

matter of dispute. Recently, we identified a novel protein complex composed of a pore-forming core (MitoK) and of a regulatory subunit (mitoSUR) located in the inner mitochondrial membrane. In planar lipid bilayer experiments in 100 mM potassium gluconate solution, performed employing the recombinant mitoK protein alone, the conductance and kinetic behaviour of the observed activity resembled those of the previously described mitoKATP channel. However, activity was not inhibited by Mg^{2+} and ATP, unless MitoK and mitoSUR were co-expressed. These two proteins together formed a channel that was sensitive to mM concentration of ATP and was activated by diazoxide, a well-known pharmacological agonist of mitoKATP. Given the observed effect of several classical pharmacological activators and inhibitors of mitoKATP, our data suggest that these two proteins might be responsible, at least under certain conditions, for mitoKATP activity and for the control of mitochondrial ion homeostasis.

doi:10.1016/j.bbabbio.2016.04.157

06.07

Modulation of the mitochondrial carnitine/acylcarnitine transporter by acetylation

Lara Console^a, Nicola Giangregorio^b, Annamaria Tonazzi^b, Cesare Indiveri^a

^aDepartment DiBEST (Biologia, Ecologia, Scienze della Terra) Unit of Biochemistry and Molecular Biotechnology, University of Calabria, Via Bucci 4C, 87036 Arcavacata di Rende, Italy

^bCNR Institute of Biomembranes and Bioenergetics, via Amendola 165/A, 70126 Bari, Italy

E-mail address: console@hotmail.it (L. Console)

The mitochondrial carnitine/acylcarnitine transporter (CACT) catalyses carnitine/acylcarnitine antiport. Its function has been defined mainly in proteoliposome experimental models. Despite CACT represents a putative site of β -oxidation regulation, few data are available about its modulation. Lysine acetylation is a post-translational modification (PTM) of a huge number of proteins. It has been shown that hyper-acetylation of long chain acyl CoA dehydrogenase (LCAD) impairs its enzymatic activity. It could be hypothesized that other components of the same pathway, such as CACT, could be regulated by a similar mechanism. Indeed, CACT is partially acetylated in rat liver as revealed by WB analysis using an anti-acetyl-Lys antibody. Acetylation can be reversed by the mitochondrial deacetylase SIRT3. After treatment of the mitochondrial extract with SIRT3, the CACT activity, assayed in proteoliposomes, increases with respect to the untreated control. The half-saturation constant is not influenced, while the V_{max} is increased. The kinetic data suggests that steric hindrance of acetyl groups impairs conformational changes, rather than substrate binding. Recently, it was shown that acetylation of mitochondrial proteins also occur by a non-enzymatic pathway under conditions of reduced Acetyl-CoA buffering [1]. Recombinant CACT which is not acetylated was incubated with acetyl-CoA and then subjected to WB with anti-acetyl-Lys antibody and transport assay. Data showed that non-enzymatic acetylation of CACT occurs and impairs its activity. In conclusion, CACT is regulated by acetylation representing a control site of beta-oxidation pathway together with LCAD.

References

1. M. N. Davies, L. Kjalarsdottir, J. W. Thompson, L. G. Dubois, R. D. Stevens, O. R. Ilkayeva, M. J. Brosnan, T. P. Rolph, P. A. Grimsrud, D. M. Muoio, The Acetyl Group Buffering Action of Carnitine Acetyltransferase Offsets Macronutrient-Induced Lysine Acetylation of Mitochondrial Proteins, *Cell Rep* 14 (2016) 243-54.

doi:10.1016/j.bbabbio.2016.04.158

06.08

Do dimers of ATP synthase form the PTP in pea stem mitochondria?

Valentina De Col^a, Carlo Peresson^a, Elisa Petrusa^a, Valentino Casolo^a, Sonia Patui^a, Alberto Bertolini^a, Valentina Giorgio^b, Vanessa Checchetto^c, Enrico Braidot^a, Giovanna Lippe^a, Ildikò Szabó^c, Angelo Vianello^a, Paolo Bernardi^b, Marco Zancani^a

^aDept. of Agricultural, Food, Environmental and Animal Sciences, University of Udine, Italy

^bConsiglio Nazionale delle Ricerche Institute of Neuroscience and Department of Biomedical Sciences, University of Padova, Italy

^cDepartment of Biology, University of Padova, Italy

E-mail address: decol.valentina@spes.uniud.it (V. De Col)

In animal cells Ca^{2+} and ROS induce a sudden change in the inner mitochondrial membrane permeability, which has been named Permeability Transition (PT). Recently, it has been proposed that dimers of F-ATP synthase form the Permeability Transition Pore (PTP), the mega-channel involved in this phenomenon [1]. This feature has not yet been characterized in plants, even if their mitochondria possess the candidate components for PTP formation. Therefore, we characterized the functional properties of PTP in plant mitochondria and verified if F-ATP synthase possesses channel function in electrophysiology experiments. Mitochondria isolated from pea stem underwent PT when Ca^{2+} was added in the presence of the ionophore ETH129. The membrane electrical potential was then collapsed and the phenomenon matched by Ca^{2+} release but not by mitochondrial swelling. As is observed with the PT of animal mitochondria, Cyclosporin A (CsA) significantly delayed occurrence of PT, which was inhibited by Mg^{2+} -nucleotides and favored by benzodiazepine Bz-423 and oxidants, such as phenylarsine oxide and diamide. In electrophysiology experiments, F-ATP synthase dimers inserted into an artificial bilayer showed channel activity characterized by a rather small conductance, which could explain the inability of plant PTP to mediate mitochondrial swelling. These data suggest that F-ATP synthase is involved in PTP formation also in plant mitochondria.

References

1. V. Giorgio, S. von Stockum, M. Antoniel, A. Fabbro, F. Fogolari, M. Forte, G.D. Glick, V. Petronilli, M. Zoratti, I. Szabó, G. Lippe, P. Bernardi, Dimers of mitochondrial ATP synthase form the permeability transition pore, *Proc Natl Acad Sci U S A*. 110 (2013) 5887-5892.

doi:10.1016/j.bbabbio.2016.04.159

06.09

Modulation of mitochondrial adenine nucleotide translocase (ANT) regulation with ageing

Philippe Diolez^a, Isabelle Bourdel-Marchasson^{b,c}, Philippe Pasdois^a, Dominique Detaille^a, Audrey Sémont^a, Richard Rouland^c, Guillaume Calmettes^d, Gilles Gouspillou^e

^aINSERM U1045 - Centre de Recherche Cardio-Thoracique de Bordeaux & LIRYC - Institut de Rythmologie et Modélisation Cardiaque, Université de Bordeaux, CHU de Bordeaux, France, France

^bCHU de Bordeaux, Pôle de gériatrie clinique, Bordeaux, France

^cRésonance Magnétique des Systèmes Biologiques, UMR 5536 CNRS - Université de Bordeaux, France

^dDepartment of Medicine (Cardiology), David Geffen School of Medicine, University of California, Los Angeles, CA, USA

^eDépartement de Kinanthropologie, Université du Québec à Montréal, Montreal, QC, Canada

E-mail address: philippe.diolez@ihu-liryc.fr (P. Diolez)