



Abstracts

S17 Systems Bioenergetics

Lectures

17L1 Mechanism of selective Na⁺ or H⁺ binding and coupled rotation in F₁F₀ ATP synthases: Insights from quantitative computer simulations

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F-ATP synthases are the most prominent ATP source across the living world. These enzymes couple the structural changes required for catalyzing the conversion of ADP and P_i into ATP to the transmembrane flow of Na⁺ or H⁺ ions down their electrochemical gradients. The key, coupling element in these molecular machines is the membrane-embedded F₀ rotor, or c-ring. The recent emergence of high-resolution structural data and the close interplay of experimental analyses with advanced, quantitative molecular simulation methods are providing novel and important insights into the mechanisms of these essential proteins. We present an overall summary of our recent progress in this area, particularly pertaining to the mechanism by which ion exchange across the lipid membrane is coupled to the rotation of the c-ring, as well as to the structural basis for the distinct ion-binding selectivity observed for different species.

doi: [10.1016/j.bbabio.2010.04.408](https://doi.org/10.1016/j.bbabio.2010.04.408)
17L2 Proportional activation/inhibition of ATP demand and supply by different hormones, respiratory substrates and electrical stimulation in various tissues

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Various external factors can affect the activity of ATP usage processes specific for particular tissues and ATP synthesizing pathways, chiefly oxidative phosphorylation. The action of such factors changes the flux through the system (oxygen consumption, work intensity and ATP turnover) and concentrations of intermediate metabolites (ATP/PCr, Δp and NADH). The theoretical method called proportional activation approach (PAA) proposed previously [1] was used to quantify the relative activation/inhibition by different external stimuli of the production and consumption of different metabolites (ΔΨ, NADH and ATP/PCr) in various tissues (liver, skeletal muscle, heart). It is shown that such high-energy hormones as adrenaline (in the heart) [2] and vasopressin (in the liver) [1, 3] as well as electrical stimulation (of the skeletal muscle) [4] activate the production and consumption of different metabolites to a similar

extent. Insulin only activates ATP/PCr production in the heart [5]. Pyruvate/lactate activates both ΔΨ production and consumption in the liver [1], while in the unpaced heart they activate ATP/PCr production, but inhibit ATP/PCr consumption. Generally, PAA has appeared to be a useful quantitative method allowing to estimate, in a system divided conceptually into production and consumption of some metabolite M, the relative activation/inhibition by some external factor of the two distinguished blocks.

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doi: [10.1016/j.bbabio.2010.04.409](https://doi.org/10.1016/j.bbabio.2010.04.409)
17L3 Electron competition process in respiratory chain: Regulatory mechanisms and physiological functions

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In mitochondria isolated from the yeast *Saccharomyces cerevisiae*, under nonphosphorylating conditions, we have previously shown that there is a right of way for electrons coming from the external NADH dehydrogenase, Nde1p. In this work, we show that the electron competition process is identical under more physiological conditions i.e. oxidative phosphorylation. Such a competition generates a priority for cytosolic NADH reoxidation. Furthermore, this electron competition process is associated with an energy wastage (the “active leak”) that allows an increase in redox equivalent oxidation when the redox pressure increases. When this redox pressure is decreased, i.e. under phosphorylating conditions, most of this energy wastage is alleviated. By studying mutant strains affected either in respiratory chain supramolecular organization or in electron competition activity, we show that the respiratory chain supramolecular organization is not responsible for the electron competition processes. Moreover, we show two distinct relationships between the respiratory rate and the quinone redox state