%\begin{abstract}

The model for the evolution of genetic code leads to the idea that the folding of proteins obeys a folding code inherited from the genetic code. The flux connections between molecules containing dark matter in macroscopic quantum phase and characterized by two integers are the basic new physics element of the model.

After some trials one ends up with a general conceptualization of the situation with the identification o magnetic flux tubes as correlates of attention at molecular level so that a direct connection with TGD inspired theory of consciousness emerges at quantitative level. This allows a far reaching generalization of the DNA as topological quantum computer paradigm and makes it much more detailed. By their asymmetric character hydrogen bonds are excellent candidates for contracted magnetic flux tubes serving as correlates of attention at molecular level.

One can consider two models. For the first model the flux tubes between amino-acids are assumed to determine the protein folding.

\begin{enumerate}

\item The constant part of free amino-acid containing $O-H$, $O=$, and NH_2 would correspond to the codon XYZ in the sense that the flux tubes would carry the \blockquote{color} representing the four nucleotides in terms of quark pairs. Color inheritance by flux tube reconnection makes this possible. For the amino-adics inside protein $O=$ and $N-H$ would correspond to YZ. Also flux tubes connecting the acceptor atoms of hydrogen bonds are required by the model of DNA as topological quantum computer. The long flux tubes between $O=$ atoms and their length reduction in a phase transition reducing Planck constant could be essential in protein-ligand interaction.

\item The model predicts a code for protein folding: depending on whether also $=O-O=$ flux tubes are allowed or not, $Y=Z$ or $Y=Z_c$ condition is satisfied by the amino-acids having $N-H--O=$ hydrogen bond. For $=O-O=$ bonds $Y-Y_c$ pairing holds true. If one identifies hydrogen bond with flux tube ($Y(n)= Z(n+k)$) the model works badly for both options. If one assumes only that the presence of a flux tube connecting amino-acids in either direction ($Y(n)= Z(n+k)$ or $Z(n)=Y(n+k)$) is a prerequisite for the formation of hydrogen bond, the model works. $Y=Z_c$ option predicts the average length of alpha bonds correctly. $Y=Z$ rule is however favored by the study of alpha helices for four   enzymes: the possible average length of alpha helix is considerably longer than the average length of alpha helix if gene is the unique gene allowing to satisfy $Y=Z$ rule. The explicit study of alpha helices for four enzymes demonstrates that the failure to satisfy the condition for the existence of hydrogen bond fails rarely and at most for two amino-acids (for 2 amino-acids in single case only). For beta sheets there

ar no failures for $Y=Z$ option.

\item The information apparently lost in the many-to-one character of the codon-amino-acid correspondence would code for the folding of the protein and similar amino-acid sequences could give rise to different foldings. Also catalyst action would reduce to effective base pairing and one can speak about catalyst code. The DNA sequences associated with alpha helices and beta sheets are completely predictable unless one assumes a quantum counterpart of wobble base pairing meaning that $N-H$ flux tubes are before hydrogen bonding in quantum superpositions of braid colors associated with the third nucleotides Z of codons XYZ coding for amino-acid. Only the latter option works. The outcome is very simple quantitative model for folding and catalyst action based on minimization of energy and predicting as its solutions alpha helices and beta strands.

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Second model represents a diametrical opposite of the first model in the sense in that it assumes flux tube connections only between amino-acids and water molecules. These flux tubes mediate an attractive (repulsive) interaction in the case of hydrophily (hydrophoby) due to the behavior of magnetic (presumably) interaction energy as a function of Planck constant (or integers characterizing the level of dark matter) assignable to the flux tube. For hydrophoby (hydrophily) the interaction energy is minimized for long (short) flux tubes. The interaction between amino-acids is induced by this interaction in a manner analogous to how the interaction between electrons and ions induces secondary interaction between the members of a Cooper pair. The model explains the basic qualitative aspects of protein folding and the quantitative model of folding based on amino-acid-amino-acid flux tubes allows a generalization which is however discussed at numerical level.

The third proposal asks whether protein folding could be induced by the flux tube connections of protein with water's MB rather than between proteins as in the first two models. This model is certainly an idealization since S-S valence bonds are known to play an important part in the folding. These flux tube connections could be accompanied by hydrogen bonds - even longer than usual if h_{eff} as spectrum for water as has been proposed. This involves more detailed ideas about the origin of hydrophobia and hydrophilia at the level of magnetic body (MB). Hydrophilic amino acids would tend to form flux tube connections with the MB of water unlike hydrophobic amino acids. The formation of flux tube connection would serve as a correlate for attention at molecular level.

Decade after writing this chapter the vision about the role of DNA

in TGD Universe evolved with inspiration coming from the model of water memory and homeopathy and the realization that homeopathy might represent a core elemement in the functioning of immune system involving new physics in an essential manner. The key idea is that dark variants of amino-acid sequences would have coded for the 2-braiding of the magnetic flux tube patterns defining invader molecule as a dynamical process: dark proteins would mimic physically the braiding of invader molecule's magnetic body. Dark DNA sequences would have coded this braiding symbolically and their translation to dark amino-acids would transform symbolic representation to a concrete physical one. The emergence of ordinary DNA and amino-acids would have realized the same at biochemical level and amino-acid sequences representing the invader would serve as antigene attaching to the invader molecule. Not only the pattern produced in protein folding but also the temporal pattern of protein folding would be coded by DNA.

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