



Biological Reactions of Electron Transfer Proteins and its Significance

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DESCRIPTION

Electron transfer (ET) reactions are an important step in various biological transformations from photosynthesis to aerobic respiration. A powerful theoretical form has been developed that explains the ET rate in terms of two parameters, nuclear reorganization energy and electron bond strength. Studies on the ET reaction of ruthenium-modified proteins have examined in several metalloproteins (cytochrome c, myoglobin, azulin). This study shows that protein reorganization energies are sensitive to the medium surrounding the redox site, especially in an aqueous environment leading to large reorganization energies. Electron bond strength analysis suggests that the efficiency of long-range ETs depends on the secondary structure of the protein. Beta sheets appear to mediate bonds more efficiently than α -helix structures, and hydrogen bonds play an important role in both.

Biological reaction of electron transfer protein

Photosynthetic reaction centers and cytochrome c oxidases are just two of the many biological systems in which the ET reaction plays a central role. The unique simplicity of the ET reaction prompted the development of a powerful theoretical form that explains the speed of these processes in terms of a small number of parameters [1]. The conceptual advancement that led to the development of ET theory was the recognition of the central role played by Franck-Condon's principle. Due to the much higher electron velocities, the nuclei remain fixed during the actual transition from the reactants to the product. The transition state of this reaction must be at a point in the nuclear configuration space where the reactant and product states are degenerate. Therefore, changes in the reacting molecule and its environment can reach the transition state configuration and move electrons. Electron tunneling of proteins occurs in reactions where the electron interactions between redox sites are relatively weak. Periplasmic localization of periplasmic electron transport proteins containing cofactors raises the question of how organisms assemble these proteins [2]. This question is particularly relevant for large protein complexes with multiple redox centers. In the case of periplasmic cytochrome c, the protein travels

unfolded through the Sec pathway and the heme is covalently bound using the periplasmic or membrane-bound assembly protein. However, many other classes of periplasmic redox proteins are processed by mature enzymes and have a signal sequence containing a twin arginine motif. This motif induces proteins to the twin arginine translocase. Twin arginine translocase transports pre folded proteins with assembled redox cofactors. Some translocase substrates are so large that the diameter of the pores of the translocase device should be about 100Å to accommodate the largest substrate. The structure of the Tat complex is not yet known, but a gating mechanism is needed to maintain ion closure during transport of these large substrates [3]. The translocation process is also an energy-driven electron transport chain. This shows that the overall biochemistry and energy considerations of the periplasmic electron transport chain must consider not only the behavior of the system and also biosynthesis [4].

Synthesis of periplasmic electron transport chain

According to recent studies, iron-sulfur clusters and heme are the most common electron transport cofactors for proteins, among which the exact protection from the surrounding aqueous environment by an insulating protein matrix. It is arranged as an array of intervals. Protein-mediated electron transport was originally described for the four membrane complexes of the mitochondrial respiratory chain. It transfers two electrons from the reduction equivalent NADH and uses various redox cofactors such as flavins, iron and sulfur to transfer succinic acid to terminal electron acceptors such as oxygen [5]. The latter two are used in Complex III and are explained in this mini-review to explain the principle of electron branching. The ability of Coulomb efficiency to accelerate enzymatic reactions by currents up to 99% has been demonstrated with several oxidases and reductases and various substrates. The catalytic center of the enzyme exchanges electrons directly or indirectly with the electrode using a stable protein-bound redox cofactor or soluble redox shuttle. From the point of view of practical application, the direct process looks more attractive because there is no need to replenish the redox

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Received: 24-Feb-2022, Manuscript No. BEG-22-16047; **Editor assigned:** 01-Mar-2022, PreQC No. BEG -22-16047 (PQ); **Reviewed:** 21-Mar-2022, QC No BEG -22-16047; **Revised:** 31-Mar-2022, Manuscript No. BEG -22-16047 (R); **Published:** 08-Apr-2022, DOI: 10.35841/2167-7662 -22.10.162

Citation: Lucas D (2022) Biological Reactions of Electron Transfer Proteins and its Significance. J Bio Energetics.10:162

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mediator after the reaction product has been separated. However, the stability and efficiency of most tested enzyme systems has proven to be un optimal for real-world applications and will require further development of this technology, perhaps with rational design improvements. This approach requires a complete understanding of the structure-function relationship of electron-donating proteins.

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