Biophysical Chemistry 293 (2023) 106932

Contents lists available at ScienceDirect

Biophysical Chemistry

journal homepage: www.elsevier.com/locate/biophyschem

Thermodynamic performance of coupled enzymatic reactions: A chemical kinetics model for analyzing cotransporters, ion pumps, and ATP synthases

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ARTICLE INFO

Keywords:
ATP synthase
Molecular energy converters
Coupled enzymes
Thermodynamic optimization
Irreversible thermodynamics

ABSTRACT

Previous research has suggested that molecular energy converters such as ATP synthases, ion pumps, and cotransporters operate via spatially separate pathways for free energy donor and acceptor reactions linked by a protein molecule. We present a chemical kinetics model based on these works, with the basic assumption that all molecular energy converters can be thought of as linked enzymatic reactions, one running downhill the chemical potential gradient and driving the other uphill. To develop the model we first look at how an enzyme process can be forced to go backwards using a basic kinetic model. We then use these findings to suggest a thermodynamically consistent method of linking two enzymatic reactions. Finally, in the context of the aforementioned energy converters, the thermodynamic performance of the resulting model is thoroughly investigated and the obtained results are contrasted with experimental data.

1. Introduction

The theory of evolution through natural selection, the unity of biochemistry, and cell theory, according to Luria [1], are the three essential generalizations of biology. The unity of biological processes acknowledges that all living species share certain basic biochemical reactions because the chemical building blocks are the same: nucleic acids, proteins, and protein-producing mechanisms. Cell theory recognizes that all creatures are made up of cells, and that cells may be thought of as closed domains in which the chemical reactions required for life are carried out. One of the major duties of cells, from this perspective, is to keep the concentration of vital components high enough so that the chemical processes required for life can occur at functionally sufficient rates.

Despite the fact that cell membranes ensure high concentrations of key chemical species, many biochemical reactions would not be rapid enough without particular enzymes to speed them up. According to Berg et al. [2], enzyme catalysis is required for practically all metabolic activities in the cell to occur at rates rapid enough to support life. Enzymes, like all catalysts, can speed up naturally occurring processes, but they can't drive them up a chemical potential gradient.

In some circumstances, cells must carry out chemical processes that are not thermodynamically spontaneous. This is accomplished by the use of specific proteins (molecular energy converters) that link a favorable chemical process to an unfavorable one, allowing the first's chemical potential to propel the second up its corresponding energy gradient. Cotransporters, ion pumps, and ATP synthases are some examples.

Cotransporters are membrane transport proteins that couple one molecule's favorable movement (down its concentration gradient) with the unfavorable movement (against its concentration gradient) of another molecule [3]. Active transporters, also known as ion pumps, are ion transporters that use energy from a variety of sources, including adenosine triphosphate (ATP), sunlight, and other redox reactions, to pump an ion against an electrochemical potential gradient [4]. Finally, ATP synthases are proteins that catalyze the production of ATP. Since ATP production is generally energetically unfavorable [5,6], ATP synthases couple ATP synthesis to an electrochemical gradient, caused by a trans-membrane proton concentration differential.

Because translocation of a chemical substance can be thought of as a chemical reaction in which a molecule disappears from one compartment and reappears in another, cotransporters, ion pumps, and ATP synthases can be thought of as proteins that link two different chemical reactions and transfer energy from the thermodynamically favorable one to the unfavorable one. Previous works—see [7–17]—have proposed that molecular energy converters may work by means of spatially

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https://doi.org/10.1016/j.bpc.2022.106932
Received 21 September 2022; Received in revised form 6 November 2022; Accepted 13 November 2022
Available online 22 November 2022