Hypothetical structure for energy transformation
Evolution of cellular structures for energy transformation

János Hunyady

Department of Dermatology, Faculty of Medicine, University of Debrecen.
Nagyerdei krt. 98, H-4032, Debrecen, Hungary.

Sources of support: Szodoray Foundation, 4032 Debrecen, Nagyerdei krt. 98, Hungary

Correspondence: Prof. emeritus Dr János Hunyady, 1052 Budapest Petőfi Sándor utca 3 fsz. 6.
Tel.: 00 36 30 218 4196
e-mail: hunyadyjanos11@gmail.com.

Abstract

The present paper represents a hypothetical structure, the structure for energy transformation (SET), and its proposed evolution, which might be responsible for the proper energy transformation steps leading to the continuous production of H^+ and ATP in living cells. We predict that the electron flow is realized through the electron flow device (EFD). We suppose that there are several versions of the SET with three of them being described below. The hypothesis is based on the properties of the atoms of the protonated adenine molecule and docking computations of molecular mechanics involved, suggesting that two ascorbate molecules may occupy the empty NADPH pocket, preferably binding to the adenine binding site. We hypothesize that the adenine originates from uric acid (UA), resulting in an ATP-UA-ADP-ATP cycle. It would also mean that UA is one of the oxygen carriers in aerobic glycolysis. We also suppose that the EFD contains the well-known molecules and clusters of the electron transport chain supplemented with two additional UA originated adenine molecules and two L-ascorbic acid molecules. Based on all this, we surmise that a tetra adenine octo phosphate ring (TAR) exists, in which the UA originated adenine molecules form a ring. The molecules are linked to each other through the N7-C2 and C8-N1 atoms of the adenine molecules by $H_2PO_4^{e-}$ molecules. The four N10 atoms of the adenine molecules bind one flavin, one nicotinamide, and two L-ascorbic acid molecules. Six D-glucose molecules complete one unit of the structure. Both Fe-S and cytochrome clusters and dehydrogenase~~s~~ ensure the continuous operation of the unit. Eukaryotic cells are equipped with the mechanisms of the SET, using aerobic glycolysis of Warburg and the SET of oxidative phosphorylation; thus, they can live in an anoxic environment as well. It is hoped that the concept of the SET developed here will help to better understand the complex process of energy transformation.

1. Introduction

1.1 Anaerobic glycolysis, aerobic glycolysis, and oxidative phosphorylation

The function of the energy generating system of cells is well known. The efficiencies of anaerobic glycolysis, aerobic glycolysis, and oxidative phosphorylation are different. They produce 2, 4, and 36 adenosine triphosphate (ATP)/mol^{-1} glucose, respectively. We know less about the composition and development of the structure responsible for energy production.

We believe that cells with 2, 4, or 36 ATP/mol^{-1} glucose efficiencies have distinct structures for energy transformation (SETs). The structure providing continuous electron flow has already been established in the world without O_2. Later, new SETs have evolved. Eventually, the eukaryotic cell was formed through the symbiosis of an ancient cell using aerobic glycolysis and a modern cell with oxidative phosphorylation [1]. The cellular energy system may have gradually evolved. We assume that the energy systems of cells of different nature are made up from the same building blocks. Here, we describe the putative phylogenetic origin of these structures.

Eukaryotic cells can also function under anaerobic conditions, ensuring the body's ability to regenerate. The aerobic-anaerobic shift is enabled by the hypoxia inducible factor (HIF) [2, 3]. Malignant tumors are composed of heterogeneous cell populations. Most cells use aerobic glycolysis to produce energy, while a minor proportion of cells use oxidative phosphorylation to produce energy. However, in the literature dealing with the characterization of tumor cells, the existence of the dual-energy system is usually not mentioned.

1.2 Mitochondria contain vitamin C

Korth et al. supposed that two L-vitamin C (ascorbic acid, L-AA) molecules are in the NADPH pocket, presumably near the adenine binding site in the inner membrane of the mitochondria [4]. Their conclusion is based on molecular mechanistic docking computations.

1.3 Properties of the atoms of the protonated adenine molecule

Turecek and Chen investigated the features of the atoms of the protonated adenine molecule in the gas phase, water clusters, and bulk aqueous solution. They calculated that protons in the adenine ion 1^+ undergo fast migrations among positions N1, C2, N3, N10, N7, C8, and N9, which results in an exchange of hydrogen atoms before the loss of a hydrogen atom forming adenine cation radical at a 415 kJ mol^{-1} dissociation threshold energy [5]. We suppose that the proton displacement acts as a signal to determine the path of electrons migrating in the adenine molecule. Thus, according to the results of Turecek and Chen, the adenine molecule has two entering points for electrons (N1 and N7), while electrons might leave the molecule through the N10 atom [5] (Illustration 1).

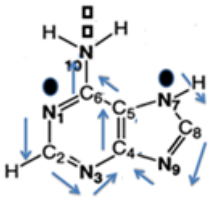


Illustration 1. Two entering points (● N1 and N7) and one leaving point (□ N10) of electrons of the adenine molecule.

1.4 Fe-S clusters

Many Fe-S clusters are known in organometallic chemistry and as precursors to synthetic analogs of the biological clusters. The most abundant Fe-S clusters are of the rhombic [2Fe-2S] and cubic [4Fe-4S] types, but [3Fe–4S] and [4Fe–3S] clusters have also been described. Two probable structures for $[Fe2S2(SCH2CH2OH)]^{e2-}$ are presented in Illustration 2.

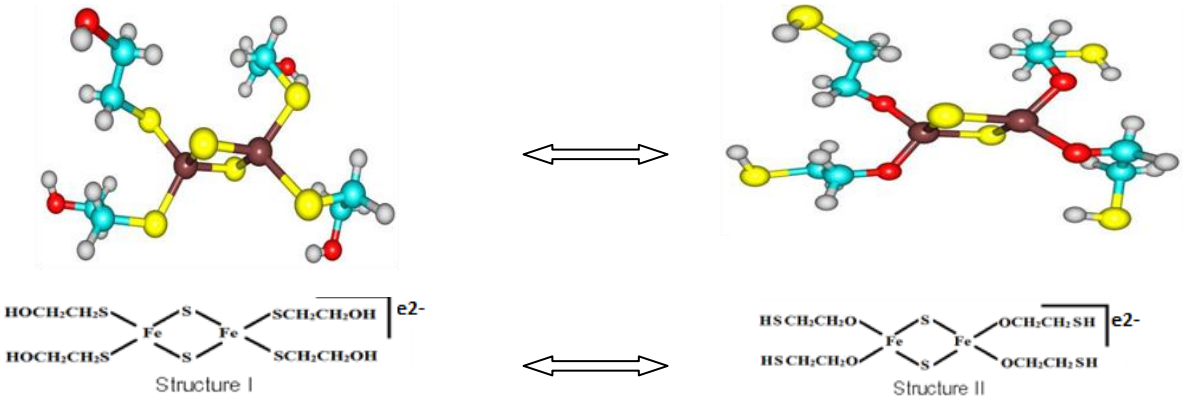


Illustration 2. Two probable structures for $[Fe2S2(SCH2CH2OH)]^{e2-}$ and their density functional theory optimized structures. Structure I is when Fe coordinates SCH_2CH_2OH through S, while Structure II is when Fe coordinates SCH_2CH_2OH through the oxygen donor site.

The structure of oxygen, sulfur, and iron atoms allow the realization of glycolysis and glycogenesis in plants. There are six electrons in the outer electron shell of oxygen and sulfur (Table I).

Table I. Some Essential Characteristics of Oxygen, Sulfur, and Iron Atoms

	Electron configuration	**Electrons per shell**	**Atomic number**
Oxygen	[He] $2s^2\ 2p^4$	2, 6	8
Sulfur	[Ne] $3s^2\ 3p^4$	2, 8, 6	16
Iron	[Ar] $3d^6\ 4s^2$	2, 8, 14, 2	26

In sulfur and oxygen molecules, the distance of the outermost electron shell from the nucleus is different. Therefore, the strength of their attachment to iron is also different. O^{e2-} binds more strongly to Fe^{++} than sulfur, so oxygen takes the place of sulfur in the Fe-S complex. The flow of electrons in the complex results in the back change of sulfur-oxygen.

The properties of oxygen, sulfur, and iron allow the oxygen and sulfur atoms to swap places in the Fe-S cluster. The exchange is mediated by the electron change mediated by the environment.

1.5 The currently prevailing view of electron transport: The electron transport chain and the structure of mitochondria

The mitochondrial multienzyme complexes of oxidative phosphorylation are well known. They are: Complex I: NADH-Coenzyme-Q reductase: prosthetic group flavin mononucleotide, or FMN; six to seven iron-sulfur clusters; Complex II: succinate-Coenzyme-Q reductase, five subunits: FAD, covalently bound; three iron-sulfur clusters; cytochrome b560; Complex III: Coenzyme-Q-cytochrome c reductase: cytochrome b562; cytochrome

b566; one iron-sulfur cluster; cytochrome c1; Complex IV: cytochrome c oxidase: cytochrome a; cytochrome a3; and Complex V.

Periplasm is the place of energy transformation in the bacterial ancestor cells. In the mitochondria, its equivalent is the ~20 nm gap between the outer membrane and the part of the inner membrane that is known as the mitochondrial inner boundary membrane.

The outer membrane separates the mitochondria from the cytoplasm. It surrounds the inner membrane, which separates the intermembrane space from the protein-dense central matrix. The inner membrane is differentiated into the inner boundary membrane and the cristae. The two regions are continuous at the crista junctions, but there is a unique gate, the mitochondrial contact site, and the cristae organizing system (MICOS) to inhibit the free protein and ion flow between the intermembrane space and the cristae. The cristae extend more or less deeply into the matrix and are the main sites of mitochondrial oxidative phosphorylation [6, 7].

All matrix proteins imported into the mitochondria from the cytoplasm must pass through the outer and inner membrane as well as the intermembrane space. Protein translocases of the outer (TOM) and inner (TIM) membrane form a supercomplex that has been visualized by cryo-electron tomography (cryo-ET) [8]. The TOM/TIM supercomplex spans the intermembrane space and appears to be held together by the polypeptide in transit. The inner boundary membrane must contain large numbers of the carrier proteins that shuttle ions, ATP, adenosine diphosphate (ADP), and small metabolites between the cytoplasm and the matrix. These small membrane proteins include, most notably, the 33 kDa ATP/ADP carrier as well as numerous other related and unrelated membrane transporters [9].

1.6 The inner membrane cristae

The inner membrane forms invaginations called cristae that extend deeply into the matrix. The cristae define the third mitochondrial compartment, the crista lumen. The crista membranes contain most, if not all, of the fully assembled complexes of the electron transport chain (ETC) and ATP synthase. The lumen of cristae contains large amounts of the small soluble electron carrier protein cytochrome C. The mitochondrial cristae are thus the primary site of biological energy transformation in all non-photosynthetic eukaryotes [6].

Cristae are disk-like lamellar, tubular or bag-like extensions of the inner boundary membrane and are continuous with it at the crista junctions. Crista junctions in the mitochondria of post-mitotic heart or liver cells are small circular apertures of ~25 nm diameter [10, 11]. In the mitochondria of all organisms, the MICOS system [12], an assembly of one soluble and five membrane-bound proteins, anchors the cristae to the outer membrane. Cryo-ET of intact mitochondria, which resolves large membrane protein complexes in situ, did not reveal any such assemblies (for example, ATP synthase or Complex I) in the boundary membrane [6].

1.7 ATP synthase forms rows of dimers in cristae membranes

The mitochondrial F1-FO ATP synthase is the most conspicuous protein complex in the cristae. ATP synthase is an ancient nanomachine. It uses the electrochemical proton gradient across the inner mitochondrial membrane to produce ATP by rotator catalysis [13, 14].

1.8 Open questions

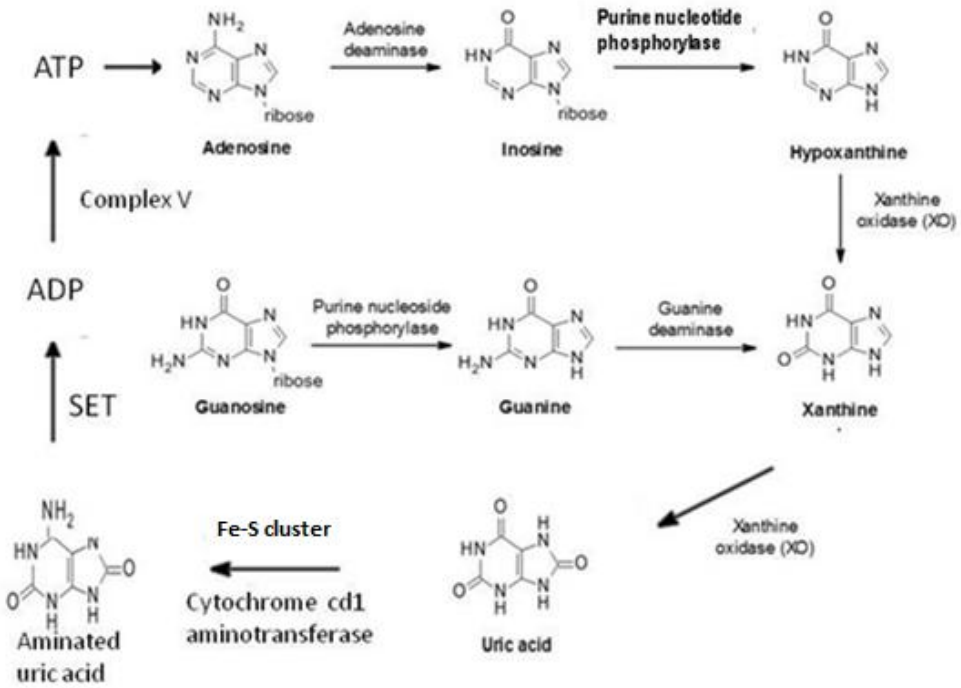
We still do not know:

1. How exactly Complex I works, especially which way is electron transfer coupled to proton translocation?
2. Are there six or seven Fe-S clusters in Complex I?
3. Where and exactly how do the respiratory chain complexes and ATP synthase assemble?
4. Where does the ADP in Complex V come from?
5. How the continuous electron transfer and ATP production is managed?

2. Hypotheses

2.1 ATP-uric acid-ATP cycle

The view that uric acid (UA) is the end-product of ATP metabolism is generally accepted. Gounaris et al. reported that the hypoxanthine molecule could develop as an effective capture of inorganic nitrogen species. These authors have also reported that hypoxanthine, the biochemical precursor of adenine and guanine, was able to capture nitrite ions and be reductively transformed into adenine [15]. A similar reaction may occur by UA amination. Thus, UA is not an end-product, but one element of an ATP-adenosine-inosine-hypoxanthine-xanthine-UA-aminated UA-adenosine-ADP-ATP cycle (Illustration 3).



SET: structure for energy transformation

Illustration 3. The hypothetical ATP-uric acid-ATP cycle. From the ATP, uric acid is created by the well-known metabolic way. Later, from the uric acid, an aminated uric acid, then adenosine, ADP, and finally ATP are generated.

2.2 Hypothetical structure for energy transformation

2.2.1. The complex energy transformation results in the production of energy by the oxidation of the carbon atoms of the glucose, the generation of ATP, and the provision of membrane potential by H^+.

For the engines of cars, petrol must be produced from crude oil. Similarly, sugar (glucose), the cell's energy molecule, needs to be converted into an ATP molecule. When life began, this process could take place in the membrane of the first cells. Nowadays, mitochondria are specialized in this task in eukaryotic cells. During evolution, the essential elements of the energy supply system were formed. These elements, like the molecules encoding the genetic trait, are fundamental structures of the living world.

We created a hypothetical structure that supplies the cell with energy. The hypothesis is based on well-known data, such as the oxidative pentose pathway, the electron transport system in the mitochondria [16], the biochemical nature of $H_2PO_4^{e-}$, the results of Turecek and Chen in connection with the nature of adenine [5], and the oxidative experimental findings supported by stoichiometric computations, suggesting that there are two vitamin C molecules found in the NADPH pocket [4].

The JSME Editor courtesy of Peter Ertl and Bruno Bienfait was applied for calculating the presented three-dimensional (3D) structures of the hypothesized structures [17]. The computer program helped in the creation of the vision of the SET. The figures mostly represent part of the structure under study. All pictures made by this program are signed with “JSmol.”

Our hypothesized SET consists of the well-known Complexes I, II, III, IV, and V, completed with two adenine, two L-vitamin C, and two D-glucose molecules. We believe that the tetra adenine octo phosphate ring (TAR) is the engine of the five multienzyme complexes in the mitochondria.

2.2.2 Evolution of the energetic system in the living world

Maintenance of life requires continuous electron flow. Cells provide this through permanent glycolysis. In cells, glucose is transformed into the ATP molecule, while CO_2, energy, and H^+ are produced, which provides a continuous membrane potential.

We assume that, in every cell, SETs provide the cell with the proper energy supply and H^+. The SET directs the processes of glycolysis and glycogenesis in plants. We think that the units of the SET consist of the same building blocks.

We suppose that the enzyme aminotransferase may create aminated UA molecules through Fe-S clusters and dehydrogenases. The question is whether nitrogen is coming from NO_2^{e-}, as suggested by Gounaris et al. [15], or from biogenic amines.

Fe-S clusters take up oxygen atoms from the C1 position of UA molecules. At the same time, UA will be nitrified with the help of the aminotransferase enzyme. The clusters obtain four oxygen atoms from four UA molecules. They produce four aminated UA molecules and four H_2O molecules.

4 UA+ 4 NH_3 (biogenic amines) + aminotransferase + $[Fe_2S_2(SCH_2CH_3)]^{e2-}$ cluster = 4 NH-UA^{e-} + 4 H_2O.

It is generally expected that the ETC is responsible for electron transport in the cells. We propose that the SET consists of the mitochondrial clusters and enzymes supplemented with two further UA originated adenine molecules, two L-AA molecules, and two D-glucose molecules. This structure is 3D. Thus, we named it the electron flow device (EFD). The complete structure of the SET contains dehydrogenases and both Fe-S and cytochrome clusters, in addition to the EFD.

2.3. Structures for energy transformation

2.3.1. Adenine binding place of NADPH contains four aminated uric acid/adenine molecules

We suppose that the known NADPH pocket contains four adenine molecules. They are bound to each other by eight H_2PO_4 molecules through the N7-C2 and C8-N1 atoms of the adenine molecules. They form the TAR. Adenine is created from aminated UA; thus, at the start of energy transformation, the ring can be best described as a tetra-aminated UA ring.

The TAR can facilitate electron transfer. According to our hypothesis based on the results of Turecek et al. [4], the N1 and N7 atoms of the adenine molecules are the entering points, while the N9 and N10 atoms might be the exit points for the electrons. The electron capture points are linked by $H_2PO_4^{e-}$ molecules. In the TAR, electrons are arriving from the $H_2PO_4^{e-}$ molecules (2^{e-}).

2.3.2. Basic units of structures for energy transformation

According to our hypothesis, a unique SET is responsible for the continuous H^+ and ATP production of living cells. We predict that the electron flow is realized through the EFD. We suppose that there are several versions of the SET. Three of them are described below. They are the SET of anaerobic glycolysis (SET-ANG), the SET of aerobic glycolysis (SET-AG), and the SET of oxidative phosphorylation (SET-OP).

2.3.3. Amide-carbonyl hydrogen bond

The amide-carbonyl hydrogen bond determines the proper function of the SETs, as all forms of the SET units consist of four amide-carbonyl connections (2 x ascorbic acid-adenine, flavin-adenine, and nicotinamide-adenine). Accordingly, dehydrogenases are important protein structures catalyzing the reactions at the connecting points of the SET units.

2.3.4. Molecules determining the structures for energy transformation

The SET units consist of the EFD (four UA originated adenine, one nicotinamide, one flavin, two L-Ascorbic-acid-6-phosphate and six 5-phospho-D-glucose molecules). The EFD comprise the mitochondrial multienzyme complexes, complemented by two 5-phospho-D-glucose two L-AA and two adenine molecules that are derived from UA molecules. This structure organizes the mitochondrial multienzyme complexes into functional units. The SET is made up of structural and base molecules. The structural molecules are clusters of both Fe-S and cytochrome, flavin and nicotinamide, dehydrogenases, membrane transporters, and mitochondrial multienzyme complexes. The base molecules are UA, L-AA, D-glucose,

$H_2PO_4^{e-}$ and biogenic amines. They arrive consecutively to ensure continuous ATP production and electron flow.
The composition of the building structures determines the products of the given SET unit. The TAR is formed by four aminated UA molecules as a tetra UA ring. In that way, eight oxygen atoms are offered by the four UA molecules and eight oxygen atoms provided by the eight $H_2PO_4^{e-}$ molecules.

All the SETs contain the ADP-producing unit (ADP-pu) supplemented with further clusters of both Fe-S and cytochrome. The characteristics of these clusters determine the nature and products of the structure.

The ADP-pu consists of the EFD complemented with six $[Fe_2S_2\ (SCH_2CH_3)]^{e2-}$ clusters. Four of the clusters are responsible for the oxidation of the 6th carbon atoms of six D-glucose molecules and of the two L-AA molecules. The 5th $[Fe_2S_2\ (SCH_2CH_3)]^{e2-}$ cluster oxidizes the 5th carbon atoms of the two L-AA molecules, while the 6th cluster, together with the aminotransferase enzyme and dehydrogenase, is responsible for the catalysis of the aminated UA molecules.

The SET unit of anaerobic glycolysis (U-ang) consists of five $[Fe_2S_2\ (SCH_2CH_3)]^{e2-}$ clusters and one further cluster (3Fe-3S?), which is responsible for the production of six O^{e2-}. Thus, the U-ang can produce two ATP molecules.

The SET unit of aerobic glycolysis (U-ag) consists of seven $[Fe_2S_2\ (SCH_2CH_3)]^{e2-}$ clusters, accordingly it can produce four ATP molecules.

The SET-OP consists of nine ADP-pus. It also contains one pyruvate dehydrogenase complex (PDC), which produces 36 ATP molecules.

Other numbers of clusters of both Fe-S and cytochrome can result in additional SETs.

2.3.5. The nest of structure for energy transformation

We suppose that, both in the mitochondrial cristae of eukaryotic cells and in the periplasm of all kinds of cells, pre-formed sites (nests) exist for energy transformation. The nest is identical with the positions of the Complexes I, II, III, IV, and V within the inner membrane [6]. Base molecules arrive into the nest where the successive production of both ADP and ATP molecules as well as H^+ starts. When the energy transformation is completed, ATP, CO_2, and H^+ leave the nest and new base molecules will arrive.

2.3.6. The reaction of the Fe-S cluster with aminated uric acid and $H_2PO_4^{e-}$

In each of the four connecting points of the EFD, two aminated UA molecules and two $H_2PO_4^{e-}$ molecules react with one Fe-S cluster. We believe that the SET units use the aminated

UA molecules. Aminated UAs arrive at sites defined by four Fe-S clusters (Illustration 4). Illustration 4A shows the nest of the EFD before the start, and Illustration 4B shows when oxygen atoms (O^{e2-}, circled) are already prepared for the oxidation of carbon atoms.

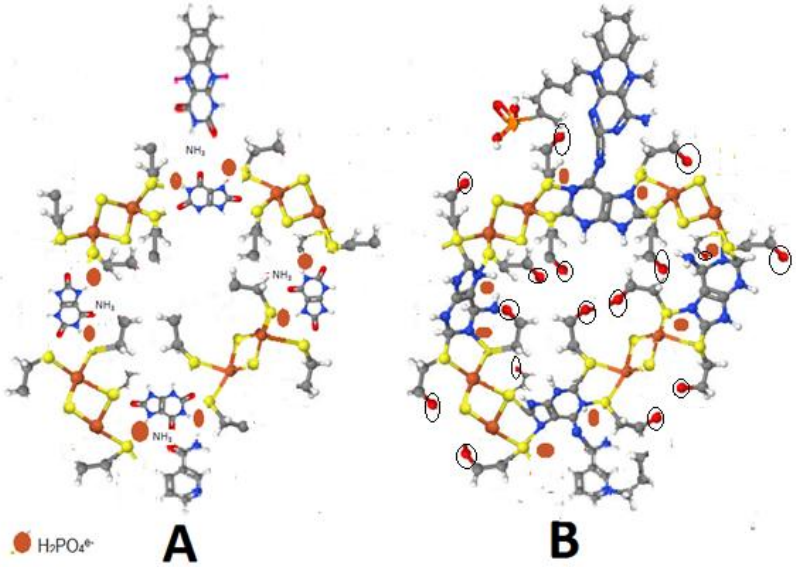


Illustration 4. A: Four $[Fe_2S_2\,(SCH_2CH_3)]^{e2-}$ clusters, flavin, and nicotinamide molecules are waiting for the basic molecules (eight H_2PO_4, four NH_3 [biogenic amines], and four uric acid) of the EFD. The D-glucose and L-ascorbic acid molecules are not presented. B: Oxygen atoms (O^{e2-}, circled) of four aminated uric acid molecules and eight H_2PO_4/PO_3 molecules are ready for the oxidation of carbon atoms.

In each of the four Fe-S clusters, the sulfur atoms are replaced by oxygen derived from $H_2PO_4^{e-}$ (eight oxygen atoms) and aminated UA molecules (eight oxygen atoms).

One of the four connecting points is presented in Illustration 5, with arrows indicating the supposed electron flow. In each connecting point of the EFD, two electrons are transferred. I think that when adenine molecules are organized into the TAR, the electrons pass the molecule not only in the direction of the N10 atom, as presented in Illustration 1, but also in the direction of the N9 atom (Illustration 5). The 3D picture is available at https://set.suicidevolution.com/.

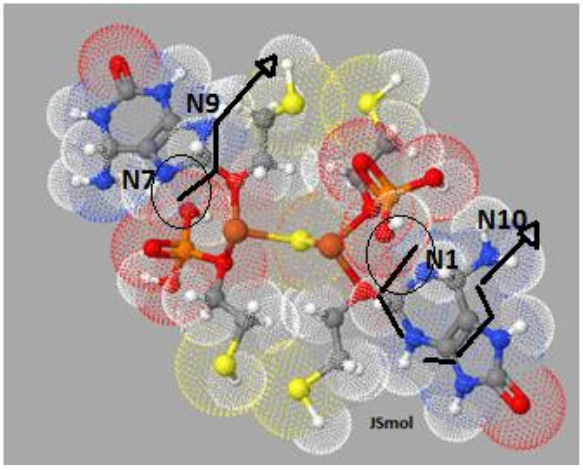


Illustration 5. Two aminated uric acid molecules and two H_2PO_4 molecules arrive in one $[Fe_2S_2\,(SCH_2CH_3)]^{e2-}$ cluster. The aminated uric acid molecules and $H_2PO_4^{e-}$ molecules are bound in the Fe-S cluster. $H_2PO_4^{e-}$ is not yet bound to the aminated UA (circle). Arrows indicate the supposed electron flow.

As a result, the tetra UA/adenine ring is formed. Its interfaces have electron entering and leaving points. The $H_2PO_4^{e-}$ molecule, which is bound by oxygen through the Fe-S cluster, is located near an electron entering point (circle) that allows electrons to enter the adenine molecule (Illustration 5). First, at each entry point, two electrons coming from two hydrogen atoms will leave behind two protons. Finally, the four UA originated adenine molecules and the eight H_2PO_4 molecules form one TAR.

2.3.7. Process of uric acid-adenine conversion during energy transformation

Four aminated UA molecules arrive in four of the seven Fe-S clusters of the U-ag, where the oxygen atoms of the UA molecules are bound by four of the iron-sulfur complexes. The Fe-S clusters also bind eight $H_2PO_4^{e-}$ molecules to one of their oxygen atoms.

In the next step, eight $H_2PO_4^{e-}$ molecules are bound to the newly formed four adenine molecules, linking their N7-C2 and C8-N1 atoms. Subsequently, 8 x 2 electrons arrive at the EFD via the electron-accepting points of the adenine molecules (N1 and N7), leaving them at the four N9 and N10 atoms. The connection of the Fe-S cluster with UA forms the possibility of electron transfer in the direction of the nitrogen atoms (N9 and N10) of the adenine molecules (Illustration 5).

2.3.8. Nicotinamide, flavin, and vitamin C molecules connected to tetra adenine ring

The N10 atoms of the aminated UA molecules connect to additional molecules as well. The supposed binding of UA originated adenine molecules to flavin, nicotinamide, and L-vitamin C molecules are presented in Illustration 6. The tetra adenine ring binds nicotinamide, flavin, and two L-ascorbic acid molecules with the help of dehydrogenases. The double bond between the N10 atoms of adenine and these molecules allows the electron flow. It provides the ability to quickly connect and separate these molecules in the EFD (Illustration 6). The 3D pictures are available at https://set.suicidevolution.com/.

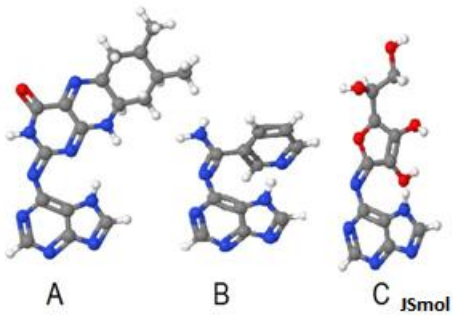


Illustration 6. Presumed interfaces of adenine-flavin (A), adenine-nicotinamide (B), and adenine- L-ascorbic acid (C) molecules.

One $[Fe_2S_2\,(SCH_2CH_3)]^{e2-}$ cluster is responsible for the oxidation of the 5th carbon atom of the two L-AA molecules. The reaction will result one lactone ring. In this case, the four oxygen atoms are probably obtained from the OH of the 5th and 6th carbon atoms of the two L-AA molecules.

2.3.9. The synthesis of adenosine

Before the electron flow starts, the unit is completed by six D-glucose molecules (Illustration 7). Four 5-phospho-D-gluconate molecules (1–4) are bound to the adenine molecules via a β-N9-glycosidic bond (Illustration 7A), one 5-phospho-D-gluconate (5) to the nicotinamide, and one (6) to the flavin molecule (Illustration 7B). Most probably, the phosphorylation of the D-glucose molecules takes place at the connecting points of the TAR.

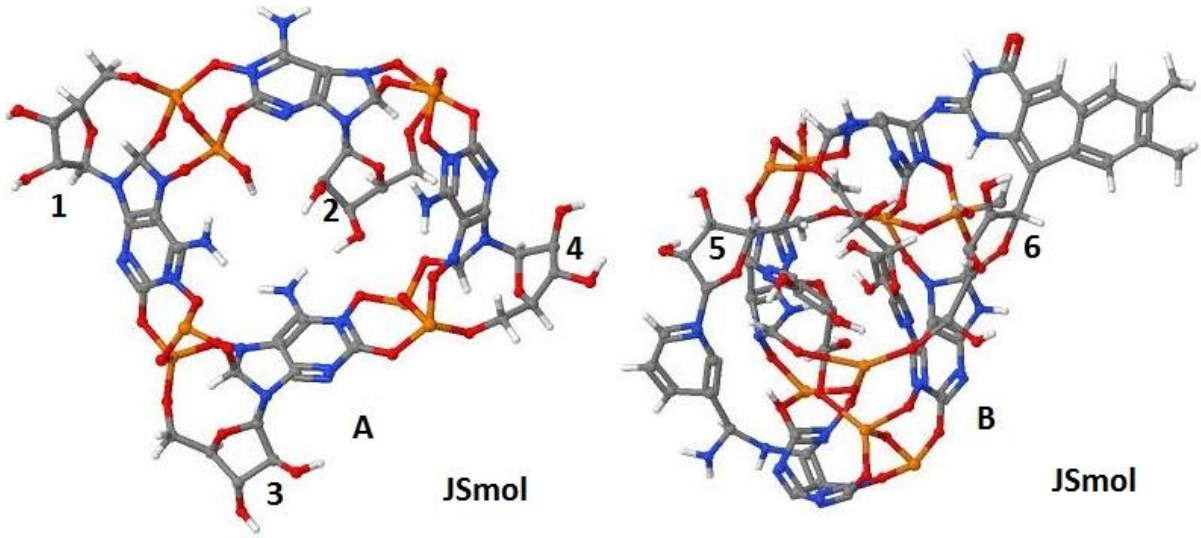


Illustration 7. Six D-glucose molecules in one unit of the SET in the tetra adenine octo phosphate ring. Pictures A and B illustrate the same unit of the SET. Picture A presents four 5-phospho-D-gluconate molecules (1–4), and picture B presents two further 5-phospho-D-gluconate molecules (5, 6), along with one flavin, one nicotinamide, and two ascorbic acid molecules. The 6th carbon atoms of the glucose molecules are oxidized (not presented).

The 6th carbon atoms of the 5-phospho-D-gluconate molecules are targets of the oxidation process. The two electrons arriving at that point separate from the 6th carbon atoms of the glucose molecules (or help to form H_2O at the 6th carbon atom). Finally, $CO_2 + 2H^+$ will be produced by the $2O^{e2-}$ arriving from the Fe-S cluster.

The 3D pictures of the structures are available at https://set.suicidevolution.com/.

2.3.10. Origin of oxygen used for ADP synthesis during anaerobic glycolysis, aerobic glycolysis, and oxidative phosphorylation

Both in anaerobic and aerobic conditions, in the U-ag, 12 oxygen atoms (4 x 3) will be obtained from four UA molecules, eight from $H_2PO_4^{e-}$ of the TAR, four from the two vitamin C molecules (of the 5th and 6th carbon atoms) and additional four from four $H_2PO_4^{e-}$ molecules.

In the Uag, 10 x 2 O^{e2-} will oxidize 10 carbon atoms, with the remaining eight O^{e2-} creating four aminated UA molecules, four PO_3^{e3-} molecules, and 2 x 4 H_2O molecules.

Ten carbon atoms, six from the 6th carbon atoms of glucose and four from the two L-AA molecules (the 5th and 6th carbon atoms), are oxidized in a similar manner in all SET units both in oxygenated and anoxic environments. In SET-OP, 9 x 6 additional carbon atoms (two

pyruvate molecules = six carbon atoms) are oxidized by its PDC, resulting in 36 CO_2 + 36 H^+ ($C_3H_8O_3$ + 3 $2O^{e2-}$ = 3 CO_2 + 3 H_2O + 2 H^+).

2.3.11. Rebirth of vitamin C

Nicotinamide, flavin and vitamin C molecules in the units of structure for energy transformation

The location of the flavin mononucleotide molecule within one EFD is shown in Illustration 8A. One adenine (a) will be bound to flavin, which will also bind one 5-phospho-D-gluconate molecule. An additional 5-phospho-D-gluconate molecule will bridge this structure to another adenine (c) via a β-N9-glycosidic bond (not presented).

The location of the nicotinamide riboside molecule within one EFD is shown in Illustration 8B. One adenine (c) will be bound to nicotinamide, which will also bind one 5-phospho-D-gluconate molecule. An additional 5-phospho-D-gluconate molecule will bridge this structure to another adenine (a) via a β-N9-glycosidic bond (not presented).

The 1st, 2nd, and 3rd carbon atoms of the 5-phospho-D-gluconate molecules bound to flavin and nicotinamide will create two pyruvate/lactate molecules (circle) (Illustration 8).

The 5th and 6th carbon atoms of the two L-AA molecules will be oxidized (triangle). Two x 2 carbon atoms (quadrilateral) will be connected to the remaining two lactone rings of the L-AA molecules (arrows), forming two renewed L-AA molecules (Illustration 8).

The 3D versions of the pictures are available at https://set.suicidevolution.com/.

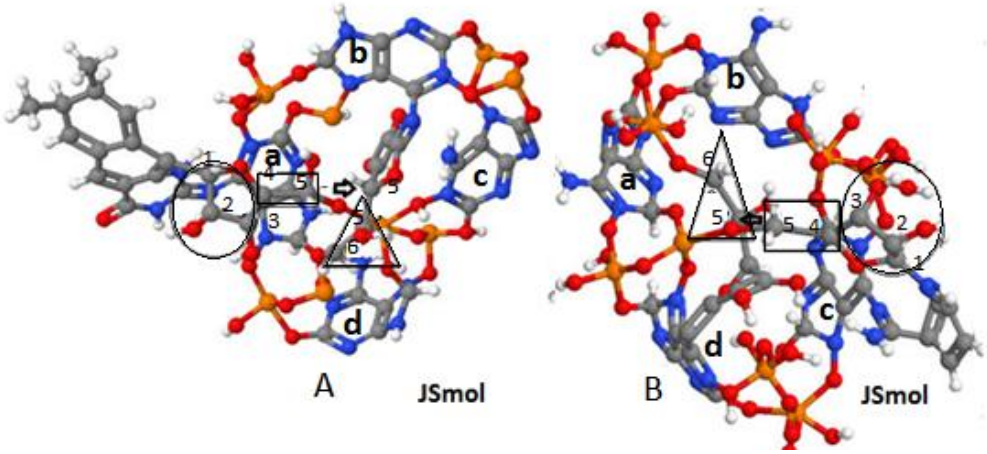


Illustration 8. Two pictures of the same unit (A and B). A: Flavin mononucleotide molecule and one L-vitamin C molecule in the tetra adenine octo phosphate ring. B: Nicotinamide riboside molecule and one L-vitamin C molecule in the tetra adenine octo phosphate ring. The 5th and 6th carbon atoms of the two L-AA molecules will be oxidized (triangle). Two x 2 carbons (quadrilateral) will be connected to the remaining two lactone rings of the L-AA molecules (arrows). Two pyruvate molecules are situated in the two circles.

In an oxygenated environment, pyruvate molecules of NAD and FAD will be oxidized by the PDC. Accordingly, in an anoxic environment, 9 x 10, and in an oxygen-containing milieu, 9 x 16 carbon atoms, respectively, will be oxidized in the SET-OP.

2.4. Aminated uric acid, PO_3^{e3-}, and H^+ production and the electron flow in the electron flow device

2.4.1 Processes of amination and PO_3^{e3-} production

We suppose that $[Fe_2S_2\ (SCH_2CH_3)]^{e2-}$ clusters are responsible for the amination of the UA molecules.

In the SET-AG, oxygen atoms of the UA molecule at the C1 position will be taken up by $[Fe_2S_2\ (SCH_2CH_3)]^{e2-}$ clusters and converted to four O^{e2-}. At the same time, with the help of the aminotransferase enzyme and dehydrogenases, 4 NH-UA^{e-} + 4 H_2O molecules are formed.

The reaction is as follows: 4UA + 4NH_3 (biogenic amines) + Fe-S cluster = 4 NH-UA^{e-} + 4 H_2O.

We suppose that $[Fe_2S_2\ (SCH_2CH_3)]^{e2-}$ in the SET-AG and high molecular weight cytochrome (Hmc) clusters in the SET-OP are responsible for PO_3^{e3-} production.

The reaction is as follows: $H_2PO_4^{e-}$ + Fe-S or cytochrome clusters = PO_3^{e3-} + H_2O.

2.4.2. Electron flow in the electron flow device

Fe-S clusters are producing electrons. The EFD transfers them to the points where carbon atoms are oxidized. The electrons enter the UA/adenine molecule when the $H_2PO_4^{e-}$ molecule is attached to adenine (Illustration 5). One proton will remain at the site of the hydrogen molecule, while the electron migrates to a new location in the EFD. It creates hydrogen atoms using one proton at the place of CO_2 liberation. Thus, the proton pump might be realized as proton conduction using the aquaporin canals. In each of the entering points, two electrons are arriving to the structure through the N1 and N7 atoms of the four adenine molecules and leaving them through the N9 and N10 atoms (Illustration 5).

2.4.2.1 The N9 route of electron transfer

The electrons are moving to the N9 atom (Illustration 5), passing through the 5-phospho-glucose molecules bound here. They are responsible for the detachment of the 6th carbon atom (or for helping with creation of H_2O) of the four glucose molecules.

2.4.2.1 The N10 route of electron transfer

In the EFD, the other path of the electrons is realized through the N10 atoms (Illustration 5) of the four adenine molecules. The electrons directly reach the 6th carbon atoms in the two L-AA molecules. Nicotinamide and flavin help with the transfer of the electrons to the 6th carbon atoms of the two 5-phospho-glucose molecules that bind to the nicotinamide and flavin molecules.

2.4.3 The results of the ADP-pu

In all the SET units, the disconnected carbon atoms will be oxidized by eight $2O^{e2-}$ produced by the four Fe-S clusters. At the same time, an additional Fe-S cluster prepares two $2O^{e2-}$, which are responsible for the oxidation of the 5th carbon atoms of the two L-AA molecules.

The result of the reaction is four ADP, two ribose (which will be converted to two pyruvate and two citric acid molecules) and two lactone rings, 10 H_2O, 10 CO_2, and 20 H^+. The lactone rings will bind the citric acid molecules, resulting in two renewed L-AA molecules. Thus, the end- product of the reaction is four ADP, two pyruvate, 10 CO_2, and two renewed L-AA molecules as well as 20 H^+.

2.5. Continuous electron and ATP production

2.5.1. ATP synthase (Complex V)

ATP synthase couples ATP synthesis during cellular respiration to an electrochemical gradient created by the difference in proton (H^+) concentration across the mitochondrial membrane in eukaryotes or the plasma membrane in bacteria. During photosynthesis in plants, ATP is synthesized by ATP synthase using a proton gradient created in the chloroplast stroma. ATP synthase consists of two main subunits, FO and F1, which have a rotational motor mechanism allowing for ATP production [18].

Because of its rotating subunit, ATP synthase is a molecular machine. The binding change mechanism involves the active site of the β subunit cycling between three states. In the "**loose" state**, ADP and phosphate ***enter*** the active site. The enzyme then changes shape and forces these molecules together, with the ***active*** site in the resulting **"tight" state,** binding the newly produced ATP molecule. Finally, the intense site cycles back to the **open state**, ***releasing*** ATP [19].

2. 5. 2. The three steps of ATP production

In all the SET units, EFD, Hmc, and cytochrome C are located in such a way as to allow for close cooperation between them. In addition, the connections of the three nicotinamide and three flavin molecules result in the possibility of cooperation between the three SET units (Illustration 9). In this way, one of the units is always active. The coordinated operation of the three subunits ensures continuous electron and ATP production. The SET-ANG and SET-AG have three U-angs and three U-ags, respectively, while the SET-OP has nine ADP-pus.

Three flavin molecules bind three adenine molecules (A) on the surface of the inner membrane facing the cytoplasm or matrix, and 1.5 nm away, three nicotinamide molecules bind three adenine molecules (C) in the inner membrane so that the adenine molecules (C) are superimposed on the flavin-bound ones (A). Adenine molecules A and C form a TAR using two additional adenines (B and D) (Illustration 9). The 3D versions of the pictures are available in https://set.suicidevolution.com/.

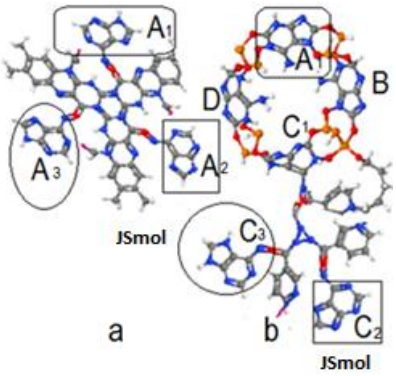


Illustration 9. a: three flavin + three adenine. b: three nicotinamide molecules, two adenine molecules, and one tetra adenine octo phosphate ring. A_1 of picture a is identical to the A_1 of picture b. A_2 is connected with C_2, while A_3 is connected with C_3 by further adenine molecules, creating two further tetra adenine octo phosphate rings.

We suppose that the synchronized operation of the three SET units allows continuous electron and ATP production, as one of the units is always active.
Complex V and the EFD are three-stroke nanomachines. Their working states are:

1. **Open state.** In the open state, the products are leaving the EFD and Complex V.
2. **State of construction ("loose" state)**. During this state, base molecules are arriving into the SET unit and Complex V.
3. **Active state ("tight" state).** In the active state, ADP and H^+ are produced in the ADP-pu**,** while ATP molecules are produced in Complex V.

We assume that the functions of Complex V and the EFD units are synchronized. When the EFD is in an open state (releasing ADP), Complex V is in a loose state (able to accept the ADP molecules).

2.5.3. Cooperation of electron flow device, high molecular weight cytochrome clusters, and Complex V

Four aminated UA, eight $H_2PO_4^{e-}$, two L-ascorbic acid, and six D-glucose molecules are entering the EFD, where in the active phase of the reaction, four ADP molecules are produced. Complex V creates ATP from the PO_3^{e3} and ADP molecules arriving from the EFD.

In the SET-ANG, SET-AG, and SET-OP, the collaboration between the EFD and Complex V might be promoted by their close contact.

In the mitochondria, the ATP synthase forms dimer rows at the cristae tips. Complex V, the EFD, and Hmc clusters are connected by the lumen of cristae in the mitochondria, which provides the transport of ADP and PO_3^{e-} to Complex V.

Both the SET-ANG and SET-AG are built from three units, while the SET-OP consists of nine ADP-pus. This composition ensures continuous electron transfer, as one unit of the structure is always in the active state. In the case of the SET-OP, three units are active simultaneously. Active cooperation exists between the EFD, Complex V, Fe-S clusters and Hmc clusters.

The molecular organization of cristae membranes have been widely studied [6, 13, 20]. Based on these publications and the concept of the function of the SET, we concluded that the EFD is a key component of the electron transport protein-mediated electron flux.

In the first step, aminated UA and PO_3^{e3-} molecules are produced by Hmc or Fe-S clusters (as described in 2.4.1 and 2.4.2). The aminated UA molecules will form TARs in the inner membrane. The second step of energy transformation is ADP production by the EFD. In the third step, ATP synthase (Complex V) will finish the reaction, resulting in the formation of ATP from ADP + PO_3^{e3-}. Hmc clusters catalyze the conversion of pyruvate molecules to CO_2. H^+ is liberated during the reaction catalyzed by the EFD and Hmc clusters. Protons created by Hmc clusters in the cristae space flow back into the matrix through the ATP synthase rotor, driving ATP production (Illustrations 10 and 11).

Illustration 11 is created based on the publication of Hakjoo et al. [6]. I assume that, for mitochondrial function, an EFD instead of an ETC is responsible. The EDF is the place where ADP is produced, which is converted to ATP in Complex V. Hmc clusters provide 36 PO_3^{e3-} and 36 H^+. The 36 H^+ are the result of the 18 pyruvate - 54 CO_2 transformation (pyruvate + three $2O^{e2-}$ = three CO_2 + three H_2O + two H^+). While H^+ produced in the EFD are mainly responsible for the membrane potential of the cell, H^+ produced by Hmc clusters will be used up by the 36 ADP - ATP conversion.

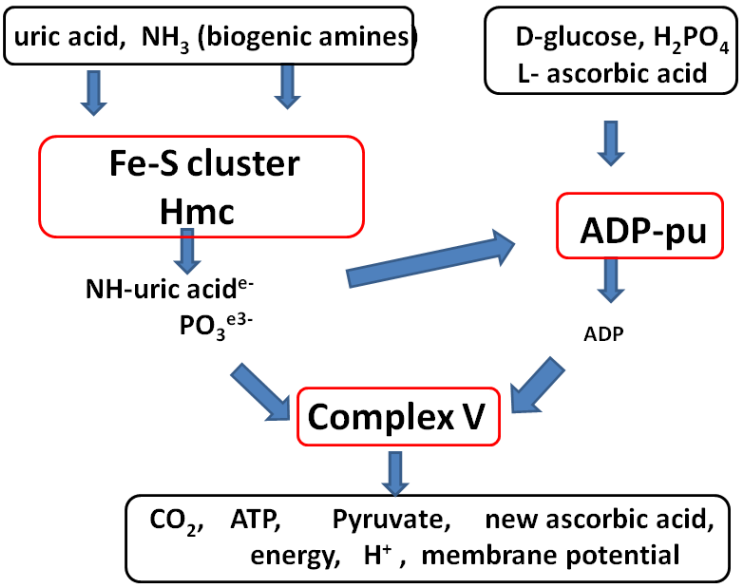


Illustration 10. Cooperation between Fe-S, high molecular weight cytochrome (Hmc) clusters, and Complex V in the structures for energy transformation.

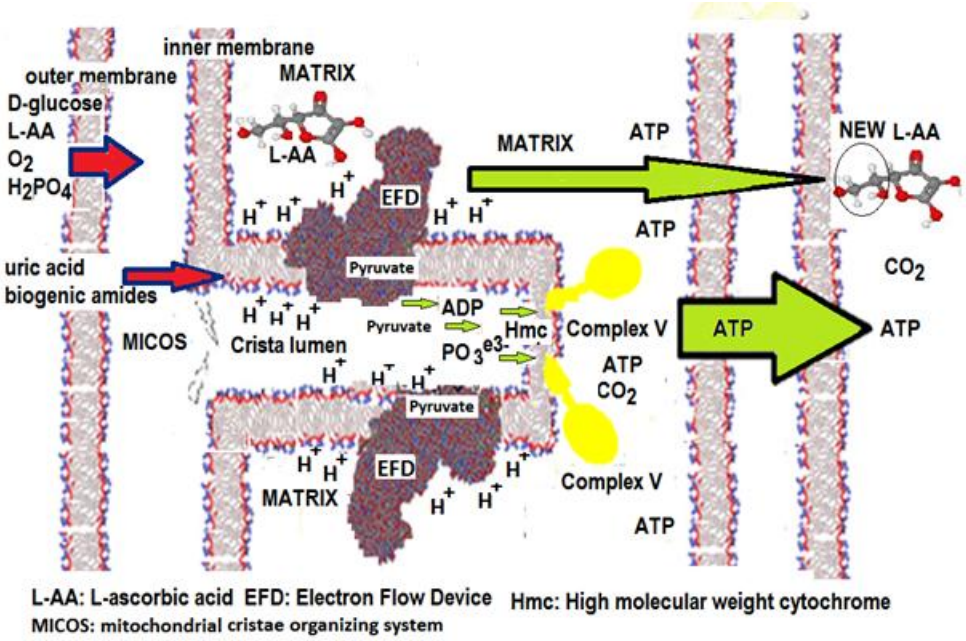


Illustration 11. The supposed cooperation between the electron flow device (EFD), Complex V, and Hmc clusters. Basic molecules (uric acid, H_2PO_4, biogenic amines, O_2, D-glucose, and L-ascorbic acid) arrive at the EFD where ADP, pyruvate, CO_2, and H^+ are produced. Pyruvate is oxidized by Hmc clusters; the ADP-ATP transformation is realized in Complex V. The renewed L-AA molecules contain two carbon atoms (circled) obtained from the glucose of the NAD and FAD molecules.

2.6. Phylogenetic evolution of SET

2.6.1. The development of the cellular energy supply

The structure providing continuous electron flow has already been established in the world without O_2. Later, new SETs have evolved, and eventually, the eukaryotic cell was formed through the symbiosis of an ancient and a modern cell [1]. The cellular energy system may have gradually evolved. The supposed steps in the evolution of energy supply are summarized in Table II.

2.6.1.1. Development of structures for energy transformation in the world without O_2

Formation of energetically important molecules (such as Fe-S clusters, uric acid, and carbon hydrates) in the age of biopolymers.

In the age of biopolymers, molecules of the energy system were developed. Na^+, K^+, Mg^+, ortho-H_2O, CO_2, biogenic amines, $H_2PO_4^{e-}$, Fe, and S were present. Furthermore, based on Miller's experiments, the UA and different carbohydrate molecules have become available [21].

The first important step towards the development of life was the appearance of Fe-S clusters. The existence of a $[Fe_2S_2(SCH_2CH_3)]^{e2-}$ cluster that catalyzes 2 x $2O^{e2-}$ can be assumed.

Table II Evolution of Energy Supply of Cells

Primitive cell membrane	Fe-S clusters, UA, L-AA, nicotinamide, flavin, $H_2PO_4^{e-}$, NH_3 (biogenic amines)		
Primitive cell	Fe-S clusters; Complex V TAR + six [2Fe-2S] clusters (6 x 2 x 2O $^{e2-}$) = SET-ADP-pu		
	←	↓	←
	O_2 is missing Anaerobic glycolysis	O_2 is missing Aerobic glycolysis (Warburg)	O_2 Oxidative phosphorylation
	U-ang	U-ag	U-op = ADP-pu
	EFD + 5 [2Fe-2S] clusters + one [3Fe-3S] cluster	EFD + seven [Fe-2S] clusters	EFD + six [Fe-2S] clusters
	SET-ANG = 3 U-ang	SET-AG = 3 U-ag	SET-OP= 9 U-op PDC
Eukaryotes	SET-AG + SET-OP		

The development of a multicolored complex living world along with the Darwinian evolution.

UA: uric acid; L-AA: L-ascorbic acid; Fe-S: $[Fe_2S_2(SCH_2CH_3)]^{e2-}$; TAR: tetra adenine octo phosphate ring; EFD: electron flow device; ADP-pu: ADP-producing unit; U-ang: unit of anaerobic glycolysis; U-ag: unit of aerobic glycolysis; SET-ANG: SET of anaerobic glycolysis, SET-AG: SET of aerobic glycolysis, U-op: unit of oxidative phosphorylation; SET-OP: SET of oxidative phosphorylation, PDC: pyruvate dehydrogenase complex.

2.6.1.2. ADP-pu of SET

The EFD + 6 $[Fe_2S_2\ (SCH_2CH_3)]^{e2-}$ forms the ADP-pu, which is responsible for ADP production. It produces 10 CO_2, two renewed L-AA, two pyruvate/lactate, and four ADP molecules, which are used for creating ATP.

2.6.1.3. Unit of anaerobic glycolysis

The U-ang has five $[Fe_2S_2\ (SCH_2CH_3)]^{e2-}$ clusters contributing to the emission of 10 CO_2 molecules. Additionally, it contains one [3Fe-3S] cluster forming four NH-UA^{e-} and two PO_3^{e3-} ions. Accordingly, the unit will produce two ATP, two ADP, two pyruvate/lactate, 10 CO_2, and two renewed L-AA molecules.

TAR + 5 [2Fe-2S] + 1 [3Fe–3S] cluster for 3 x $2O^{e2-}$ = U-ang; products: 10 CO_2 + 2 ADP+ 2 ATP + 2 pyruvate/lactate + 2 renewed L-AA molecules.

2.6.1.4. Unit of aerobic glycolysis

The U-ag has seven $[Fe_2S_2\ (SCH_2CH_3)]^{e2-}$ clusters contributing to the emission of 10 CO_2 molecules. ADP-pu + one $[Fe_2S_2\ (SCH_2CH_3)]^{e2-}$ cluster = U-ag; products: 10 CO_2 + 4 ATP + 2 pyruvate/lactate + 2 renewed L-AA molecules.

Fe-S clusters are the dominant structures of anaerobic glycolysis, aerobic glycolysis, and oxidative phosphorylation. Oxygenation of these clusters is controlled by oxygen atoms obtained from UA (4 x 3), L-AA (2 x 2), and $H_2PO_4^e$ (8 x 1).

Cyanobacteria (blue-green algae) produce oxygen (O_2) by photosynthesis (6 CO_2 + 6 H_2O + energy - $C_6H_{12}O_6$ + 6 O_2), which allows the further development of the SET

2.6.1.5. World with O_2, development of SET unit of oxidative phosphorylation

The combination of ADP-pu and various cytochrome clusters may have resulted in several types of energy converting structures. Probably the most effective of these was the SET-OP containing nine ADP-pu + PDC combination.

In the SET-OP, PDC, including 4 x Hmc clusters, and nine ADP-pus are situated. The products of the SET-OP are 36 ATP and 9 x 16 CO_2 in an oxygenated environment. In the case of anoxia, it produces 36 ADP + 9 x 10 CO_2 because Hmc clusters are active only in the presence of O_2 molecules.

PDC and Hmc cluster complexes are responsible for the oxidation of the pyruvate molecules (9 x 2) and also for producing PO_3^{e3-} (3 x 12). Four Hmc clusters are offering 4 x 18 $2O^{e2-}$ atoms for the reaction.

PDC, including four Hmc clusters + 9 ADP-pus = SET-OP, producing 9 x (10 + 6) = 144 CO_2 + 36 ATP.

$[Fe_2S_2\ (SCH_2CH_3)]^{e2-}$ clusters are producing 9 x 10 CO_2 in the nine ADP-pus. Each unit produces two pyruvate molecules (9 x 2 = 18 pyruvate = 3 x 18 carbon atoms = 54), and they will be oxidized by four Hmc clusters. Each of the Hmc clusters is responsible for the production of 18 x $2O^{e2-}$. Thus, four Hmc clusters are producing 72 x $2O^{e2-}$. Fifty-four $2O^{e2}$ will produce 54 CO_2. The remaining 18 $2O^{e2-}$ will produce 36 PO_3^{e3-} as follows: 2 $H_2PO_3^{e-}$ + $2O^{e2-}$ = 2 PO_3^{e3-} + 2 H_2O.

2.6.2. The supposed complete structures for energy transformation

The SET may consist of the following units: ADP-pu, U-ang, and U-ag and functional elements, such as $[Fe_2S_2\ (SCH_2CH_3)]^{e2-}$, Complex V, PDC, and Hmc clusters.

We assumed that each SET was made up of three units. In the SET-ANG and SET-AG, three similar units are forming the SET. Each of the units is complemented by Complex V. The SET-OP consists of 9 ADP-pus and one PDC, which consists of six Complex V molecules (Table III).

Table III. Creative Elements and Products of the Various Structures for Energy Transformation

			Products	
			ATP	CO_2
SET- ANG	3 U-ang	1 Complex V	3 x 2	3 x 10
SET-AG	3 U-ag	2 Complex V	3 x 4	3 x 10
SET-OP	9 ADP-pu	6 Complex V 1 PDC 4 Hmc clusters	9 x 4 = 36	9 x 10 + 9x2x3

SET: structure for energy transformation; SET-ANG: SET of anaerobic glycolysis; U-ang: unit of anaerobic glycolysis; SET-AG: SET of aerobic glycolysis; U-ag: unit of aerobic glycolysis; SET-OP: SET of oxidative phosphorylation; ADP-pu: ADP-producing unit; PDC: pyruvate dehydrogenase; Hmc: high molecular weight cytochrome.

2.6.3. The location of structures for energy transformation within the cell

The SET-ANG and SET-AG are situated in the plasma membrane of the cells, while the SET-OP is in the mitochondrial cristae.

2.7. Cooperation between SET-AG and SET-OP in eukaryotes regulated by hypoxia-inducible factors

Hypoxia-inducible factors are transcription factors that respond to decreases in the available oxygen in the cellular environment [21, 22]. They are highly conserved essential proteins that regulate oxygen delivery to tissues. The alpha subunits of HIF are hydroxylated at conserved proline residues by HIF prolyl-hydroxylases, resulting in a rapid degradation by the proteasome [23, 24]. This occurs only in normoxic conditions. In hypoxic conditions, HIF prolyl-hydroxylase is inhibited, since it utilizes oxygen as a co-substrate [25, 26]. HIF-1 α has been found to drive the expression of hundreds of genes [27, 28] involved in many biological processes, including neovascularization, angiogenesis, cytoskeletal structure, survival/apoptosis, adhesion, migration, invasion, metastasis, glycolysis, and metabolic bioenergetics [29]. It is also known that vitamin C is indispensable for oxygen sensing [30].

The survival and regeneration of human and vertebrate bodies are ensured by the ability of eukaryotic cells to live in an anoxic environment. In that case, the system of the HIF will regulate the process of regeneration of the damaged structure. The failure of proteolysis due to anoxia will result in the up- or down-regulation of about 200 genes [2, 3] and start the SET-AG, resulting in neovascularization. Finally, when O_2 arrives through the new blood vessels, HIF-1 α will become degraded, and the SET-OP starts to work again (Table IV).

Table IV. Regulation of Energy Supply by HIF-1 α in Eukaryotic Cells

O_2	HIF-1 α	SET-AG	SET-OP
Yes	No	No	Dominates
No	Yes	Dominates	No

In the eukaryotic cell living in an anoxic milieu, only 3 x 4 ATP will be produced in the SET-AG, and at the same time, 36 ADP are provided in the SET-OP, resulting in the

overproduction of ADP. Accordingly, serum samples from cancer patients revealed elevated levels of *in vitro* ADP-ribosylation through non-enzymatic binding of ADP-ribose to free acceptor sites on serum proteins; thus, increased ADP-ribosylation might be used as a tumor marker [31].

2.8. The size of the structures for energy transformation

We calculated the sizes of the SETs using the JSME Editor courtesy of Peter Ertl and Bruno Bienfait [17]. Based on these data, we estimate the SET-ANG and SET-AG as a sphere with a 1.5 nm diameter. The SET-OP consists of 9 ADP-pus. Thus, most probably, it is one 1.5–2.5 nm spherical structure (Illustration 12). The 3D pictures are available at https://set.suicidevolution.com/.

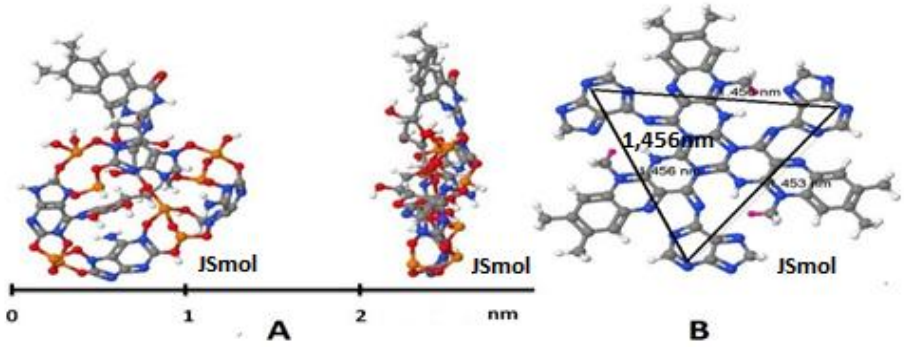


Illustration 12. The size of units of the structure for energy transformation. One tetra adenine octo phosphate ring + one vitamin C + one flavin + one glucose molecules (A) and the distance between the three units (B).

3. Conclusions

The model of the SET helps to answer the questions described in the introduction. Ad 1: Complex I and the electron transfer chains work in a 3D structure as the EFD, which might be responsible for the proton-electron translocation. Ad 2: the number of Fe-S clusters is seven in the SET-AG, while there are six in the ADP-pu of the SET-OP. Ad 3: the EFD and Complex V are working in a synchronized way in the inner membrane of the cell and the lumen of the cristae in the mitochondria. Ad 4: the EFD produces ADP in all units of the SET. Ad 5: the continuous ATP production and membrane potential provided by continuous H+ production is realized by the synchronized operation of three or nine units. In the SET-OP, three of the nine ADP-pus are active.

4 The energy-producing twin motor of cells

All cells are powered by one synchronous, three-stroke twin-engine system that is provided by three or nine subunits. The system operates by well-known clusters, complexes, and structural proteins. Complex V and EFDs make up the twin motor. The coordinated operation of three EFD units and Complex V ensures that, in the SET-ANG and SET-AG, one of the three units (or three of the nine ADP-pus) are always active, resulting in a continuous membrane potential and ATP production.

Operating phases of the three-stroke engine:
The first (loose) phase:
EFD: Essential molecules enter EFD.
Complex V: ADP and PO^{3e3-} enter Complex V.
The second phase (active state):
EFD: Enzymes transform the parent molecules to form ADP molecules.
Complex V: ATP is formed from ADP and PO3e3-.
The third phase (open state):
EFD: ADP leaves EFD.
Complex V: ATP leaves complex V.

When the EFD is in the open state, releasing ADP, Complex V is in a loose state, ready to uptake ADP.

5. Possibilities for proving the hypothesis

The hypothetical SET model described above is a simplified idea. The SET is undoubtedly an extremely complex system with different modalities in different organisms.

We believe that experimental testing of the SET model is justified and warranted. If the model is correct, the following major results would serve to confirm it:

1. Delivery of radiolabeled vitamin C should result both in *in vitro* and animal experiments in the appearance of labeled CO_2, if the 5th and or 6th carbon atoms were labeled. In contrast, the CO_2 labeling is omitted, if the C1, C2, C3, or C4 atoms of L-AA were labeled.
2. Metabolism of ^{13}C labeled D-glucose will yield ^{13}C labeled L-AA. The change can be detected by nuclear magnetic resonance spectroscopy.
3. Radiolabeled UA molecules will result in labeled adenine molecules.

6. Hypothetical statements of the concept of energy transformation system

We assume that:

- an ATP-UA-ATP cycle exists;
- adenine molecules originate from the UA molecule;
- two adenine, two L-AA, and two 5-phospho-glucose molecules complete the ETC, creating one EFD;
- four adenine and eight $H_2PO_4^{e-}$ molecules create the TAR;
- TAR + two L-ascorbic acid 6-phosphate + nicotinamide + flavin + six 5-phospho-glucose molecules create the EFD;
- the EFD is responsible for the glucose-ADP transformation and for the realization of electron flow;
- one energy-producing twin motor of cells implements continuous power generation, membrane potential, and ATP production;
- proton pumps might be materialized as proton conduction using the aquaporin pores.

Keep in mind that the structure I assume works only with the help of the known enzymes and environmental proteins with a defined structure.

Notions and Abbreviations

Table V.

Notions		**abbreviations**
Electron Transport Chain = Complex I, II, III, and IV		**ETC**
New notions		
Tetra uric acid/adenine octo phosphate ring = four uric acid originated adenine + eight H_2PO_4		**TAR**
Electron Transfer Device = TAR + nicotinamide + flavin + 2 L-AA + 6 D-glucose		**ETD**
Structure for energy transformation		**SET**
ADP-producing unit		**ADP-pu**
Unit of anaerobic glycolysis		**U-ang**
Unit of aerobic glycolysis		**U-ag**
SET of anaerobic glycolysis	**3 U-ang**	**SET-ANG**
SET of aerobic glycolysis	**3 U-ag**	**SET-AG**
SET of oxidative phosphorylation	**9 ADP-pus**	**SET-OP**

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