Quantum Tunneling in DNA

Megan Wolfe
Department of Physics and Astronomy
Drexel Univerisity
mjw365@drexel.edu

June 7, 2013

Abstract

DNA contains all of the genetic information necessary to grow and sustain life and it is designed in such a way as to be remarkably stable despite it's complexities. This paper discusses the inherent quantum mechanical nature of the hydrogen bonds in DNA nucleotides, specifically the occurrence of proton tunneling within the hydrogen bond and the implications this has on the integrity of DNA replication as a whole. This paper also touches upon the effect radiation has on the frequency of proton tunneling in hydrogen bonds and the deleterious results it has on DNA replication integrity.

Introduction

DNA (deoxyribonucleic acid) is the molecule that encodes all necessary genetic information for use in living organisms–as the atom is said to be the building block of the universe, DNA can be thought of as the building block, or perhaps more accurately as the blueprint for life. Much research has gone into understanding this incredibly important molecule, and in 1953 Watson and Crick suggested a model in which DNA consists of a double helix [1]. In DNA, genetic information is encoded as a sequence of nucleotides: adenine (A), thymine (T), guanine (G), and cytosine (C). These nucleotide bases are paired A-T, G-C through hydrogen bonds and are attached to sugar-phosphate chains that make up the two backbone strands in the double helix. DNA is well-suited for biological information storage because the double-stranded helix structure provides the molecule with a built-in duplicate of the encoded information. This means that if one strand of the double helix has a specific base sequence (for example ATGACTG) then the other strand must have the complimentary sequence (TACTGAC).

In order to study the idea of complimentarity further examination of the nucleotide bases–which take part in the formation of the hydrogen bonds–are necessary. The reason why A pairs with T and G pairs with C all comes down to matching electron lone pairs. In essence the hydrogen bond is a single proton shared between two lone electrons (two separate atoms,

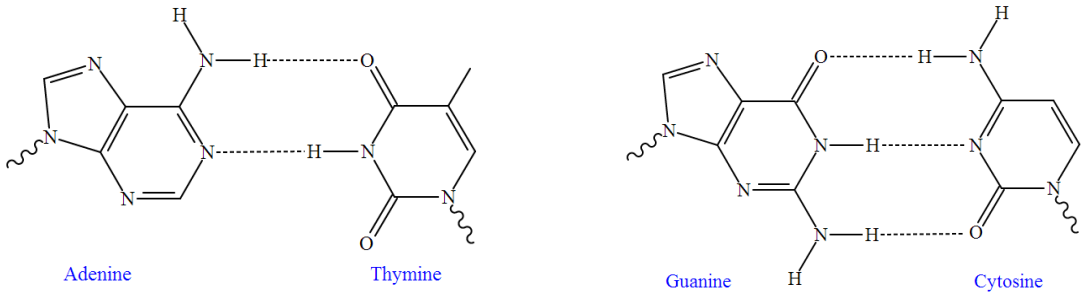


Figure 1: Left, an A-T base pair with two hydrogen bonds. Right, a G-C base pair with three hydrogen bonds.

each containing an extra unpaired electron in their outer orbital shell compete for possession of the single proton). Figure 1 shows the bonding structure of the A-T and G-C base pairs.

In addition to the normal forms, the tautomeric forms of the nucleotide base pairs must also be considered. Tautomeric forms are obtained by moving a proton from its original (or normal) lone pair into another position. This changes the inherent complementarity between the bases and as such the tautomeric bases pair differently. The diagram below gives a direct comparison between the normal forms and the tautomeric forms with their complementary bases:

Normal	Tautomeric
A - T	A* - C
T - A	T* - G
G - C	G* - T
C - G	C* - A

These changes from the normal to the tautomeric forms introduce errors into the DNA replication process–creating point mutations–and can irreparably effect the genetic code. These point mutations, if not checked after initial replication, can be amplified through continued replications, ultimately leading to severe mutations in the cell. It is not unreasonable to suggest that these changes from normal to tautomeric forms correspond to a sort of "quantum jump" where the proton transfer within the hydrogen bond parallels jumping between various stationary states[2].

Quantum Theory of the Hydrogen Bond

In order to investigate the properties of the hydrogen bond the electronic structure of the atoms involved must first be understood. In DNA there are several molecules that have multiple electron lone pairs, all jostling in competition to catch the protons in the surrounding environment, and this is what leads to the formation of the hydrogen bonds.

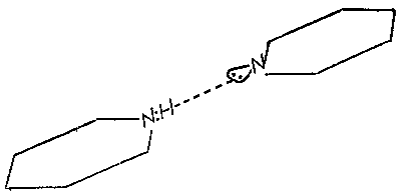


Figure 2: Hydrogen bond formed when two electron lone pairs compete to get the same proton.

The attraction of an individual electron lone pair on a proton can be modeled by a single-well potential. Since, however, there are two electron lone pairs competing for a single proton in a hydrogen bond, the hydrogen bond can be represented as a superposition of two such potentials, i.e. a double-well potential. In the double-well potential there is a bump, or potential barrier, separating the two equilibrium positions.

$$N : H - - - : N \qquad N : - - - H : N$$

Above is a representation of the two equilibrium positions. Assuming that the probability of being in either state is the same then one can predict that under certain circumstances the proton may jump from one position to another. In a quantum mechanical system the proton can be represented by a wave packet, which allows for the proton to penetrate into areas that were forbidden before in the classical system. It is then possible for the proton to travel from one equilibrium state to another by means of tunneling through the potential barrier, achieving this "quantum jump" from one state to another.

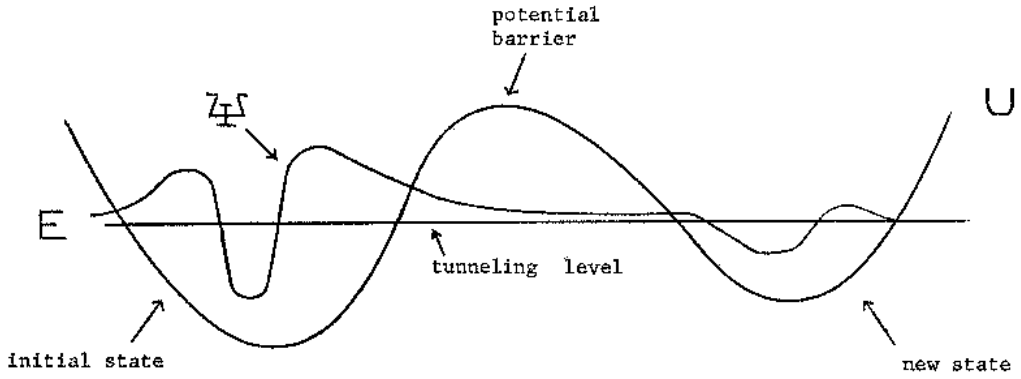


Figure 3: Quantum tunneling effect allows a quantized wave packet to penetrate through the barrier and move from one potential well to another.

The behavior of the proton in the double-well is regulated by the time-dependent Schrödinger equation:

$$\mathcal{H}\Psi = -\frac{h}{2\pi i}\frac{\partial \Psi}{\partial t} \tag{1}$$

where $\mathcal{H}$ is merely the conventional Hamiltonian operator. A solution by means of expression in terms of stationary states is then easily obtained. If the initial value of the wave function is Ψ_o at time t = 0, then the time-dependent wave function can be rewritten as follows:

$$\Psi(t) = e^{-\frac{2\pi i}{h}\mathcal{H}t}\Psi_o \tag{2}$$

It is convenient for solutions to the eigenvalue problem $\mathcal{H}\Phi_n = E_n\Phi_n$ to be made up of an orthonormal set Φ_n and taking advantage of the identity $1 = \sum_n |\Phi_n >< \Phi_n|$ the time-dependent wave function becomes

$$\Psi(t) = \sum_n e^{-\frac{2\pi i}{h}E_n t}\Phi_n < \Phi_n|\Psi_o > \tag{3}$$

This form is known as the "expansion into stationary states"[3]. If the double-well potential is symmetric the quantum mechanical wave functions for the stationary states are necessarily *gerade* or *ungerade*, which corresponds to a 50-50 distribution of the proton over both positions. However, by denoting the proton orbitals associated with the two potential minima as a and b, and making the assumption that at time t = 0 the proton is fully in one position or the other (i.e. $\Psi_o = a$ or $\Psi_o = b$) we are assuming that the proton is initially localized in one of the potential wells (meaning that the system is in a nonstationary state). Assuming that $\Psi_o = a$, the initial position state can be broken down into its symmetry components:

$$a = \frac{1}{2}(a+b) + \frac{1}{2}(a-b) \tag{4}$$

Then plugging this into the stationary state expansion [Eq 3] we see that

$$\begin{aligned}\Psi(t) &= \frac{1}{2}(a+b)e^{-2\pi i h E_g t} + \frac{1}{2}(a-b)e^{-\frac{2\pi i}{h}E_u t} \\ &= \quad [\frac{1}{2}(a+b) + \frac{1}{2}(a-b)e^{-2\pi i \nu t}]e^{-\frac{2\pi i}{h}E_g t}\end{aligned} \tag{5}$$

where $\nu = (E_u - E_g)/h$ is the Bohr frequency associated with the two energy levels and by introducing the period $T = 1/\nu$, the proton distribution becomes:

$$|\Psi(t)|^2 = |\frac{1}{2}(a+b) + \frac{1}{2}(a-b)e^{-2\pi i t/T}|^2 \tag{6}$$

Let us now return to the hydrogen bond and the double-well potential. It is evident that a proton can move even in classically forbidden regions, which gives rise to an overlap

between the orbitals associated with the potential minima (a and b). The oscillations of the proton may thus be considered an example of tunneling. It should be observed that the oscillating proton is not in a stationary state, it is instead oscillating between the two classical equilibrium positions with a frequency determined by the energy difference between the ungerade and the gerade states. These general arguments, although essentially aimed at a symmetric potential, can be extended to an asymmetric double well potential as well.

Proton Tunneling in DNA

When looking specifically at proton tunneling in DNA the scope of the problem must be expanded slightly. Due to the nature of the nucleotide there will always be at least two hydrogen bonds involved in any calculations (refer back to Figure 1) and thus the question becomes one of motion and stability of *two* proton. In other words this becomes a quantum mechanical two body problem. For ease, we can assume these two double-well potentials are fixed. And for maximum stability in the double helix model of DNA it is reasonable to assume that the double-well potentials are highly asymmetric. This is to provide as large a potential barrier as possible in order to reduce the frequency in which tautomeric nucleotides are formed and to ensure as high a purity of DNA replication possible. Due to the asymmetry it is then assumed that the proton will occupy the potential well of lowest energy and therefore outside sources aside, the only way for tautomeric nucleotide bases to form is through proton tunneling. Löwdin predicted that the tunneling times for the protons would depend upon the height and form of the barrier.

Tunneling Probabilites and Rates

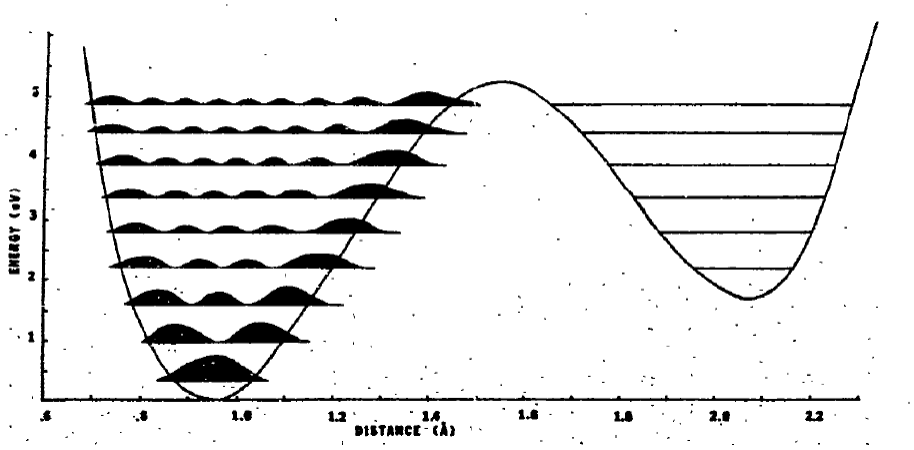


Figure 4: The proton distribution ($|\Psi(t)|^2$) for the tautomeric base combination G*-T

The above figure shows the shape of the potential for the tauromeric base combination

G*-T. Because this potential is so asymmetrical the proton is assumed to be located in the lowest level of the left well. Due to the well shape, tunneling is impossible into the right well until the proton is excited to at least the 4th energy level in the left well. Note however that tunneling into the left well would be possible from even the lowest energy level in the right well if for whatever reason there was a proton in the right well initially. This thought will be further expanded upon in the tunneling and radiation section.

So using the WKB approximation suggested by Löwdin, the probability of a proton tunneling through the barrier is dependent upon the quantity

$$s = \frac{2\pi}{h} \int_{x1}^{x2} (2m[V(x) - E])^{1/2} dx \tag{7}$$

where m and E are the mass and energy of the proton, V(x) is the potential energy at position x, and x_1 and x_2 are the limits of the barrier region (i.e. the potential barrier where V(x) $\geq$ E between x_1 and x_2). The tunneling probability then is given by:

$$g = e^{-2s} \tag{8}$$

Thus if the proton has a frequency ν than the tunneling rate per second will be

$$c = gv \tag{9}$$

For tunneling from left to right the frequency ν_1 can be estimated as the classical oscillation frequency (or as previously stated $\nu = (E_u - E_g)/h$); however, for right to left tunneling the frequency ν_2 is best estimated directly from the curvature of the minima[4].

Tunneling and Radiation

Again referring back to Figure 4 we see that tunneling can take place in both directions through the potential barrier. Reverse tunneling, or tunneling from the right well to the left can happen in two ways. Normally the proton would not initially populate the right well; however, it may be excited to those levels by some outside energy source applied to the system such as radiation[5]. Another way reverse tunneling may occur is when the proton population on the right side of the barrier builds up through normal proton tunneling until the protons begin tunneling back through to the left side. The tunneling rates in the two directions are given by

$$c_1 = \nu_1 g \qquad c_2 = \nu_2 g \tag{10}$$

And from these we define an effective tunneling time

$$\tau_{1,2} = \frac{1}{c_1 + c_2} = (c_1 + c_2)^{-1} \tag{11}$$

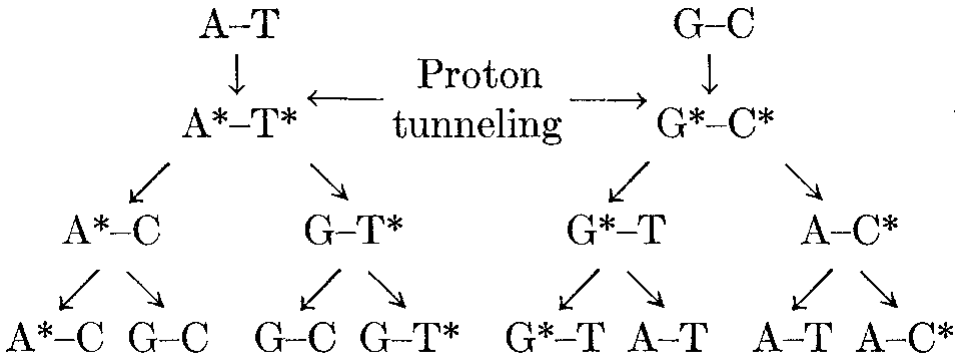
In most cases, but especially true for the upper energy levels, the lifetime of the proton is longer than the corresponding tunneling time, indicating that proton tunneling is a realistic phenomena occurring within the hydrogen bond. The introduction of radiation into the

system excites the protons to the upper energy levels, and from there it becomes much easier to tunnel through the potential barrier. For example, in the A-T ground state the lowest tunneling level has a proton lifetime of $0.165\text{x}10^{-2}$ seconds with a corresponding tunneling time of $\tau_{1,2} = 0.3463x10^{-4}$ seconds, whereas the highest A-T state has a lifetime of $0.3656\text{x}10^{-2}$ seconds and a tunneling time of $\tau_{1,2} = 0.2467x10^{-11}$ seconds[5].

Discussion

It is important to distinguish between the two cases of proton tunneling which have presented themselves through the course of this paper. The phenomena of proton tunneling appears to occur in one of two ways–with bases of equal charges or with bases of unequal charges.

In the case of bases with equal charges, the tunneling of a proton in one direction will trigger a reverse tunneling of a proton in the opposite direction. This most often happens when the protons are stimulated via some outside energy source (such as radiation) or when there is a buildup of protons on one particular side of the potential well (such as was briefly discussed in the previous section). The simultaneous proton tunneling leads to the production of pairs of tautomeric bases. A-T becomes A*-T* and G-C becomes G*-T*. This leads to compounding mutations during replications.



Mutations of this type have been called transitions and they are characterized by the fact that they are reversible, meaning the mutant DNA strands may continue replicating and if a transition happens again, they will revert back to their original ordering. Most often though in this type of mutation the once functioning DNA strand turns into junk DNA and so fails to pass on its encoded information and directions, or even worse, turns into malfunctioning DNA which gives destructive information.

In the case of bases with unequal charge, one of the bases in a nucleotide pair has obtained an extra charge, changing the shape of the double well potential. The tunneling of a proton occurs only in one direction in this case. This results in transitions of the type A-T to A^+-T^- or A^--T^+ which does not appear in the Watson-Crick model. There is no nucleotide which

can or will combine with the transitioned A^+ and G^+ so the genetic code is lost, deleted from the larger DNA strand. This means that this type of mutation is irreversible–once lost, the genetic information can never be recovered.

Conclusion

By treating the proton as a quantum "wave packet" it becomes possible to model the hydrogen bond as a quantum body problem. Due to quantum tunneling, however, there is a small but finite probability that the protons will change place within the hydrogen bond, altering the genetic code, and giving rise to mutations. These mutations, whether they are reversible or not, could be the cause of several medical conditions that come about as a result of degraded or corrupted genetic material such as aging or cancer.

References

[1] J. D. Watson and F. H. C. Crick, A Structure for Deoxyribose Nucleic Acid. *Nature*, **171**, 737 (1953).

[2] Per-Olov Löwdin, Proton Tunneling in DNA and its Biological Implications. *Rev. Mod. Phys.* **35**, 724 (1963).

[3] Per-Olov Löwdin, Advances in Quantum Chemistry (Academic Press, New York).

[4] Robert Rein and Frank E. Harris, Studies of Hydrogen-Bonded Systems. II. Tunneling and Tautomeric Equilibria in the N-H $\cdots$ N Hydrogen Bond of the Guanine-Cytosine Base Pair. *The Journal of Chemical Physics* **42**, 2177 (1965).

[5] B.R. Parker and J. Van Everv, Quantum tunnelling in {DNA}. *Chemical Physics Letters* **8**, 94 (1971).