



ΕΡΕΥΝΗΤΙΚΟ ΙΝΣΤΙΤΟΥΤΟ ΧΗΜΙΚΗΣ ΜΗΧΑΝΙΚΗΣ ΚΑΙ ΧΗΜΙΚΩΝ ΔΙΕΡΓΑΣΙΩΝ ΥΨΗΛΗΣ ΘΕΡΜΟΚΡΑΣΙΑΣ

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ΣΕΜΙΝΑΡΙΟ

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ΘΕΜΑ: **HIGH RESOLUTION FLUX DETERMINATION USING STABLE ISOTOPES AND MASS SPECTROMETRY**

ΤΟΠΟΣ: Αίθουσα Σεμιναρίων ΕΙΧΗΜΥΘ-ΙΤΕ

ΗΜΕΡΟΜΗΝΙΑ: Τετάρτη, 19 Σεπτεμβρίου 2001

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ΠΕΡΙΛΗΨΗ

Cellular physiology is a combination of many different functions that have to be accurately probed individually and then precisely correlated to each other, in order to reveal the language used by the cell to communicate changes from the environment to gene expression and vice versa. Recently, DNA microarrays allowed the measurement of the full gene expression profile under a particular set of environmental conditions and genetic backgrounds. To understand, however, the correlation between gene expression and the actual metabolic state of the cell, the latter needs to be also determined with high accuracy. This requires that a comprehensive set of variables is defined to describe metabolic activity and reliable methodologies are developed for the accurate determination of such variables. Defining flux as the rate at which material is processed through a metabolic pathway, the fluxes of a metabolic reaction network can be employed to provide an overall measure of metabolic activity. In addition, the changes of metabolic fluxes in response to genetic or environmental perturbations provide insightful information about the distribution of kinetic and regulatory controls in metabolism.

In this context, my research focused on the development of methods for high-resolution metabolic flux determination using stable isotopes, mass spectrometry and bioreaction network analysis. Metabolic fluxes cannot be measured directly, they are rather estimated from measurements of extracellular metabolite consumption and production rates along with data of isotopic-tracer distribution at various metabolites after the introduction of labeled substrates. This indirect estimation is possible because unknown fluxes and measurements are connected through mass and isotopomer balances. I am going to present my work on investigating the feasibility of obtaining a complete and accurate flux map from potential data based on the degree of observability of the unknown fluxes from the measurements. My research focused primarily on examining whether mass spectrometric measurements can be used as sensors of the metabolic fluxes. Finally, I will describe the determination of fluxes in the central carbon metabolism of *Corynebacterium glutamicum* from mass isotopomer distribution measurements of biomass hydrolysates in a continuous culture.

Για περισσότερες πληροφορίες μπορείτε να επικοινωνείτε με την Κλεάνθη Ζαχαροπούλου
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