Some TGD inspired comments about biocatalysis

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Abstract

In this article biocatalysis, Pollack effect, and catabolism and anabolism as aspects of metabolism are considered from the new physics perspective in the TGD framework. The new physics elements are the new view of space-time involving the notions of field body and of monopole flux tube as a carrier of phases of ordinary matter labelled by a hierarchy of effective Planck constant and behaving like dark matter. Pollack effect and OH-O^-+dark proton qubit, proposed to be topological qubit, are key elements in biological applications. In particular, the mysterious notions of high energy phosphate bond and the existence of two different phosphates, the organic and inorganic phosphate, are discussed. Also a mechanism of bio-catalysis based on the notion of a field body as a controller is considered in more detail.

Contents

1 Introduction

It seems that the Pollack effect [I2, L1, I4, I3] could play a fundamental role in living matter. In the TGD framework, Pollack effect has several applications generalizations (see [L1, L2, L5, L3, L6, L4]). OH-bonds, typically associated with acids, are fundamental and they could be dynamical so that Pollack effect and its reversal, that is the transformation $OH \leftrightarrow O^- + p$, where p is dark proton at the monopole flux tube, could be central in quantum biology [L7]. Pollack effect would generate exclusion zones (EZs) with negative charge and also the electrons could be dark. What follows is an attempt to test this proposal.

There are good reasons to believe that this qubit is topological and TGD analog of condensed matter Majorana fermion requiring respecting fermion number superselection rule [L9]. This topological qubit would make possible fully topological quantum computations based on braidings of monopole flux tubes [K1, K4, K3].

Catalyst action by a gel phase bounding water is necessary for the Pollack effect. It could be needed to kick the OH bond near to the criticality against the splitting to $O^- + p$ induced by the Pollack photon. One should also understand catalyst action in the TGD framework. I have proposed that here magnetic monopole flux tubes and large value of h_{eff} behaving like dark matter could play a central role: the latest discussion can be found in [L8]. Magnetic body could serve in the role of midwife or energy investor in bio-catalysis which together with the Pollack effect would make it possible to overcome the potential barrier making the reaction very slow.

In the sequel biocatalysis, Pollack effect, and catabolism and anabolism as aspects of metabolism are considered from the TGD point of view. In particular, the mysterious notions of high energy phosphate bond and the existence of two different phosphates, the organic and inorganic phosphate are discussed.

2 Basic facts about biomolecules

It is good to start with some basic biochemical notions relevant for what follows.

1. Acids (see this) is a molecule able to donate a proton (Brönsted-Lowry acid) or to form a covalent bond with an electron pair (Lewis acid). The hydronium ion H_3O^+ is an example of Arrhenius acid. Base (see this) is a substance which dissociates in aqueous solution to form hydroxide ions OH^-. Base is typically metal hydroxide such as NaOH, which dissociates to $Na^+ + OH^-$.

   According to TGD, in Pollack effect the -OH associated with a water molecule can dissociate and give rise to a water ion OH^- and dark proton at monopole flux tube. In the case of base like NaOH one would obtain Na^+ and HO^-. The strange effects of ELF em fields observed by Blackman [J1] and others suggest that Na^+ is a dark ion [K2]. These dark ions would play a key role in the TGD inspired biology. Could acids and bases differ in that the acids can donate ordinary proton and bases can donate dark proton or dark metal ion? Or are dark ions

   Note that besides ions, also radicals involving one unpaired electron, making them highly reactive, are important. H-O radical is a basic example.

2. Reduction means that the reactant gains electrons and oxidation that the reactant loses electrons (see this). One speaks of redox reactions.

3. Catalysts play a central role in biology by increasing the reaction rates dramatically. Enzymes (see this) are proteins acting as catalysts and ribozymes (see this) are RNA sequences serving for the same purpose. Also metal ions such as Mg++ can serve as catalysts. Co-factors NAD, NAD^+, NADP, NADP, $NADP^+$, NADPH, FAP involving phosphates (see this), FAP (this) act as catalysts.

   Within the enzyme, generally catalysis occurs at a localized site, called the active site.

2.1 Some facts about the binding energies of bonds appearing in biomolecules

It is useful to have some basic understanding about the binding energies of various bonds appearing in biomolecules. There are tables about bond energies: usually the bond energies are given using kJoule/mol as a unit. With particle physics background, eV is a more conventient unit and the energies can be translated to eV:s by using the equation eV= 96.45 kJ/mol. The chemical bonds can be classified to ionic-, valence- and hydrogen bonds.

1. Ionic bonds (see this) typically between ions with opposite valences at opposite ends of the row of periodic table (such as NaCl ionic bond) have energies in the range 1.8-15.6 eV and therefore rather high.

2. Covalent bonds (see this) involving sharing of electrons between bonded atoms. Single -, double -, and even triple bonds can appear. Often the rule that in stable states the total number of bonds is the number of states at the shell, is satisfied. Covalent bonds also have also rather high bonding energies in few eV range (see for instance this). The bond energies are usually given by using kJoule/mol as a unit. eV is a more convenient unit and the energies can be translated to eV:s by using ev= 96.45 kJ/mol.

   The following list gives biologically interesting examples of bond energies. The energies are given in eVs and the subscript $_3$ refers to a triple bond.

$$
\begin{array}{l}
H-H=4.5 \\
\\
C-H=4.3 \quad C-C=3.6 \quad C=C=6.2 \quad C-_3C=8.7 \\
\\
O-H=4.8 \quad O-C=3.7 \quad O=C=8.3 \quad O-_3C=11.1 \\
O-O=1.5 \quad O=O=5.1 \\
\\
N-H=4.0 \quad N-C=3.2 \quad N=C=6.4 \quad N-_3C=9.2 \quad N-O=2.1 \\
N=O=6.3 \quad N-N=1.7 \quad N=N=4.3 \quad N-_3N=9.8 \\
\\
P-H=3.3 \quad P-C=2.7 \quad P-O=6.0 \quad P=O=5.6 \quad P-P=2.1
\end{array}
\tag{2.1}
$$

   In the list the so-called high energy phosphate bond, assumed to appear between organic phosphates, is not mentioned. This notion is poorly understood and in the sequel a TGD based model for it will be discussed.

   ADP (see this) and ATP (see this) molecules would possess high energy phosphate bonds. The metabolic energy currency associated with single ATP molecule is about .22 eV carried by an ATP molecule (see this). ATP synthase (see this)is a molecular machine analogous to a power plant producing about 3 ATP molecules per single rotation and therefore giving energy .66 eV. The glycolysis portion of cell respirations produces two 2 ATP molecules making .44 eV. This energy is often called metabolic energy currency.

   On must be very careful with the meanings of the words when one talks about energies in order to avoid a total confusion. The bond energy associated with P-O bond is about 6.0 eV so that its splitting requires energy. On the other hand hydrolysis of ATP under standard conditions in presence of water by a cleavage of a single phosphate by water (creating ADP + Pi, where Pi is inorganic phosphate) yields -.32 eV change of Gibbs free energy (see this). The cleavage of pyrophosphate by water (creating AMP + PPi) yields .47 eV so that in both cases one can talk about high energy phosphate bond. Other triphosphates, such as UTP, CTP, TTP, and GTP yield equivalent amounts of energy, indicating that the energy source is the triphosphate, not the base in the nucleotide.

   The binding energy of C-N bond or peptide bond (see this, appearing between amino-acids in proteins and between phosphate group and ribosome in DNA, RNA and tRNA, is 3.1 eV. The bond is very stable and split by catalytic action. Peptide bond is formed by dehydration in which O=C-OH of the first amino acid and H^2N of the second amino acid fuse to O=C-N-H. This means that the O-H group disappears and only the second end of the peptide has OH group proposed to act as OH-O^- qubit besides OH groups in the side chains of amino-acids. There are 5 amino-acids which contain an OH group in the side chain implying that they also have OH group also when in proteins and these correspond to charged amino-acids Thr, Tyr, Ser, Glu, Asp. An interesting question is whether they are somehow special from the point of view of catalysis. For instance, could these amino acids correspond to active sites of enzymes?

3. Hydrogen bonds (see this) appear as H...O bonds between hydrogens and oxygens in water molecules. They appear also as N...HN and NH_2...O bonds between the bases of DNA strands. Their bond energy varies between .01 eV and 1.67 eV.

The rule is that the basic building bricks of biomolecules have large bond energies whereas the dynamical structures have much smaller binding energies. Catalyst are necessary in the ste structural changes.

2.2 Some important organic molecules

Also a list of some organic molecules important for what follows is in order.

1. DNA, that is deoxyribonucleic acid, as building bricks DNA nucleotides (see this). The nucleotides have a common building block phosphate making them acids and deoxyribose (sugar). The varying part of the DNA nucleotide is a base. There are 4 different bases: pyrimidines A,T and purines C,G. In DNA double strand the bases form pairs (see this) A-T resp. G-C, with A and T connected by 2 and C and G connected by 3 hydrogen bonds DNA. DNA codon consists of 3 nucleotides forming its letters. RNA codons are pyrimidines U,T and purines C-G.

   DNA codons code for 21 amino-acids having constant part O=C-OH part responsible for the acid property. Proteins are formed as sequences of amino acids in which peptide bonds -O=C-N are formed by dehydration (splicing of a water molecule) so that -O=C-OH and H_2N- is replaced with -O=C-(NH)-.

2. Carbohydrates are decomposed into monosaccharides (sugars). Glucose $C_6H_{12}O_6$ is basic example of monosaccharide. Carbohydrates, lipids and metabolic energy storage

3. Lipids or fats have carbohydrate sequences having O=C-OH carboxyle group at their ends (see this).

4. Alcohols (see this) are organic compound that carry at least one hydroxyl (OH) functional group bound to a saturated carbon atom.

5. Esters are building bricks of fatty acids which in turn are building bricks of lipids composing cell membranes. Ester is obtained from acid by replacing one H in at least OH group by organyl group R with at least one free valence electron in carbon atom so that there is C=O present (see this). Glyceride fatty acid is an ester of glycerol, in which H in at least one OH group is replaced with R. Glycerol is an alcohol.

Phosphate is an enigmatic molecule and deserves a separate discussion.

1. There are two kinds of phosphates (see this). High energy phosphate bond distinguishes between inorganic and organic phosphates. Is the organic phosphate excitation of inorganic phosphate which is near the splitting of OH bond to produce dark proton. Plants load the phosphate bonds with energy. Also animals can do this. Bacteria in soil use the energy of organic phosphates and produce inorganic phosphate.

   The metabolic energy of proteins can transform inorganic phosphate to organic phosphate. This requires energy to generate high energy phosphate bond. Is the energy already present in NAD and ANDP or is it liberated in the catabolism of nutrients and used to excite the inorganic phosphate? Does the formation of organic compound containing phosphorus liberate this energy as a binding energy? PO^4 binds to the molecule by valence bond (see this.

   Phosphorus cycle (see this) is a key cycle in biology. Plants provide the phosphorus needed by metabolism and the formation of bones and teeth. Soil microbes recycle organic phosphate to inorganic form for plant uptake. Plants transform the inorganic P (in soil and water) to organic phosphate.

2. Cofactors (see this) are metallic ions (such as Mg^{2+}) or complex organic molecules in which case they are called coenzymes. Coenzymes NAD(P)H and $NAD(P)^+$ (see this) contain nicotinamide and diphosphate thought to have what is called higher energy phosphate bond. These coenzymes are needed in catabolism and metabolism and are necessary to produce ATP from ADP. The transformation ADP $\rightarrow$ ATP requires as a coenzyme NAD, NAD^+ containing 2 phosphates.

3 Metabolism, catabolism and anabolism

Catabolism and anabolism are the destructive and creative aspects of metabolism.

3.1 Catabolism

The basic goal of catabolism (see this) as a way to release metabolic energy stored temporarily to ATP molecules and break the molecules involved to basic building bricks so that they can be rebuilt in anabolism.

Catabolism decomposes polysaccharides, lipids, nucleic acids, and proteins to smaller molecules containing large numbers of OH bonds associated with carbons. In particular, molecules such as carbohydrates and fats serving as metabolic energy sources are decomposed to smaller units such as monosaccharides and fatty acids.

Monosaccharides, fatty acids, and proteins can be decomposed further to produce energy. OH groups are transformed to O-phosphate groups used to transform ADP to ATP. This requires phosphate which is basically obtained as inorganic phosphate from soil and water and transformed to organic phosphate characterized by high energy phosphate bond.

1. Glycolysis (see this) is a set of reactions that converts glucose to pyruvate or lactate. This metabolic pathway can be considered as a paradigm of metabolic pathways. Glycolysis is also called the Embden-Meyerhoff pathway. Glycolysis involves two phases: the investment phase during which energy provided by ATP molecules is used and the phase in which energy is stored to ATP molecules. Glycolysis adds phosphates from NAD:s and NADPs to ADPs to build ATP which carries the energy to the molecule using it.

2. In lipid catabolism (see this) the triglycerides produced in glycolysis are decomposed to fatty acids (see this), which are main components of lipids appearing as building bricks of cell membranes.

   Fatty acids exist as three main classes of esters: triglycerides, phospholipids, and cholesteryl esters and serve as dietary sources of fuels and structural components for the lipid layers of cells.fats are decomposed into fatty acids and glycerol which is a simple alcohol, with 3 carbons with OH in each carbon (see this). Lipids or fatty acids are used to store metabolic energy.

   Ketone bodies (see this) serve as energy storages. Ketone bodies are water-soluble molecules or compounds that contain the ketone groups produced from fatty acids by the liver (ketogenesis). Ketone bodies are transported into tissues outside the liver, where they are converted into acetyl-CoA (acetyl-Coenzyme A) which then enters the citric acid cycle (Krebs cycle) and is oxidized for energy. Krebs cycle releases the energy stored in nutrients through the oxidation of acetyl-CoA derived from carbohydrates, fats, proteins, and alcohol.

3. Also proteins can be used as a metabolic fuel when glucose is not available. Also extra proteins are converted to glucose and triglycerides. Catabolism and anabolism are competing processes and a kind of self-amplifying loop in which too much anabolism induces catabolism and vice versa might emerge and must be avoided.

Coenzyme A or briefly CoA (see this) has a key role in Krebs cycle releasing metabolic energy in catabolism.

1. CoA contains a phosphate associated with adenine (A) and monophosphate associated with Acetyl (see this). CoA has a role similar to that of NAD(P). CoA is involved with fat metabolism and attaches to the fatty acyl group (see this), which involves a double-bonded oxygen atom and an organyl group (R C=O) or hydrogen in the case of formyl group (H C=O). CoA serves as an Acyl carrier protein.

2. CoA-acyl group bond to the sulspher of =O-S has a negative bond energy: -0.33 eV slightly below the metabolic energy currency and thus serves as a temporary energy storage and could have a role similar to that of phosphate bond. Note that the metabolic energy carried by a single ATP molecule is .22 eV. Also NAD(P) has a high energy bond so that it can serve for catalytic purposes by providing this energy temporarily.

3. The energy of the high energy phosphate bond is 489.7 kJ/mol= 5.1 eV and therefore much higher than metabolic energy currency. This energy scale is the same as that of valence bonds. A natural guess is that in biocatalysis this energy is used to kick the reactants over the potential barrier making the reaction very slow. The reactants would receive this energy temporarily and give it back after the reaction has occurred.

3.2 Anabolism

In anabolism these building brick molecules obtained in catalysis used to rebuild polysaccharides, lipids, nucleic acids, and proteins. From nucleic acids and aminoacids DNA, RNA and proteins are constructed in cells. Also bones are constructed in anabolism. Carbohydrates are constructed in plants and some bacteria by photosynthesis. Photosynthetic carbohydrate synthesis in plants and certain bacteria is an anabolic process that produces glucose, cellulose, starch, lipids, and proteins from CO_2. Lipids are constructed in both plant and animal cells and some lipids animal cells are obtained only in diet.

4 The TGD perspective

In the following TGD perspect of metabolism, in particular the role of phosphate and mechanism of catalysis is discussed. The new elements are the new view of space-time, in particular the notions of field body and magnetic monopole flux tubes; the predicted hierarchy of effective Planck constants h_{eff} meaning the existence of hierarchy of dark matter-like phases of the ordinary matter with arbitrarily long quantum coherence scales; Pollack effect interpreted as a transfer of ordinary protons to dark protons of field body; and the topological reactions of monopole flux tubes proposed to play a key role in biocatalysis.

4.1 The phosphate mysteries

Phosphate is the black sheet of the standard bio-chemistry. It involves two mysteries. The existence of two kinds of phosphates, the inorganic and organic phosphate, is the first mystery. The high energy phosphate bond is the second mystery.

1. There are two kinds of phosphates: inorganic phosphate ${PO_4}^{3-}$ and organic phosphate R-O-(O=P(OH)$_2$ appearing in di- and triphosphates and plants. The -OHs in the organic phosphate can become negatively charged. The organic phosphates in ATP would provide the metabolic energy to the inorganic phosphate.

   Phosphate cycle is fundamental for living matter. After the biological death, organic phosphate of the body transforms in the soil to inorganic phosphate by bacterial activity, which would use the organic phosphate as a metabolic energy source.Plants would in turn use the inorganic phosphate and transform it to organic phosphate by using the energy provided by photosynthesis. Animal cells would in turn use plants as nourishment and get the organic phosphate in this way. Animals can also use the inorganic phosphate and presumably transform them to organic phosphate by providing the needed energy. This cycle is known as the phosphate cycle.

   What distinguishes between these two kinds of phosphates?

2. There is also the mystery of high energy phosphate bonds. ATP and ADP and various compounds appearing in biology involving more than one phosphate are assumed to have what is called high energy phosphate bonds. The notion of high energy phosphate bond plays a central role in catabolism providing metabolic energy, which is assumed to be temporarily stored to the ATP serving. ATP would provide the metabolic energy currency of about .22 eV to the receptor molecule by forming a connection consisting of a flux tube pair. The bonding energy of the O-P bond in ATP is however 5 eV and has the wrong sign: the splitting of the bond requires this energy. Something goes wrong.

These mysteries inspired two TGD inspired questions.

1. Does the high energy phosphate bond exist at all? Could the TGD counterpart of a high energy phosphate bond be identifiable as a monopole flux loop carrying a dark proton created in the splitting of OH to O^-+p by Pollack effect, where p is dark proton at monopole flux tube [L7]. Could the dropping of the dark proton in the transition $O^-+p \to OH$ provide the metabolic energy currency and lead to the disappearance of the illusory high energy phosphate bond.

2. Could the difference between organic and inorganic phosphate be that the negative charge in the case of organic phosphate is due to the transfer of the proton of -OH to a dark proton at magnetic flux tube producing $-O^-$ ion + dark proton. Also the electron of the O^- in the organic phosphate could be dark? In the case of inorganic phosphate there would be no dark proton and the electron would be ordinary?

If the answers to these questions are affirmative then the notion of a field body (magnetic/electric) could solve the mysteries related to the phosphates.

4.2 Catalyst action in the TGD framework

Catalysts make possible biochemical reactions by providing temporarily the energy needed to drive the system near the top of the potential barrier making the reactions slow. How biocatalysts that are enzymes (proteins), ribozymes (RNA) and also metal ions, can provide this energy. Catalyst must provide the energy needed to almost overcome the energy barrier preventing the reaction and measured in few eVs. It would seem that the metabolic energy currency .22 eV provided by ATP$\to$ ADP is much smaller than this energy and can only give the additional energy allowing to overcome the energy barrier. After the reaction has occurred the catalyst would get back the energy.

In the general TGD based picture, the reaction might look as follows.

1. Catalyst, reactants, and ATP possess U-shaped monopole flux tubes acting as tentacles. In the first step a reconnection between the tentacles of the catalyst molecule and those reactants and ATP takes place and connects them by flux tube pairs. The same could occur also for tentacles of reactants. The U-shaped monopole flux tube pairs connecting catalyst to reactants and in the case of enzymes (and perhaps also ribozymes, which however have phosphates) also to ATP molecules would carry energy making it possible to overcome the energy barrier(s) associated with the reaction.

2. This makes it possible for the flux tube pairs to find each other. The reduction of the value of h_{eff} for the flux tube pair would reduce the value of the dark cyclotron energy (proportional to h_{eff}) and possibly also the value of classical magnetic energy. The energy ΔE liberated in this way would help the reactants to get near the top of the potential wall. In the case of cyclotron energy, this would require a large value of h_{eff} and of gravitational Planck constant for the Earth would provide it. ATP could provide the remaining energy of order .22 eV making it possible to get over the potential barrier so that the reaction would take place.

3. After the reaction the reaction products would have additional energy and would have a recoil momentum. They would be associated with the ends of the flux loops connecting the catalyst to the reactants. These would get longer as a consequence and split by a reconnection, a phase transition increasing the value of h_{eff} back to its original value would occur and the the energy ΔE borrowed from the catalyst would be returned to it. This suggest that the catalyst acts like a shell surrounding the reactants and explodes and takes back the energy ΔE.

This view can be compared with the following proposal that I found in the web (see this).

1. Each reaction in a cell has a specific enzyme. Each enzyme has binding sites for, say, two molecular species *and* for an ATP molecule. When a reaction takes place, the two species bind to the enzyme, and a little later, an ATP molecule binds.

Comment: The contraction of the flux tube pairs would provide the system consisting of catalyst and reactants with an energy ΔE measured in eVs taking it near to criticality for the reaction to occur. .

2. For some reason (why ?), the ATP→ ADP reaction is now energetically favourable, so the high-energy bond breaks.

   Comment: The ATP→ ADP +Pi reaction would be essentially the reversal of a Pollack effect and involve a dropping of a dark proton from the field body liberating the metabolic energy currency .22 eV. This reaction can occur if the sign of the energy difference of -OH and -O^-+ dark proton states changes sign. This could be due to the presence of an electric field modifying the energy difference. I have proposed that this mechanism is central in bio-control [L7].

3. This releases electromagnetic energy as a photon at some characteristic frequency.

   Comment: The photon would be the counterpart of the Pollack photon allowing the reaction to occur if the system is near the criticality that is already near the top of the potential barrier.

4. Certain bonds in the enzyme have a resonant frequency that allow them to absorb this electromagnetic energy (the EM energy disturbs molecular dipoles?).

   Comment: The first step involving the contraction of the flux tube pairs would have driven the system, near criticality for the reaction. The absorption of the Pollack photon would break the camel's back and initiate the reaction.

5. The 3D structure of the enzyme is disturbed (i.e. it bends) in such a way that the 2 molecular species are mechanically forced together, providing sufficient activation energy for the reaction in question.

   Comment: The geometry and charge distribution would change this and the reaction to occur.

6. The newly formed species no longer binds nicely to the enzyme (why ?) so it detaches, as does the ADP, which also doesn't bind as nicely as ATP.

   Comment: TGD would suggest that catalyst molecule should surround the reactants and that catalyst receives recoil momentum forcing the lengthening of the flux tubes and increase of h_{eff} made possible by the energy ΔE that it invested to the reaction.

These considerations raise some questions about the energetics of the field bodies serving as controllers.

1. Field bodies (magnetic or electric), actually flux tube loops, serve as kinds of energy investors in biocatalysis. While reactants and ATP are affected in the reaction, the catalyst leaves the reaction without essential change and gets its energy investment back. The temporary energy gain ΔE needed to overcome energy barriers would come from the shortened flux tube pairs connecting the catalyst to the reactants rather than from the catalyst as is assumed in textbooks. ATP would provide the Pollack photon making it possible to overcome the potential barrier which is already made very low by the energy provided by the field body of the catalyst.

   Catalyst would serve as a kind of midwife. What distinguishes it from the reactants? The active site of a heterogeneous catalyst (heterogeneous catalyst is in a different phase than reactants) is identified as an ensemble of atoms which directly catalyzes the reaction. Biocatalysts can be regarded as a special case of heterogeneous catalysts. Does the active site distinguish heterogeneous catalysts from the reactants? Does the active site correspond to a higher level of the h_{eff} hierarchy as compared to the reactants?

2. Does the energy provided in biocatalysis correspond to the classical magnetic energy of the flux tubes, the dark cyclotron energy associated with the dark particles at the magnetic body, or to both? The first option would conform with the temporary reduction of h_{eff} shortening the flux tubes and liberating classical magnetic energy proportional to the length of the flux tube. The reduction of h_{eff} would in turn liberate cyclotron energy.

4.3 Catabolism and Pollack effect

In the TGD framework, the Pollack effect is proposed to be the basic mechanism of metabolism and lead to the formation of ATP with ionized phosphate and dark protons taking care of the distribution of the metabolic energy as a standard metabolic currency. Essentially a generation of dark protons would be in question. The OH bonds are potential providers of dark protons and monosaccharides (see this) as end products of catabolism of carbohydrates, in particular glucose, are optimal in this respect. For $(\text{H-C-OH})_n$-CHO the number of OHs is maximed so that also the number of potential dark protons is maximized. The process involves oxidation and oxygen obtained in breathing is therefore needed. Carbon dioxide and water is the final outcome of the process.

Consider next the proposed role of Pollack effect.

1. Acid capable of donating H^+. Is the donated proton ordinary proton or is donated proton in biological systems a dark proton, which then drops to the acceptor? DNA is acidic because of phosphate groups, which are usually represented as ionized. The Pollack effect or its reversal could occur when an external electric field changes the sign of the energy difference of the states -OH and $-O^-$ + dark proton. Note that also the electron of $-O^-$ could be dark in organic phosphate.

   The transformation of proton to dark proton or its reversal would in the TGD framework correspond to a process analogous to the change of a value of bit. This leads to the proposal that OH-O^- qubit and more generally, the generalization of this qubit could play a fundamental role in biology and even in systems involving cold plasma [L7]. In fact, OH-O^- could give rise to a topological qubit analogous to Majorana qubit [L9].

   Amino-acids in proteins lose their OH as the peptide bond (C-N bond) between two subsequent amino acids is formed by dehydration so that only the second end of the protein contains O=C-OH group. The 5 amino-acids Thr, Tyr, Ser, Glu, and Asp contain the -OH group in their residue so that Pollack effect could be possible for them. Note that the amino acid Cys (see this)) contains an -SH residue at least chemically analogous to -OH residue. It is frequently observed in functionally important (catalytic, regulatory, cofactor binding, etc.) sites of protein. Among the unique properties of Cys are its ability (i) to react with another Cys forming a disulfide bond, and (ii) to functionally interchange with another amino acid, selenocysteine (Sec).

   Also fatty acids (see this) contain O=C-OH groups at their ends and are potential providers of dark protons.

2. For phosphates the -OH is assumed to split spontaneously to O^- + dark proton, at least in the illustrations. The formation of ATP would generate dark protons. The use of metabolic energy reduces the number of dark protons as they drop back from the magnetic body in the transformation ATP$\rightarrow$ ADP+Pi. The essence of catabolism would be generation of dark protons assignable to the phosphates of ATP and ADP. As proposed, there is no need for a high energy phosphate bond since the dark proton would carry the metabolic energy currency.

3. Pollack effect generates exclusion zones which behave strangely: in particular the arrow of time seems to be reversed. This is possible in the zero energy ontology of TGD. If the electrons in EZs are dark, the duration of the period with the reversed arrow of time would be scaled up. It would not be surprising if both dark electrons and dark protons at field bodies would distinguish between biochemistry and non-organic chemistry.

   How does the Pollack effect relate to bases? Bases are able to donate electrons. Is this electron ordinary electron or could it be a dark electron, possibly formed in Pollack effect.

O=C-OH groups are potential providers of protons eventually transformed to dark protons by Pollack effect. The feed of metabolic energy makes possible Pollack effect and phosphate ions and dark protons are formed. The final outcome is APT containing phosphates (see this, this). Each amino acid contains O =C-OH group but proteins contain this group only at its second end.

1. The oxidation of sugars produces water and carbon oxide. Monosaccharides or simple sugars (see this) are optimal in this respect and are the final outcome of the catabolic process. For

(H-C-OH)$_n$-CHO the number of OHs is maximized so that also the number of potentially dark protons is maximized.

Glycolysis could essentially mean the transformation of protons to dark protons and the transformation ADP→ATP in which inorganic phosphate would receive this dark proton carrying metabolic energy currency of about .22 eV. ATPAse machinery would pump 3 ordinary protons per rotation and transform them to dark protons of the phosphate added to ADP.

2. Alcohols contain OH-group bound to a saturated C atom.which therefore has valence bonds to 3 residues this. Also alcohol burning liberates energy. The psychological effects of sugars and alcohols would relate to the heightening of the level of consciousness as dark protons are created.

3. Dehydration means loss of OH groups because water is formed (see this). The ability for the Pollack effect is reduced in dehydration.

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