

e-MITOCHONDRIA RESEARCH FOR SYSTEMS BIOLOGY AND PROTEOMICS

Hyun Joo, Jae boum Youm, Taeho Kim, Nari Kim, Won sun Park, Sunghyun Kang,
Dang Van Cuong, Hyoung kyu Kim, Tran Min Khoa, Vu Thi Thu, Hyunju Kim, Hyejin
Moon, Hyunsuk Lee, Euiyong Kim and Jin Han

Mitochondrial Signaling Laboratory, Department of Physiology and Biophysics,
College of Medicine, Cardiovascular and Metabolic Disease Center, Biohealth
Products Research Center, Inje University, Busan 614-735 Kore

Abstract

Virtual mitochondria project is a consortium network to concentrate and standardize mitochondrial functions in human. Here we describe a strategy for constructing and investigation of large-scale mitochondria models of energy metabolism. The development of realistic-working model for energy metabolisms (oxidative phosphorylations), signaling networks, and ROS (Reactive Oxygen Species) generations are accomplished in several steps. The first step is to elucidate a static model of the mitochondrial functions: ion-gating proteins, metabolic intermediates, enzymes, co-factors, and other key players. The second stage is to generate simultaneous dynamic equations to describe all processes involved in the maintenance of mitochondrial membrane potential. To aid mitochondrial proteomics approach, the model is linked to an internal mitochondrial proteome database (DB) and genome-wide proteins searching and annotation tool. They include computational predictions of signaling sequences and the results of mitochondrial 2-DE and Mass spectrometry analyses. Taken together, the constructed model and DB may lead to a comprehensive grasp of the mitochondrial functions, and give us a possibility for understanding the control and regulatory phenotype of mitochondria-related disorders. The ultimate goal of this work is to provide improved diagnostics, therapy and prevention of mitochondria-related diseases.