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On the Dynamics of Ion-Transporting Membrane Enzymes

S. F. Timashev

Karpov Institute of Physical Chemistry, Moscow, 103064 Russia
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Abstract—Recent high-resolution data on transport ATPases (electron density distribution and x-ray structure) allow refining the earlier model suggestions about the mechanisms whereby the energy of ATP hydrolysis is used for active transmembrane ion transfer.

More than two decades ago it was suggested that ion-transporting membrane enzymes use the energy of ATP hydrolysis or light excitation through redistribution of charge density to create intramembrane local electric fields opposite to the average membrane field (see e.g. [1]). Such a possibility was illustrated with simple models of partial electron density transfer, determined by the absorbed energy and giving rise to an additional pair of separated (~1 nm) charges $D^{\delta+}$–$A^{\delta-}$ in the vicinity of an ion channel (like those in bacteriorhodopsin or ATPase ion pumps). It was shown that the Coulombic field of this pair can alter the potential energy profile at certain critical points of the channel and thus ensure ion movement against the overall field.

The recently published high-resolution data on the structures of P-type ion pumps (H^+-, Na^+, K^+-, and Ca^{2+}-ATPases) suggest common principles of their operation in the plasma membrane and cell organelles, and reveal certain functionally important details, such as the amino acid residues most close to the transported ions at the energy-driven stages, or a large water cavity in the plasmalemmal proton pump [2–5]. Detailed analysis of the static structures of various complexes is a step toward understanding the dynamics of the enzyme function. An outstanding question is how the energy of ATP hydrolysis (with the characteristic time of the chemical event hardly exceeding 10^{-10} s) is stored and used in the much longer process (~10^{-2} s) of ion transfer against the concentration gradient. The local field idea [1] is quite consistent with the new structural informa-tion; in this framework, the question is which residues can generate the charge-separated $D^{\delta+}$–$A^{\delta-}$ pair. What is needed further is experimental studies on the enzyme dynamics on various (especially pico- to nanosecond) scales [6–9]. The problem of extracting the information from such time series may be alleviated by using, e.g., flicker noise spectroscopy [10].

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