SOME NEW DATA ON F_0F_1-ATP-SYNTHASE STRUCTURE AND FUNCTION

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Introduction. The question how energy of oxidation of fueling molecules is transformed and conserved in the universal form of ATP in the cell is an issue of critical importance for scientists in the field of bioenergetics for some 5-6 last decades. Many theories were proposed to answer this question, but the most rational explanation was given by the Nobel laureate Peter Mitchell in his chemiosmotic model. The author postulated that working electron transport chain creates the electrochemical potential on the inner mitochondrial membrane - $\Delta\mu_H^+$, and this potential is the proton-motive force which drives the biosynthesis of ATP. Such force makes protons to cross the membrane from the intermembrane space back into the mitochondrial matrix via proton pores in F_0 of the ATP synthase complex. The same force provides the energy for ATP synthesis by F_1 connected to F_0.

Aim. On the eve of Millennium II it was shown that ATP synthase revealed a turbine activity. The F_0 domain that is plunged into the inner mitochondrial membrane includes 3 types of subunits – a (1), b (2) and c (varies from 8 to 15 depending on organism species) – and contains a proton pore. The c subunits are identical, small hydrophobic proteins arranged in a ring which is rotated as hydrogen ions cross F_0. The F_1 domain is composed of 9 subunits of 5 types – α (3), β (3), γ, ϭ, ε. Each of the β subunits carries a catalytic area where ATP biosynthesis occurs. These catalytic areas may be present in 3 different conformations with different nucleotide-binding sites. Three conformational states gave rise to the names of β subunit status – β-ATP, β-ADP and β-empty. All the 9 subunits form a stalk and a pileus of a microscopic "mushroom" headed into the matrix.

Results and discussion. Another Nobel laureate Paul Boyer who for a long period of time strongly defended a "conformational" theory of oxidative phosphorylation, now with high probability considers a rotational mechanism of ATP synthesis. According to the mechanism a given β subunit starts to participate in ATP synthesis in the β-ADP conformation. It binds ADP and Pi from the medium and turns into the ATP state. Being in the ATP conformation, the subunit fulfils the ATP formation and firmly keeps the molecule of ATP on its surface. Then the conformation of the unit is changed to β-empty. Such conformation possesses a low affinity to ATP, and the new molecule of ATP easily leaves the subunit.

Conclusion. What energy supplies all these conformational transformations? This is the energy of protons moving across the inner mitochondrial membrane through the F_0 domain of ATP synthase. The proton-driving force makes the cylinder of c subunits rotate together with the connected γ subunit (the stalk), which at each120° turn switches onto a new pair of αβ subunits (3 αβ pairs) changing the conformation of β unit into the β-empty form. At the same time one neighboring β subunit takes the β-ADP conformation, and the third β subunit – the β-ATP one. The rate of the cylinder rotation in intact mitochondria can reach 100 rotations per second.