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Spin phase links up the genetic code with the protein synthesis - a long-expected answer on how the genetics works

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ABSTRACT

The anticodon-codon (A-C) segment and the tRNA charging segment (7 nanometers apart) are coupled through the spin torque current arising as a response to the triplet-singlet (T-S) crossing (the T and S energies are equal) on the A-C segment. If the direction of the torque vector at the tRNA end matches with the spin direction on the attachable amino acid (AA) - spin directions must be opposite - the AA bonding to the tRNA (the tRNA charging) is allowed, if not the bonding is forbidden. The finding works flawless and has multiple applications, including the creation of new materials with quantum properties.

INTRODUCTION

In physics, theoretical and experimental, use of the phase concept is common[1]. In chemistry, the phase concept is mostly unclaimed[2]. The reason is obvious. Chemical reactions operate with Avogadro number of molecules, which collisions cancel randomly dispersed phases. In contrast, the major biological aggregates, including DNA/RNA molecules, A-C segments and coupled with them synthesized proteins, are highly selective about information storage, transfer, and processing. The processing initiates spin-dependent reactions which selectivity is much higher than commonly known electrophilic or nucleophilic substitution reactions in bioorganic chemistry[2]. Spin-dependent reactions are inevitably sensible to phase that up to sign and value from both reactants (mathematically, the carrier (spin) gains a tensor character[3]) ensures their fidelity to make or not to make bonds[4].

Here we aim to show that the A-C and the charging tRNA (by 'charging' we mean a single AA bonding to the unchangeable tRNA end – C-C-A-OH[4]) segments (7 nanometers apart) are coupled through a spin flow (a spin torque flow, in general)[3] arising as a response to the triplet-singlet (T-S) energy (E) crossing, $E^T \cong E^S$ – a result of tRNA and mRNA recognition through the Watson-Crick pairing[4], Figure 1. When the torque vector direction on the tRNA end matches the spin direction on the AA candidate (totally, there are 64 possible amino acids[4]) – the spin directions must be opposite – the tRNA charging is allowed; if not the charging is forbidden.

The fidelity of protein synthesis is very high – one mistake of 10.000 correctly assembled amino acids[4]. This flawless operation stems from a perfectly-tuned communication between the A-C (the codon consists of three nucleotides; the anticodon is its counterpart bound to the codon through the Watson-Crick hydro-

Regular Paper

gen bonds[4]) reading segment[4] (tRNA-mRNA) and the tRNA charging segment[4]. How these segments see each other at a nanoscale distance is shrouded in mystery. This leaves the genetics, despite its indisputable practical achievements[4], a mysterious branch of science.

EXPERIMENTAL AND MODELING

The data rest on the DFT:(L)APW+lo computations, the Wien2k code[5]. The unit cell in tRNA is a single nucleotide, Figure 1. Here we use the set of plane waves[5], spreading over the most part of tRNA and sandwiched between the A-C segment and the tRNA end. The localization automatically switches the plane wave code to the DFT:B3LYP (6-31G** basis set). The localization occurs on the A-C segment, the tRNA end, AA, OH, and AMP fragments, Figure 1. The computations are carried out on the New York Blue Gene/L supercomputer parallel complex (NYCCS center). In our computations we use a simplified tRNA-mRNA structure, Figure 1, (this is a necessary requirement because of system's complexity; the full structure of tRNA can be found elsewhere). The mRNA in our computations consists of five nucleotides, G-C-G-U(C,A,G)-G (in brackets are the nucleotides that can replace the U with no influence on the right AA attachment – the genetic code is degenerated[4]); the core nucleotides, C-G-U(C,A,G), are complementary to the tRNA – the A-C segment. The tRNA end is able to interact with one of the amino acids, AA = Arg (the right amino acid predicted by the genetic code[4]), Gly, Ser, Gln (the wrong amino acids; they show a mismatch with the genetic code[4]); •AMP and •OH, Figure 1 (the dot stands for a radical, see below). We treat the tRNA-mRNA core as "frozen" (the atomic positions are those from the PDB, Japan). The computation variables are the distances (the computational step in localized regions does not exceed 0.05 Å) between the tRNA and mRNA (C-G-U(C,A,G) nucleotide sequence), AA, AMP, OH, and the A-OH fragment in the two water volumes – 10×4×4 Å[3] (the A-C segment) and 18×32×23 Å[3] (the tRNA end together with the named molecules, Figure 1). Besides finding the optimal structure within the segments, the computations include the hyperfine coupling constants (*hfc*, scalar and vector; they come from interaction between the ^{31}P nuclei, 100% natural abundance[4], and the electron), and the spin tensor torque, **Q**(**r**) (the imaginary object, in general[1,3,6]), over the tRNA (PW + *hfc*[6]). At the tRNA end the torque gives a final spin vector direction s on the Poincare sphere[1,6]. The appropriate system of coordinates and the spin orientation angle, θ, are in Figure 2. The spin density, N(**r**)= Tr[σ_0**Q**(**r**)] (σ_0 is the first Pauli matrix), as a part of four **Q** (hereinafter we omit r) tensor components – Tr[σ_i**Q**] (i =0÷3)[3,6], is computed on the AA, AMP, OH, and

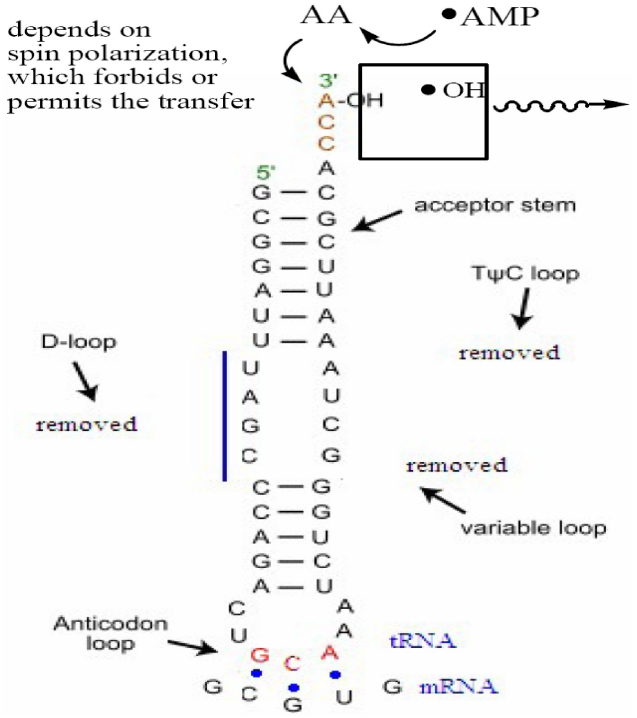

Figure 1 : A simplified structure of the tRNA used in quantum computations. The blue dots indicate H-bonding in the A-C segment. The atoms in the box produce water. The curved arrows show local spin transfers. The horizontal lines display the hydrogen bonds in the tRNA. The blue vertical line shows the nucleotides with no hydrogen bonding – the analogue of real RNA

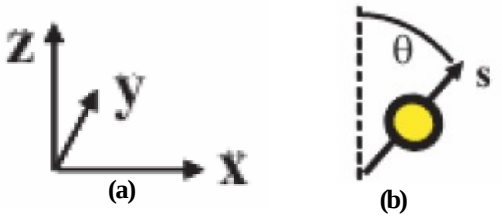

Figure 2 : (a) The system of coordinates. The x direction coincides with that of the electron movement along the tRNA – from the A-C segment to the tRNA end. (b) the spin s is oriented in the x-z plane at the variable angle θ with respect to z direction

the A-C segment[6]. The radicals, •AMP and •OH, arise as a response to the ATP (ATP serves as the energy source in biochemical processes) cleavage upon its binding to Mg cation/cations (it could be one or two[7]), which, first, convert the (Mg)-ATP into a triplet (T) state (here we also have a crossing point, $E^T=E^S$[8],) and, second, decompose it with a radical pair (•AMP and •OH, both spins are parallel that forbids their recombination[9]) production and the energy release of 14.51 kcal/mol (the ATP cleavage producing a radical pair is detailed in ref.[7]). This energy goes into overcoming the two barriers[10], 7.23 kcal/mol and 7.28 kcal/mol, in the two chemical reactions: A + •OH = •A + H_2O and •A + •AA = A-AA (the details see in ref.[10]). The initial atomic positions in the A-C and tRNA segments are those obtained earlier[10,11].

RESULTS AND DISCUSSION

The outlined structure reveals some intriguing facts. The complementary pairing, mRNA-tRNA (the A-C segment), shows a triplet-singlet (T-S) crossing[8]. Initially, both electrons are on the mRNA in the T state (the analogue of quantum dots and wires[12]). This state is energetically unfavorable. It favors the transfer one of the named electrons on the tRNA with no spin flip (the T symmetry remains unchangeable; $\Delta E = -0.007$ cm^{-1}) – the evidence of the computations. Further, the electron on the tRNA goes as far as possible from its counterpart (electrons of the same orientation experience a repulsion[9]) and occupies the A-OH terminus nucleotide (in bold) – C-C-**A**-**OH**, Figure 2a,b. The transfer takes 1.9 ns that we track directly. This is the time when the **Q** of the moving electron sets right on the A nucleotide leaving the rest tRNA body empty of spin. Such an observable time interval comes up thanks to the *hfc* existing on each nucleotide (without the *hfc* the Q makes no sense). The θ value varies in the interval $30\text{-}33^0$ depending on the nucleotide nature. The data do not pretend to be QMD computations which today are still unavailable for such complex systems as ours[13]. The electron transfer converts the tRNA end into a radical C-C-A•. The unpaired electron, in turn, changes spin orientation on the •OH radical, thus opening the way to the •AMP-•OH pair recombination (T→S). The recombination, however, does not occur since the HO•-H-O-A interaction is more favorable, $\Delta E = -0.7$ kcal/mol[10]. The interaction breaks the H-O bond in the sugar core[10]. Consequently, we have the water molecule and the biradical •(O-A•), or simply •A•. The two electrons on the A are unable to exist. Having the same spin orientation, T, they experience a new, much stronger, spin repulsion, 0.024 cm^{-1}, than the previous one on the A-C segment. One electron stays on the A (we see it in our computations), the other moves back to the A-C segment (we see its flow back in a time interval of 1.4 ns) where it undergoes a flip (the flip is a response of the electron trapping between the two identically oriented spins, Figure 3). When in S, the incoming electron transfers back onto the mRNA, $\Delta E = -0.009$ cm^{-1}. This, in turn, shifts the reading frame (tRNA-mRNA) to a new position (mRNA experiences the H-bond elongation of 0.1 Å that removes the named earlier T-S crossing)[4]. The outlined scenario is displayed in Figure 3. Totally, the spin flips are energetically negligible, ≤ 0.024 cm^{-1}. The energetically consuming are the processes with •OH, •A, and •AA (see above). Noteworthy, even these processes, despite their high energy barriers, release no energy (this leaves the E^T and E^S practically equal during the computations), which

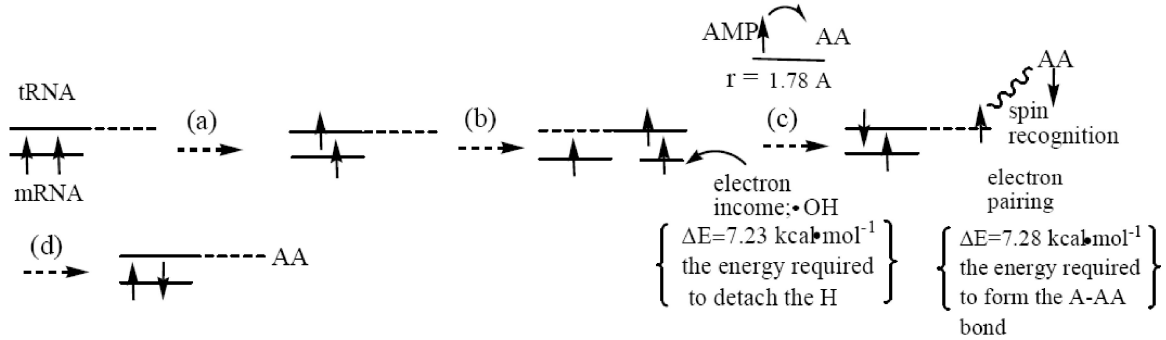

Figure 3 : A simplified picture of the spin flow in the mRNA-tRNA structure (the spin has two orientations – 'up' or 'down'; the back flow is not shown). The wavy line shows interaction between the AA and A. The details are in text

Regular Paper

supports the idea that biological reactions in living cells do not produce heat in normal state[4].

The most important thing for us is that the spin polarization of the remaining unpaired electron on the •A (the computation uniquely determines the spin polarization unit vector **n** on the Poincare sphere[1]) feels the polarization vector on the •AA which gains spin density from the •AMP ((c) stage, Figure 3; the process has no barrier and looks like a spin density flow from the •AMP to the •AA (both molecules are separated by 1.78 Å, Figure 3) with a negligible energy gain, 0.012 cm^{-1}. If •AA and •A spin vectors are of opposite direction and of the same value, TABLE 1, Figure 4a, the AA attaches to the oxygen atom of A (S state; initially, the AA and A are separated by 4.38 Å) through its carbon atom, thus making the tRNA charged[4]; if not (Figure 4b) – there is no interaction (•AA = Gly, Ser, Gln; the spin vector on the AA is practically normal to the spin vector on the A). Even if we change the spin vector direction through the AA rotation, it makes the carbon-oxygen (AA-A) interaction impossible since the rotation removes the named atoms from each other).

TABLE 1 : Dot product of the spin density N and the n = ± x vector with the origin at AA (+x) or A (-x)

AA	x	tRNA terminus	-x
Arg	0.995	A	-0.995
Gly	0.005	A	-0.005
Ser	0.002	A	-0.002
Gln	0.003	A	-0.003

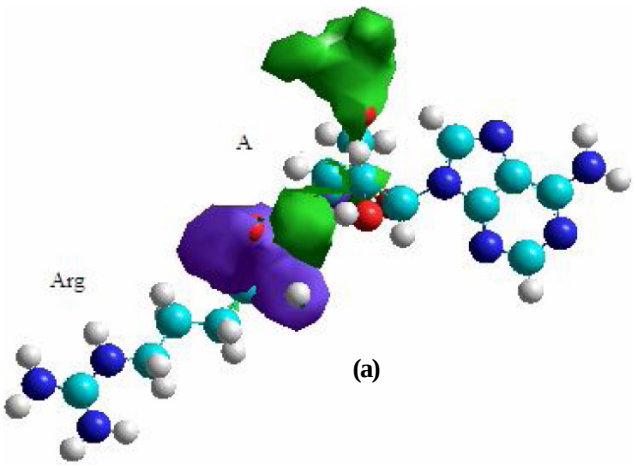

Figure 4a : Spin density distribution on the A terminus nucleotide and the arg amino acid (the right AA predicted by the genetic code, see text and ref.[4]). Green and violet colors show that the spin directions are opposite

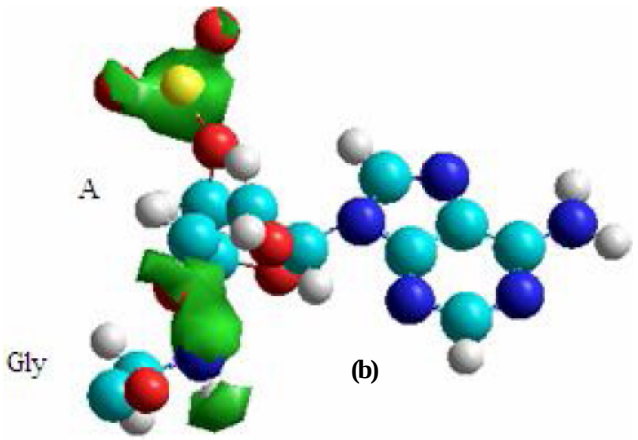

Figure 4b : Spin density distribution on the A terminus nucleotide and the gly amino acid (the wrong AA forbidden by the genetic code, see text and ref.[4]). Green colors show that the spin directions on the A and AA are identical

The TABLE 1 confirms the previous words. The right AA (AA = Arg) predicted by the genetic code[4] (the A-C segment) shows a high value of the spin density identical, up to sign, to that on the A terminus nucleotide (the dot product $\mathbf{S} = N \cdot \mathbf{n}$ in the $\mathbf{n} = \pm\mathbf{x}$ direction considered as a link between the AA and A). The wrong AA shows a very small value of the named dot product.

The outlined mechanism of the genetic code operation (the A-C segment) explains the fidelity of the process of tRNA charging. Physically, the origin of communication between the A-C segment and the charging segment on tRNA stems from the presence of the T-S crossing ($E^T \approx E^S$) and the *hfc*. The latter, the analogue of the spin-orbit (SO) coupling[3], is responsible for the total spin current ($\mathbf{J} = j + \Sigma_i \tau_i \mathbf{x}$ (j – bare spin current, $\tau_i = (1/i\hbar)[\sigma_i^x, H]$; H – the Hamiltonian) defines the torque on the tRNA). The *hfc* creates the vector field **A** which becomes a function of the spin and, in turn, determines the magnetic field $\mathbf{B} = \nabla \times \mathbf{A}$.[1] For organic systems with periodically inserted ^{31}P nuclei, the *hfc* coupling constant G_{ij} is giant and reaches, according to experiment and theory[14], the value 0.07 ÷ 0.1 T (MHz ÷ low GHZ region). Note that the highest value of the ^{31}P-electron coupling is reached at 298-310^0 K, the MD DFT computations[11]. Mathematically, the $\int_l A dx$ is a curvature along the path *l*. If *l* is a closed path, we deal with the Berry phase[15], assuming the spin flip upon the *l* closure. So when the electron comes back to the A-C segment, its spin orientation is fully opposite to that it

had before starting its 'journey' along the *l*.

CONCLUDING REMARK

A spin current necessarily suggests existing of a spin phase. The phase plays its crucial role thanks to energy equality between the T and S states. In turn, the phase is associated with the spin direction. A three-nucleotide combination (a codon) creates a unique direction of spin vector depending on the nucleotide sequence in the codon. The phase is transmitted to the tRNA end – the adenine nucleotide – where the spin vector gains its final orientation. The rest scenario is discussed above.

ABBREVIATIONS

A – adenine, C- cytosine, G – guanine, U – uracil, ATP – adenosinetriphosphate, AMP – adenosinemonophospate, Arg – argenin, Gly – glycine, Ser – serine, Gln – glutamine, tRNA – transport RNA, mRNA – messenger RNA, A-C – anticodon-codon segment, AA – amino acid.

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