Could the replication of mirror DNA teach something about chiral selection?

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Abstract

Chiral selection is one of the deep mysteries of biology. Amino-acids are left-handed and DNA and RNA double strands form a right-handed screw. One can assign handedness with individual DNA nucleotides and with DNA double strand. The challenge is to understand the origin of chiral selection. The recently reported replication and transcription of mirror DNA using mirro variant of DNA polymerase provides some hints in this respect.

According to TGD inspired model chiral selection would be induced from that in dark matter sector identified in terms of phases of ordinary matter with non-standard value of Planck constant $h_{eff}/h = n$ [K5, K6]. In living matter dark matter would reside at magnetic flux tubes and control ordinary matter. TGD predicts standard model couplings, in particular weak parity breaking. For $h_{eff}/h = n$ the scale below which weak bosons behave as massless particles implying large parity breaking is scaled up by n. Large parity breaking for dark matter becomes possible in even biological length scales for large enough h_{eff}.

The crucial finding is that the states of dark proton regarded as part of dark nuclear string can be mapped naturally to DNA, RNA, tRNA, and amino-acid molecules and that vertebrate genetic code can be reproduced naturally. This suggests that genetic code is realized at the level of dark nuclear physics and induces its chemical variant. More generally, biochemistry would be kind of shadow of dark matter physics. A model for dark proton sequences and their helical pairing is proposed and estimates for the parity conserving and breaking parts of Z^0 interaction potential are deduced.

1 Introduction

I received a link to a very interesting popular article (see `http://tinyurl.com/zqgutdv`) from which I learned that short strands of mirror DNA and mirror RNA - known as aptamers - have been be produced commercially for decades - a total surprise to me. Aptamers bind to targets like proteins and block their activity and this ability can be utilized for medical purposes.

Now researchers at Tsinghua University of Beijing have been able to create a mirror variant of an enzyme - DNA polymeraze - catalyzing the transcription of mirror DNA to mirror RNA also replication of mirror DNA [I2]. What is needed are the DNA strand to be replicated or transcribed, the mirror DNA nucleotides, and short primer strand (see `http://tinyurl.com/j3o8cyx`)) since the DNA polymeraze starts to work only if the primer is present. This is like recalling a poem only after hearing the first few words.

The commonly used DNA polymerase containing about 600 amino-adics is too long to be built up as a right-handed version and researchers used a much shorter version: African swine fever virus having only 174 amino-acids. The replication turned out to be very slow. A primer of 12 nucleotides was extended to a strand of 18 nucleotides in about 4 hours: 3/2 nucleotides per hour. The extension to a strand of 56 nucleotides took 36 hours making 44/36= 11/9 nucleotides per hour. DNA and its mirror image co-existed peacefully in a solution. One explanation for the absence of mirror life is that the replication and transcription of mirror form was so slow that it lost the fight for survival. Second explanation is that the emergence of mirror forms of DNA polymerase and other enzymes was less probable.

Can one learn anything about this?

1. Chiral selection is one of the deep mysteries of biology. Amino-acids are left-handed and DNA and RNA double strands form a right-handed screw. One can assign handedness with individual DNA nucleotides and with DNA double strand but web sources speak only about the chirality of double strand. If the chirality of the DNA nucleotides were not fixed, it would have been very probably discovered long time ago as an additional bit doubling the number of DNA letters.

2. What could be the origin of the chirality selection? Second helicity could have been loser in the fight for survival and the above finding supports this: fast ones eat the slow ones like in market economy. There must be however a breaking of mirror symmetry. Weak interactions break of mirror symmetry but the breaking is extremely small because the weak bosons mediating weak interaction are so massive that the length scale in which the breaking of mirror symmetry matters is of order 1/100 times proton size. This breaking is quite too small to explain chiral selection occurring in nano-scales: there is discrepancy of 8 orders of magnitude. The proposal has been that the breaking of mirror symmetry has been spontaneous and induced by a very small seed. As far as I know, no convincing candidate for the seed has been identified.

According to TGD inspired model chiral selection would be induced from that in dark matter sector identified in terms of phases of ordinary matter with non-standard value of Planck constant $h_{eff}/h = n$ [K5, K6]. In living matter dark matter would reside at magnetic flux tubes and control ordinary matter. TGD predicts standard model couplings, in particular weak parity breaking. For $h_{eff}/h = n$ the scale below which weak bosons behave as massless particles implying large parity breaking is scaled up by n. Large parity breaking for dark matter becomes possible in even biological length scales for large enough h_{eff}.

The crucial finding is that the states of dark proton regarded as part of dark nuclear string can be mapped naturally to DNA, RNA, tRNA, and amino-acid molecules and that vertebrate genetic code can be reproduced naturally [K2]. This suggests that genetic code is realized at the level of dark nuclear physics and induces its chemical variant. More generally, biochemistry would be kind of shadow of dark matter physics. A model for dark proton sequences and their helical pairing is proposed and estimates for the parity conserving and breaking parts of Z^0 interaction potential are deduced.

2 TGD based model for the chiral selection

In the sequel the TGD inspired model of chiral selection partially inspired by the findings of [I2] is discussed.

2.1 Dark matter and chirality selection

In TGD framework the hierarchy of Planck constants suggests an explanation for the chirality selection.

1. In TGD Universe the new physics of quantum biology involves magnetic bodies and dark proton sequences as a representation of the genetic code at the level of dark nuclear physics. The crucial observation is that dark proton states provide representations for RNA, DNA,

tRNA, and amino-acids [K2, K4] and there is also natural map between DNA and amino-acid type states giving rise to vertebrate genetic code. This looks like a miracle and I find still difficult to believe that it is true. A The extreme slowness of the wrong-handed DNA replication as compared to the ordinary replication means large breaking of parity symmetry. This is possible to understand in terms of weak interactions only if they are dark in DNA length scales so that weak bosons are effectively massless and weak interactions are as strong as electromagnetic interactions.

This suggests that the replication of DNA and takes place at the level of dark proton sequencies - dark nuclear strings - serving as a dynamical template for the biological replication. Also transcription and translation would be induced by dark processes. Actually all biochemical processes could have as template the dynamics of molecular magnetic bodies and biochemistry would be kind of shadow of dark matter physics.

If this is the case, then chiral selection would take place the selection at the level of dark nuclear strings and induce that the level of biochemistry. If dark and ordinary chiralities fit together like hand and glove. Dark matter at magnetic bodies could control the behavior of ordinary matter. By parity breaking the dark weak binding energy between members of proton pairs in the dark DNA strand consisting of a pair of helical dark proton strings is higher for the second helical chirality and would favour this chirality. A very naive thermodynamical estimate is that the ratio of the densities of two chiralities is proportional to the Boltzmann exponent $exp(-\Delta E_B/T)$. The transition to thermodynamical equilibrium can be however very slow so that thermodynamical argument need not make sense.

2. There is experimental support for dark proton sequences. Leif Holmlid and Berhard Kotzias [L3] (see `http://tinyurl.com/hxbvfc7`) have published an article about the superdense phase of hydrogen proposed to make possible to overcome the Coulomb wall making cold fusion impossible in the textbook Universe. In TGD superdense phase has interpretation as dark proton sequences at magnetic flux tubes with the Compton length of dark proton coded by $h_{eff}/h = n_{eff} \simeq 2^{11}$ to electron's Compton length [L1]. Remarkably, it is reported that the superdense hydrogen is super-conductor and super-fluid at room temperatures and even above: this is just what TGD predicts.

   The dark protons in TGD inspired quantum biology (see `http://tgdtheory.fi/public_html/articles/geesink.pdf`) should have much longer Compton length of the order of the distance between nucleotides in DNA sequences in order to serve as templates for chemical DNA. This gives a dark Compton length of order $\simeq 3.3$ Angstroms from the fact that there are 10 codons per 10 nm. This would give $n_{eff,p} \simeq 2^{18}$. The safest manner to estimate the dark binding energy is by scaling the binding energy about $E_B \simeq 7$ MeV per nucleon by $1/n_{eff,p}$ to give $E_{B,d} = E_B/n_{eff,p} = 28$ eV.

3. Further evidence for the importance of dark protons in biology comes from the recent finding of the group led by Thomas Carell related to the understanding the origins of life [I1] (see `http://tinyurl.com/z65kpyo`). For TGD inspired model see [L2], [K1]. Carell et al have identified a mechanism leading to the generation of purines A and G, which besides pyrimidines A,T (U) are the basic building bricks of DNA and RNA. The crucial step is to make the solution involved slightly acidic by adding protons.

   In TGD inspired quantum biology this suggest that the protons in the acidic water are dark and that the attachment of the dark protons to the amines of the amino-pyrimidine transforms them to ordinary protons and makes the amino-pyrimidine non-reactive. There would be however one exception: the amine which reacts further to give purines as a reaction product. In this case the proton would remain dark and the chemical properties of the amine would remain intact. This suggests that DNA nucleotides and DNA strands can attach to dark protons or are accompanied by them.

2.2 Model for the replication of DNA in terms of replication of dark nuclear string

One can consider a detailed model for the replication as induced by the addition of dark protons to dark proton sequence representing dark DNA strand. The added dark protons would be

accompanied or attached with the DNA nucleotides as suggested by the work of Carell et al.

1. In the replication and transcription of DNA the basic step would be the addition of dark proton to an increasing dark proton sequence. The need for primer means that there must already exist a dark proton sequence. In the presence of prime the attractive dark nuclear binding energy of the added dark proton with the prime would make the dark fusion rate higher. The addition of dark protons could proceed like a dark nuclear chain reaction. It would be made possible by the dark nuclear binding energy per proton scaling like $1/h_{eff,p}$.

   For the ordinary nuclei the binding energy per nucleon would be of the order of 7 MeV (note that charge independence of strong interactions holds in good approximation). The scaling down by $h_{eff}/h = 2^{18}$ would give $E_B \simeq 4$ eV, which corresponds to UV photon energy. Note that bio-photons assumed to correspond dark photons with same energy have energies in visible and UV range.

2. Dark nuclear energy cannot explain parity breaking. The axial part of dark weak energy between dark protons belonging to dark strand and its conjugate and having nuclei acids and its conjugate as a chemical "shadow" must be also involved. Two values of h_{eff} are involved: $h_{eff,p}$ assignable to the flux tubes containing dark protons parallel to DNA strands and $h_{eff,W}$ assignable to the transversal flux tube connecting dark protons associated with different dark strands.

   One of the assumptions of the TGD inspired model of cold fusion [L1, L3] is that the weak scale is scaled up from weak boson Compton length to about atomic length scale. This would require $h_{eff,W}/h = n_{eff,W}$ for weak bosons to be roughly

   $$n_{eff,W} \simeq \frac{m_Z}{m_p} \times n_{eff,p} \simeq 91 \times n_{eff,p}$$

   so that one would have $n_{eff,W} \simeq 2^{25}$. If this is the case weak interactions are of essentially same strength as em interaction below the scaled up Compton scale of order 3 Angstroms. This makes it possible to talk about classical Z^0 Coulomb potential and about spin dependent parity breaking Z^0 force. These two interaction energies sum up and this reduces the binding energy per proton in double strand for the other chirality.

3. The parity conserving Z^0 Coulomb interaction energy between two protons at different strands connected by a flux tube is given by the expression

   $$V_{PC}(r_{12}) = -kV(r_{12}) \ , \quad V(r_{12}) = \frac{\hbar}{r_{12}} \ ,$$

   $$k = \alpha_Z Q_Z^2(p) \ , \qquad \alpha_Z = \frac{\alpha}{sin^2(\theta_W)cos^2(\theta_W)} \ , \quad Q_Z(p) = 1/4 - sin^2(\theta_W) \ .$$

   $$(2.1)$$

   Here units $\hbar = 1$, $c = 1$ are used. r_{12} refers to the distance between dark protons at magnetic flux tubes assignable to DNA strands. Base pair thickness is about .34 nm and thickness of DNA double strand is about 2 nm. r_{12} could be between these two limits.

4. The spin dependent and parity non-conserving Z^0 interaction potential for Dirac spinors proportional to the gradient of the Z^0 Coulomb potential can be written as

   $$V_{PNC} \quad = \quad \alpha_Z Q_Z^A(p) Q_Z^V(p) \gamma_5 V(r_{12}) \ . \qquad (2.2)$$

   Here $Q_Z^A = I_{3,A}/2 = 1/4$ is the axial weak charge of proton. The vectorial charge of proton is $Q_Z(p) = 1/4 - sin^2(\theta_W) \simeq 0.02$ so that it is much smaller than $Q_Z^A(p)$. Hence the axial force dominates by a factor $10^2/8 \sim 12.5$ for a given relative position. Usually the axial part becomes very small by symmetries as one estimates quantum averages but in the recent situation one cannot expect this since the positions of dark protons are in the first approximation fixed.

5. Using non-relativistic correspondence following from $\gamma_5 = \gamma_0\gamma_1\gamma_2\gamma_3$ and $(\gamma_5)^2 = -1$: this equation holds true also for $(\gamma^0\gamma^k p_k(m)$, and one has

$$\gamma_5 \to \frac{\overline{\sigma} \cdot p}{m_p} \quad .$$

Here $\overline{\sigma}$ denotes Pauli sigma matrices expressible as $\gamma^0\gamma^i$). Using the replacement $p \leftrightarrow i\hbar_{eff,W}\nabla$ one can write V_{PNC} as the sum of the axial energies of the two protons

$$
\begin{aligned}
V_{s_1,s_2} &= V_{s_1} + V_{s_2} \quad , \\
V_{s_i} &= \frac{\hbar_{eff,W}}{m_p}\overline{\sigma}_i \cdot \nabla_i V_{PC}(r_{12}) = (-1)^i \frac{k n_{eff,W}\hbar}{m_p}\hbar\frac{\overline{\sigma}_i \cdot \overline{r}_{12}}{r_{12}^2} \quad . \quad i = 1, 2 \quad .
\end{aligned}
$$

(2.3)

The parity breaking part of Z^0 force is proportional to $n_{eff,W}$ from the expression of momentum operator in terms of gradient operator so that dark matter physics makes itself visible and increases further the magnitude of parity breaking. The potential energy changes sign in reflection $\overline{r}_{12} \to -\overline{r}_{12}$. This gives

$$
\begin{aligned}
V_{s_1,s_2} &= -\frac{\alpha_Z}{4}(\frac{1}{4} - sin^2(\theta_W))\frac{n_{eff,W}\hbar}{m_p r_{12}}\frac{(\overline{\sigma}_1 - \overline{\sigma}_2) \cdot \overline{r}_{12}}{r_{12}}\frac{\hbar}{r_{12}} \\
&= \frac{1}{4}\frac{1}{(\frac{1}{4} - sin^2(\theta_W))}\frac{n_{eff,W}\hbar}{m_p r_{12}}\frac{(\overline{\sigma}_1 - \overline{\sigma}_2) \cdot \overline{r}_{12}}{r_{12}}V_{PC}(r_{12}) \quad .
\end{aligned}
$$

(2.4)

6. For the vectorial part one has

$$V_{PC} = -\alpha_Z(\frac{1}{4} - sin^2(\theta_W))^2 V(r_{12}) \quad .$$

(2.5)

The order of magnitude is about $V_Z = .16/x$ eV.

7. The condition that r_{12} corresponds to dark Compton length of proton implies in the first approximation $\frac{n_{eff,p}}{m_p r_{12}} = 1$ so that $n_{eff,W}$ proportionality gives factor $m_Z/m_p \simeq 91$. The order of magnitude parity breaking potential is the value potential at distance in the range $r_{12} \in [3.4, 2]$ nm. Let us expres the horizontal distance between the paired dark protons as $r_{12} = x$ Angstroms. This gives for the axial part

$$
\begin{aligned}
V_{s_1,s_2} &= \frac{1}{4}\frac{1}{(\frac{1}{4} - sin^2(\theta_W))}\frac{m_Z}{m_p}(\overline{\sigma}_1 - \overline{\sigma}_2) \cdot \frac{\overline{r}_{12}}{r_{12}}V_{PC}(r_{12}) \\
&\simeq .5 \times 10^2 \times 91 \times \frac{V_{PC}(r_{12})}{x} \times (\overline{\sigma}_1 - \overline{\sigma}_2) \cdot \frac{\overline{r}_{12}}{r_{12}} \quad .
\end{aligned}
$$

(2.6)

The order or magnitude for the axial part is roughly $4550/x$ times larger than for the vectorial part. V_{PNC} is proportional to $1/x^2$ and V_{PC} to $1/x$. The condition that the states are spin eigenstates requires that spin quantization axes must be chosen along the flux tube connecting the dark protons. This is rather natural choice.

This would give for the axial part order of magnitude $V_{PNC} \sim 728/x^2$. For 2 nm distance one would obtain $V_{PNC} \sim 1.82$ eV. For 1 nm distance one would have $x = 10$ and this would give $V_{PNC} \simeq 7.28$ eV. For this value $V_{PC} \simeq 16$ meV, which is of same order of magnitude as thermal energy $kT/2$ at room temperature.

8. The process of adding dark protons to the increasing DNA sequence must be possible irrespectively of the direction of spin. The spin eigenvalue in the direction of the horizontal axis connecting the members of dark proton pair is assumed to be opposite for the members of the dark proton pairs of dark double strand. This assumption comes from the model of the dark genetic code. This demands that V_{NPC} is considerably smaller than strong binding energy E_B. For 1 nm distance one has $V_{PNC} \simeq 7.28$ eV considerably smaller than $E_B \simeq 28$ eV.

9. What is the relation of the fermionic chirality to the geometric chirality? The reflection for dark protons induces the reflection of the entire helix turning also its direction. The reflection permutes the dark protons of each pair since their positions are related by reflection in the plane orthogonal to z-axis $(x_2, y_2) = (-x_1, -y_1)$. One has $(x_1, y_1, z) \leftrightarrow (x_2, y_2, -z)$. A further rotation of π in say (x, z)-plane around say y-axis is symmetry and gives $(x_2, y_2, -z) \rightarrow (-x_2, y_2, z) = (x_1, -y_1, z)$. Hence the net effect is $(x_1, y_1, z) \rightarrow (x_1, -y_1, z)$ and DNA strand with an opposite screw direction is generated.

   The model of dark genetic code motivates the assumption that the dark protons of the pair are spin eigenstates for the spin projection along the axis connecting the members of the pair. The direction of the spin quantization axis changes in reflection from that given by (x_1, y_1) to that given by $(x_1, -y_1)$ so that the states are not anymore eigenstates of the spin projection along this axis. Thus the fermionic chirality indeed correlates with the the chirality of double strand and the two chiralities are in physically different position.

   What happens at the level of classical fields? Kähler magnetic field transforms like angular momentum in reflections and rotations as is easy to see from its expression in terms of vector potential. Hence it does not change its direction in reflection but changes its direction in the rotation. Hence the magnetic flux along flux tube changes to opposite in the reflection. This also affects the physics and induces effects at the level of dark strong interactions. The magnetic energy is of form $s \cdot B$ and vanishes classically. Quantum mechanically it does not vanish since s is operator and one can wonder what this implies physically.

2.3 Differences between standard model and TGD based description

The above estimate relies on standard model, which is quantum field theory in Minkowski space, and one can wonder what new elements TGD brings in.

1. In TGD framework space-time is 4-surface in $M^4 \times CP_2$ and this description must be replaced with a description using 8-D imbedding spinors. At space-time level massive M^4 Dirac equation $p_k \gamma^k \Psi = m \Psi$ is replaced by 8-D chiral symmetry implying separate conservation of quark and lepton numbers with the analog of massless Dirac equation for the Kähler-Dirac gamma matrices, which are superpositions of M^4 and CP_2 gamma matrices. K-D gamma matrices are contractions of canonical momentum current densities of Kähler action with the imbedding space gamma matrices. If the action is volume term, one obtains induced gamma matrices. The twistorialization of TGD by replacing the imbedding space with the product of twistor spaces of M^4 and CP_2 and lifting space-time surfaces to their twistor spaces with induced twistor structure leads to the addition of volume term to Kähler action [K7]. This term corresponds to cosmological constant and is extremely small in the recent cosmology.

2. One can decompose K-D gamma matrices to their M^4 and CP_2 parts: $\Gamma^\alpha = \Gamma^\alpha_{M^4} + \Gamma^\alpha_{CP_2}$ and write the K-D equation as $\Gamma^\alpha_{M^4} D_\alpha \Psi = -\Gamma^\alpha_{CP_2} \Psi$. The presence of $\Gamma^\alpha_{CP_2}$ parts breaks conservation of M^4 chirality and serves as a signal for massivation. This operator is kind of mass operator acting non-trivial in electroweak spin degrees of freedom assignable to CP_2 and the action of its square is analogous to the the action of mass squared operator.

   The understanding of particle massivation at this level does not seem however possible and the proper approach relies of p-adic thermodynamics for super-Virasoro representations for which ground states are characterized by the modes of imbedding space spinors which are massless in 8-D sense and are eigenstates of M^4 mass squared operator with eigenvalues determined by CP_2 spinor Laplacian [K3]. Its action on M^4 chirality is same as action of mass in massive Dirac equation in M^4.

3. In the case of M^4 Dirac equation the multiplication of massive Dirac equation with γ_5 using anti-commutativity of γ_5 and γ_k gives $\gamma^k p_k \gamma_5 \Psi = -m\gamma_5 \Psi$ instead of $p_k \gamma^k \Psi = m\Psi$. TGD framework γ_5 anti-commutes with $\Gamma^\alpha_{M^4}$ but commutes with $\Gamma^\alpha_{CP_2}$ so that also now one has similar equation $\Gamma^\alpha_{M^4} D_\alpha \Psi = +\Gamma^\alpha_{CP_2} \Psi$.

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