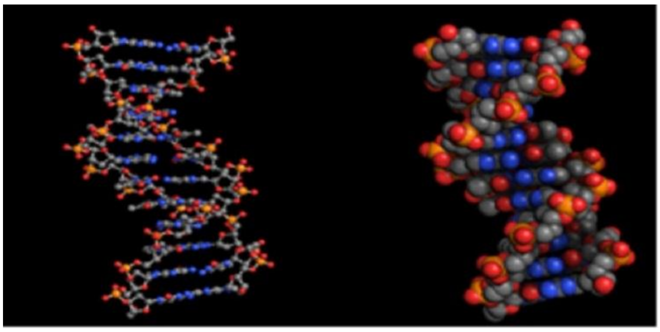

Figure 1: Double-helix structure of DNA shown in a full atomic representation bursts (left) and representation compact (right).

The physics of DNA thermal denaturation (or melting), that is the separation of the two strands upon heating, is a subject which has a long history [1]-[3], because it can be viewed as a preliminary for the understanding transcription.

The separation of the two complementary strands starts locally by the formation of small denatured regions, very similar to the transcription bubble. Another important motion of the DNA molecule is its "breathing" or fluctuational opening.

In these very large fluctuations, the base-pairs are temporarily broken, and the two bases are exposed for chemical reaction, for a very short time (10^{-7}s). These fluctuational openings can be considered as intrinsic precursors for the denaturation, and they could play a role in carcinogenesis by external molecules [4]. The wide interest in this problem is also motivated by the fact that UV absorption spectroscopy experiments [5]-[6] indicate that the whole denaturation process looks like a chain of sharp first-order-like phase transitions, in the sense that large portions of inhomogeneous DNA sequences separate over narrow temperature intervals.

The molecular deformation involved in melting or in fluctuational openings, is so large that they cannot be described by linear approximations Therefore, biomolecular dynamics is a fascinating topic for nonlinear science, because it is related to basic phenomena of life and one knows that it has to be fundamentally nonlinear.

We point out that the first model for the study of DNA denaturation is Ising-like, which represents a base-pair by a variable taking only two values, 0 and 1, i.e., closed and open. The denaturation transition is then analyzed by treating the Statistical Mechanics of this one-dimensional Ising-spin chain. The best known model in this category is that introduced by Poland and Scheraga [7]. In our case, we have adopted some model introduced by Dauxois, Peyrard and Bishop [8], with a change in the level of the interaction potential between the bases of the double-helices. The model by Dauxois, Peyrard and Bishop considers a simplified geometry for DNA chain, where one neglects the asymmetry of the molecule and represents each strand by a set of point-like masses corresponding to the nucleotides. We emphasize that, in their model, Peyrard and Bishop [8] adopted the standard Morse potential (MP) [9] that depends on three kinds of parameters. Such a potential reproduces well the main characteristics of the real potential, namely repulsive at short-distance (steric interaction) and attractive (van der Waals interaction), at high-distance.

We discuss here some aspects of DNA dynamics and we show that simple nonlinear models can provide a good description of the large amplitude distortions of the molecule, which are observed experimentally. Our basic approach can be viewed as an extension of Ising models, which have been widely used to study the Statistical Mechanics of the melting, in which we treat completely the dynamics of the bases.

In this work, we re-examine the study of the denaturation of DNA, using an extended Peyrard and Bishop model [8], where the standard MP is replaced by a more realistic one we introduce for the first time, termed q-MP, with a real parameter, q (see below). Such a new potential reduces to the standard MP for $\mathrm{q} = 0$, and to that of Dang-Fan potential [10], for $\mathrm{q} = -1$. In this sense, the q-MP is more general. In addition, the introduction of this new potential is that, the experimental adjustment of q-parameter may model various physical situations.

The remaining of presentation proceeds as follows. In Section 2, we describe the used model for DNA denaturation. A study of the denaturation transition is presented in Section 3. Finally, some concluding remarks are drawn in the last section.

A simple model for DNA denaturation:

The main characteristics of our model are as follows:

(i) One takes into account the transverse motions. The displacements from equilibrium of the n-th nucleotide are denoted as $\mathrm{w_n}$, for one chain, and $\mathrm{v_n}$, for the other. The longitudinal displacements are not considered, because their typical amplitudes are significantly smaller than the amplitudes of the smaller ones [11].

(ii) Two neighboring nucleotides of the same strands are connected by an harmonic potential, in order to keep the model as simple as possible. On the other hand, the bonds connecting the two bases belonging to different strands, are extremely stretched, when the double-helix opens locally, so that their nonlinearity must not be ignored. We use a generalized Morse potential to represent the transverse interaction of the bases in a pair. It describes not only the hydrogen bonds, but the repulsive interactions of the phosphate groups, partly screened by the surrounding solvent as well. The Hamiltonian of the model is then the following

$$\begin{aligned} H = \sum_n \Big\{ \frac{1}{2} m(\dot{w}_n^2 - \dot{v}_n^2) \\ + \frac{1}{2} K[(w_n - w_{n-1})^2 + (v_n - v_{n-1})^2] \\ + V_q(w_n - v_n) \Big\}, \end{aligned} \tag{1}$$

where m is the reduced mass of the bases. The contribution, $V_q(w_n - v_n)$, represents the interaction potential (q-MP) of the bases in a pair, whose form is the following

$$V_q(w_n - v_n) = D\left(\left(1 - \frac{b}{e^{\alpha(w_n - v_n)/\sqrt{2}} + q}\right)^2 - 1\right). \qquad \text{(1a)}$$

We assume that the real parameter q is such that $q > 0$ or $-1 \le q < 0$. In fact, the latter acts as an important deformation parameter. There, b is some parameter that is related to the minimum of the interaction potential, D is the potential depth and $\alpha > 0$ defines the potential-range. Notice that, the proposed potential is a *four* parameter exponential-type one, which is already pointed out in Ref. [12], and it may reduce to the most well-known exponential-type molecule potentials by choosing appropriate parameters (D, b, α, q). The values $q = 0$ and $q = -1$ describe the Morse and Deng-Fan potentials, respectively. Hence, the potential $V_q(w_n - v_n)$ is more general and may be a good candidate for the study of a large class of interacting molecular systems.

In Fig. 2, we report the q-generalized MP upon distance, for various values of the parameter q keeping fixed the other ones, (D, b, α). In particular, this figure shows that, the potential minimum is shifted towards its smaller values, as the parameter q is increased.

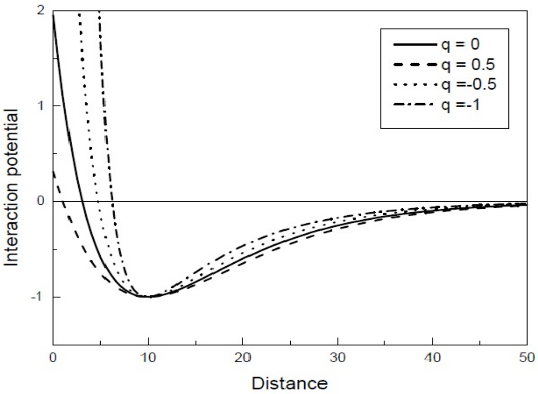

Figure 2: Reduced Morse potential, $V_q(w_n - v_n)$, versus distance, for different values of q.

Now returning to equation (1) when it is expressed in terms of the variables $x_n = (w_n + v_n)/\sqrt{2}$ and $y_n = (w_n - v_n)/\sqrt{2}$, yielding

$$H = \sum_n \Bigg[\frac{1}{2}m\dot{x}_n^2 + \frac{K}{2}(x_n - x_{n-1})^2 + \left(\frac{1}{2}m\dot{y}_n^2 + \frac{K}{2}(y_n - y_{n-1})^2\right) + D\left(\left(1 - \frac{b}{e^{\alpha y_n} + q}\right)^2 - 1\right)\Bigg]. \qquad \text{(2)}$$

The part of the Hamiltonian that depends on the variables x_n's, describes the displacement of the centre of mass of each base pair. It is well behaved, so that we can ignore this term in the Statistical Mechanics of the model. Therefore, we henceforth consider only the part of H which depends only on y_n, because it possesses the complete information on the associative dynamics of the DNA,

$$H' = \sum_n \left[\tfrac{1}{2}m\dot{y}_n^2 + \tfrac{K}{2}(y_n - y_{n-1})^2 + V_q(y_n)\right]. \qquad \text{(3)}$$

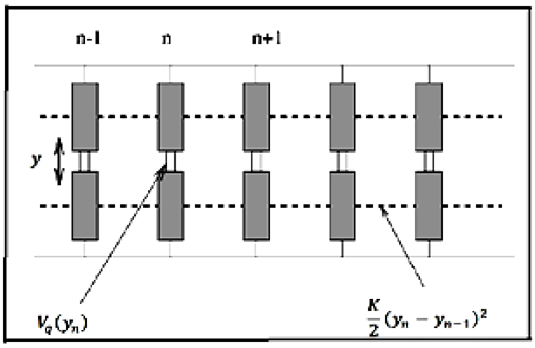

Figure 3: Schematic representation of model.

In the above expression, m is the mass of strands and $\mathrm{K} > 0$ accounts for their elastic constant.

Study of DNA denaturation and its Statistical Mechanics:

Since we are interested in the thermal denaturation of DNA, the natural approach is to make use of Statistical Mechanics. Due to the one-dimensional character of the system, and since the interactions are restricted to nearest neighbor interactions, it can be treated exactly, including fully the nonlinearities, with the transfer operator method [13].

In the canonical ensemble, the partition function of the model is related to the Hamiltonian, H_y, by

$$Z = \int_{-\infty}^{+\infty} \prod_{n=1}^{N} dy_n dp_n e^{-\beta H_y} \delta(p_1 - p_N)\, \delta(y_1 - y_N) \qquad \text{(4)}$$

with the notation $\beta = 1/k_B T$, and the Dirac-function, δ, ensures the periodic boundary conditions. The integrals over variables p_n are decoupled Gaussian integrals, which can be easily calculated to give $Z = (2\pi m k_B)^{N/2} Z_y$, and due to the one-dimensional character of the model, the configurationally part, Z_y, is a product of terms that couple two consecutive variables y_n

$$Z_y = \int_{-\infty}^{+\infty} \prod_{n=1}^{N} dy_n e^{-\beta f(y_n, y_{n-1})}\, \delta(y_1 - y_N), \qquad \text{(5)}$$

with the notation

$$f(y_n, y_{n-1}) = \tfrac{K}{2}(y_n - y_{n-1})^2 + V_q(y_n)\ . \qquad \text{(5a)}$$

Therefore, calculation of Z_y can be performed by the transfer integral (TI) method [14]-[16]. Let us define TI operator $y_{n-1} \to y_n$ and its eigenfunctions, φ_i, by

$$\int dy_{n-1} e^{-\beta f(y_n, y_{n-1})} \varphi_{i(y_{n-1})} = e^{-\beta\epsilon_i} \varphi_i(y_n)\,. \qquad \text{(5b)}$$

The δ-function in Z_y expression can be expanded in the basis of the eigenfunctions of TI operator as

$$\delta(y_N - y_1) = \sum \varphi_i^*(y_n)\varphi_1(y_1)\,. \tag{5c}$$

Performing successively integrals over variables $(y_1, y_2, y_3, \dots, y_N)$, one gets

$$Z_y = \sum_n e^{-\beta\epsilon_i} \int dy_n |\varphi_i(y_n)|^2 = \sum_n e^{-\beta N\epsilon_i}\,. \tag{5d}$$

We used the fact that the functions φ_i's are normalized to *unity*. In the thermodynamic limit $(N \to \infty)$, the above sum is dominated by the term having the smallest value of ϵ_i we denote as ϵ_1.

Therefore, according to Ref. [3], we arrive at an equation which is formally identical to the Schrödinger equation for a particle experienced a q-generalized MP,

$$-\frac{(k_BT)^2}{2K}\frac{d^2}{dy^2}\varphi_i(y) + V_q(y)\varphi_i(y) = E_i\varphi_i(y)\,. \tag{7}$$

This Schrödinger equation has been exactly solved [10], and in particular, we find that the associated ground state and the ground state energy are exactly given by

$$\varphi_0(y) = N_0 e^{Q_1 y}\left(\frac{e^{\alpha y}}{e^{\alpha y} + q}\right)^{\frac{Q_2}{\alpha q}}, \tag{8}$$

$$E_0 = -\frac{(k_BT)^2}{2K}Q_1^2\,. \tag{9}$$

with a known normalization constant, N_0, and

$$Q_1 = \frac{2KDb}{(k_BT)^2}\left(\frac{b-2q}{q}\right)\frac{1}{2Q_2} \times \frac{Q_2}{2q}\,, \tag{10}$$

$$Q_2 = \frac{1}{2}\left[-\alpha q + \sqrt{\alpha^2 q^2 + \frac{8K}{(k_BT)^2}Db^2}\right]. \tag{11}$$

We find that the free energy (per site) is given by

$$f = -k_BT\ln Z = \epsilon_0 - \frac{k_BT}{2}\ln(2\pi m k_BT)\,. \tag{12}$$

On the other hand, the computed ground state, $\varphi_0(y)$, gives the contact probability as follows

$$P(y) = C_0 e^{2Q_1 y}\left(\frac{e^{\alpha y}}{e^{\alpha y}+q}\right)^{2Q_2/\alpha q}, \tag{13}$$

with the known normalization constant, C_0. Now, notice that the system undergoes a denaturation transition, if the ground state energy, E_0, vanishes; this condition then defines the denaturation temperature given by,

$$T_d = \frac{2\sqrt{2KD}}{\alpha k_B} \times \frac{\sqrt{b}}{\sqrt{b-2q}} \tag{14}$$

that naturally depends on the parameters of the problem, which are (K, D, α, q).

Before discussing the above expression of the denaturation temperature, we emphasize that the above computed contact probability, relation (13), may be used to determine the mean-distance, $\xi = \langle y \rangle$, between adjacent strands. We find that, in the vicinity of the denaturation temperature, $\mathrm{T_d}$, this length scales as

$$\xi = \langle y \rangle = \int_0^\infty y P(y) dy \sim (T_d - T)^{-1}\,. \tag{15}$$

The divergence of this length is a signature of a denaturation transition.

Now, come back to the main result dealt with the denaturation temperature expression, relation (14).

Firstly, such a characteristic temperature depends naturally of the parameters (D, b, α, q) of the q-MP and the elastic constant, K, between neighboring strands.

Secondly, this temperature is well defined, because of the conditions: $-1 \leq q < 0$.

Thirdly, the denaturation temperature increases, as it should be, with the elastic constant, K. This means that the denaturation transition occurs at high temperature for higher elastic strands.

Fourthly, the denaturation temperature increases with increasing q-parameter.

Fifthly, in the $q = 0$ limit, we find that result from the standard MP [8], that is

$$T_{d,q=0} = \frac{2\sqrt{2KD}}{\alpha k_B}, \tag{16}$$

Finally, the value $q = -1$ defines the denaturation temperature from Deng-Fan potential [10],

$$T_{d,q=-1} = \frac{2\sqrt{2KD}}{\alpha k_B} \times \frac{\sqrt{b}}{\sqrt{b+2}}\,. \tag{17}$$

Conclusion

The aim of this work is an analytical study of DNA denaturation from a q-defomed Morse potential, using the Schrödinger equation method.

Finally, the main conclusion is that, our analytical studies reveal that the q-deformed Morse potential is a good candidate for the description of DNA denaturation and its statistical properties.

Acknowledgements:

We are much indebted to Professor T. Bickel for fruitful correspondences and helpful discussions, and for our referee, for its useful suggestions and pertinent remarks.

REFERENCES

1. D.Poland, H.A.Scheraga, Theory of helix-coil transitions in biopolymers, Academic Press, New York (1970)
2. R.M.Wartell, A.S.Benight,Thermal denaturation of DNA molecules: a comparison of theory with experiment, *Physics Reports*, **vol.126**, p 67 (1985)
3. M.Peyrard, Nonlinear dynamics and statistical physics of DNA, *Nonlinearity*, **vol.17**, p R1 (2004)
4. O.Gotoh, Prediction of melting profiles and local helix stability for sequenced DNA, *Advances in biophysics*, **vol.16**, p 1 (1983)
5. R.Thomas, Structure secondaire et denaturation des acides nucleiques, *Bulletin de la Société de Chimie Biologique*, **vol.35**, p 609 (1953)
6. A.Segerer, T.A.Langworthy, K.O.Stetter, Thermoplasma acidophilum and thermoplasma volcanium sp. nov. from solfatara fields, *Systematic and Applied Microbiology*, **vol.10**, p 161 (1988)
7. D.Poland, H.A.Scheraga, Occurrence of a phase transition in nucleic acid models, *The Journal of Chemical Physics*, **vol.45**, p 1464 (1966)
8. T.Dauxois, M.Peyrard, A.R.Bishop, Thermodynamics of a nonlinear model for DNA denaturation, *Physica D: Nonlinear Phenomena*, **vol.66**, p 35 (1993)
9. P.M.Morse, Diatomic molecules according to the wave mechanics. II. Vibrational levels, Physical Review, **vol. 34**, p 57 (1929)
10. Z.H. Deng, Y.P. Fan, Shandong University Journal, **vol. 7**, p 162 (1957)
11. J.A.McCammon, S.C.Harvey, Dynamics of proteins and nucleic acids, *Cambridge University Press* (1988)
12. J.Sheng, Z.Ying, Z.Xiang-Lin, S.Liang-Tian, Identity for the exponential-type molecule potentials and the supersymmetry shape invariance, *Communications in Theoretical Physics*, **vol.36**, p 641 (2001)
13. M.Peyrard, A.R.Bishop, Statistical mechanics of a nonlinear model for DNA denaturation, *Physical Review Letters*, **vol. 62**, p 2755 (1989)
14. D.J.Sears, R.A.M.Ferrell, Statistical mechanics of one-dimensional Ginzburg-Landau fields, *Physical Review B*, **vol.6**, p 3409 (1972)
15. J.A.Krumhansl, J.R.Schrieffer, Dynamics and statistical mechanics of a one-dimensional model Hamiltonian for structural phase transitions, *Physical Review B*, **vol.11**, p 3535 (1975)
16. A.R.Bishop, J.A.Krumhansl, S.E.Trullinger, Solitons in condensed matter: a paradigm, *Physica D: Nonlinear Phenomena*, **vol.1**, p 1 (1980)

Important: Articles are published under the responsability of authors, in particular concerning the respect of copyrights. Readers are aware that the contents of published articles may involve hazardous experiments if reproduced; the reproduction of experimental procedures described in articles is under the responsability of readers and the irown analysis of potential danger.

Reprint freely distributable – Open Access article

Materials and Devices is an Open Access journal which publishes original, and **peer-reviewed** papers accessible only via internet, freely for all. Your published article can be freely downloaded, and self archiving of your paper is allowed and encouraged!

We apply « **the principles of transparency and best practice in scholarly publishing** » as defined by the Committee on Publication Ethics (COPE), the Directory of Open Access Journals (DOAJ), and the Open Access Scholarly Publishers Organization (OASPA). The journal has thus been worked out in such a way as complying with the requirements issued by OASPA and DOAJ in order to apply to these organizations soon.

Copyright on any article in *Materials and Devices* is retained by the author(s) under the Creative Commons **(**Attribution-NonCommercial-NoDerivatives 4.0 International (CC BY-NC-ND 4.0)), which is favourable to authors.

Aims and Scope of the journal : the topics covered by the journal are wide, Materials and Devices aims at publishing papers on all aspects related to materials (including experimental techniques and methods), and devices in a wide sense provided they integrate specific materials. Works in relation with sustainable development are welcome. The journal publishes several types of papers : A: regular papers, L : short papers, R : review papers, T : technical papers, Ur : Unexpected and « negative » results, Conf: conference papers.

(see details in the site of the journal: http://materialsanddevices.co-ac.com)

We want to maintain Materials and Devices Open Access and free of charge thanks to volunteerism, the journal is managed by scientists for science! You are welcome if you desire to join the team!

Advertising in our pages helps us! Companies selling scientific equipments and technologies are particularly relevant for ads in several places to inform about their products (in article pages as below, journal site, published volumes pages, …). Corporate sponsorship is also welcome!

Feel free to contact us! contact@co-ac.com