the FEBS Journal

the FEBS Journal

Volume 282 Supplement 1 July 2015

Poster Sessions

Table of Contents

Poster Session 1

Sunday 5 July & Monday 6 July
08:30–19:30, Foyer Convention Center

Poster Session 2

Tuesday 7 July & Wednesday 8 July
08:30–19:30, Foyer Convention Center

Each poster has been given a unique number and the first part of the poster number relates to the session in which the poster was presented. Gen EX S1 = P02; Gen EX S2 = P03; Gen EX S3 = P04; Gen EX S4 = P05; Gen EX S5 = P06; Mem Biol S1 = P08; Mem Biol S2 = P09; Mem Biol S3 = P10; Mem Biol S4 = P11; Mem Biol S5 = P12; Chem Biol S1 = P14; Chem Biol S2 = P15; Chem Biol S3 = P16; Chem Biol S4 = P17; Chem Biol S5 = P18; Mol Neu S1 = P20; Mol Neu S2 = P21; Mol Neu S3 = P22; Mol Neu S4 = P23; Mol Neu S5 = P24; Sys Biol S1 = P26; Sys Biol S2 = P27; Sys Biol S3 = P28; Sys Biol S4 = P29; Sys Biol S5 = P30; Struct Biol S1 = P32; Struct Biol S2 = P33; Struct Biol S3 = P34; Struct Biol S4 = P35; Struct Biol S5 = P36; FEBS Education Session = P38; Late-breaking abstracts = LB.

high activity in a variety of different conditions, whereas enterobacterial MraY homologues from numerous pathogens were inhibited by detergents and high quality protein samples could only be produced in presence of specific compounds. The complete biosynthetic pathway starting from UDP-N-acetylglucosamine precurosr to lipid II formation could be reconstituted with cell-free expressed proteins and will provide the basis for developing new drug screening platforms in defined environments.

P32-016
Structural investigation into the comprehensive mechanism of concentrative nucleoside transport

Z. Hao[1,2], A. Lesiuk[1], R. Kolodziejczyk[1], J. D. Young[3], S. A. Baldwin[1], V. L. G. Postis[1], A. Goldman[1], M. Bartlam[4], Y. Wang[2]
[1]*Faculty of Biomedical Sciences, University of Leeds, Leeds, UK,* [2]*College of Environmental Science and Engineering, Nankai University, Tianjin, China,* [3]*Department of Physiology, University of Alberta, Edmonton, Canada,* [4]*State Key Laboratory of Medicinal Chemical Biology, Nankai University, Tianjin, China*

Nucleoside transporters (NTs) are very important in humans, and play vital roles in nucleic acid synthesis, energy metabolism and a host of physiological processes involving regulation of intra- and extra-cellular concentrations of purine and pyrimidine (deoxy) nucleosides. Furthermore, it possesses a wide range of potential applications in the development of drugs, especially for antiviral and anticancer drugs. To date, two main families of membrane nucleoside transporters have been identified in mammalian cells, including the concentrative nucleoside transporter (CNT) and the equilibrative nucleoside transporter (ENT) families. In the former family, concentrative transport of nucleosides is energized by transmembrane sodium and/or proton gradients, whereas in the latter bidirectional nucleoside transport is driven solely by the concentration gradient of the nucleosides across the membrane. However, our understanding of the molecular mechanisms of nucleoside transport remains limited. The only known structure of a CNT is VcCNT from *Vibrio cholera* in an inward-facing and partially occluded conformation. At present, we are attempting to resolve the nucleoside transport mechanism by capturing and analyzing the different conformations likely to be involved in the translocation cycles of different bacterial CNTs. Meanwhile, by comparing sodium-driven transporters such as VcCNT and homologous proton-driven transporters such as NupC from *Escherichia coli*, we aim to illustrate the basis for the differing cation selectivities of CNTs. This work should help to elucidate the molecular mechanisms of concentrative nucleoside transport by a structural approach, not only in the bacterial transporters but also in their physiologically and medically important counterparts in humans.

P32-017
MacAB efflux system of *Serratia marcescens* as a potential protective system against oxidative stress

T. V. Shirshikova[1], L. Y. Matrosova[2], I. V. Khilyas[2], M. R. Sharipova[2], L. M. Bogomolnaya[2]
[1]*Institute of Fundamental Medicine and Biology, Kazan Volga region Federal University, Kazan, Russian Federation,* [2]*Kazan (Volga region) Federal University, Kazan, Russian Federation*

Bacterial resistance to antibiotics is one of the major problems in the world. The most important in the appearance of bacterial antibiotic resistance is understanding and investigation of its molecular mechanisms. Bacteria genus of *Serratia* is opportunistic and antibiotic resistance pathogens with increased clinical significance. Efflux systems of *Serratia marcescens* involved in an excretion of a wide range of antibiotics. Analysis of genome sequence of *S. marcescens* allowed discovering a new ABC-type efflux system. This system has a high homology to MacAB system of *E. coli*. Special characteristic of MacAB efflux system of *S. marcescens* consists in defending against reactive oxygen species (ROS) addition to participating in antibiotics excretion. Goal of this research was an investigation of resistance of wild type (w.t.) and mutant Δ macAB (m.t.) *S. marcescens* to ROS. Resistance of both strains to hydrogen peroxide (HP) was explored. HP presence in the medium led to m.t. cell death and w.t. viability. Co-cultivation of both strains resulted in the emergence of resistance of m.t. to HP. W.t. supernatant provided a clear protective effect for m.t. in the presence of HP. Thermostability and sensitivity to proteinase K treatment of w.t. supernatant metabolites allowed suggesting that protective compounds have a protein essence. Thus, macAB efflux system of *S. marcescens* plays a crucial role in a cell defense against ROS and its absence prevent to extracellular protective metabolites formation. This work was funded by the subsidy of the Russian Government to support the Program of Competitive Growth of Kazan Federal University.

P32-018
Acetazolamide, an inhibitor of carbonic anhydrase, supresses photophosphorylation and stimulates light-induced ATP hydrolysis in isolated spinach chloroplast

O. K. Zolotarova, A. V. Semenikhin, E. B. Onoiko
Membranology & Phytochemistry, M.G.Kholodny Botany Institute, Kyiv, Ukraine

The chloroplast CF_1CF_o-ATPase/synthase is located in energy-transducing thylakoid membranes of chloroplasts where it catalyzes light-induced ATP synthesis and $\Delta\mu H+$ generating ATP hydrolysis. It has a membrane sector (CFo) attached to a membrane extrinsic oligomeric complex (CF1), that contains the catalytic sites for ATP synthesis and hydrolysis and noncatalytic (regulatory) sites. The noncatalytic sites can bind some oxyanions (bicarbonate, sulfite, borate etc.), activating CF_1-ATPase. We have shown recently (Semenikhin & Zolotarova, 2014) that both CF_1CF_o complex and its isolated catalytic part, factor CF_1, are able to accelerate the prosess of interconversion of carbonic acid forms: $CO_2 + H_2O \Rightarrow H^+ + HCO_3^-$, ie to exhibit carbonic anhydrase activity. The aim of the present work is studying the effect of acetazolamide, an inhibitor of carbonic anhydrase, on the rate of photophosphorylation and the light-induced ATP hydrolysis in isolated spinach chloroplasts. The rate of ATP synthesis was determined by hexokinase method in chloroplast suspension illuminated for 2 min in the presence of electron acceptors. The amount of ATP was determined enzymatically using glucose-6-phosphate dehydrogenase and NADP. Formed in the reaction NADPH was measured by fluorescent method. The amount of Pi released in ATPase reaction of thylakoids was determined by colourimetric method after illumination of the chloroplast suspension for 2-5 min. The data show that acetazolamide inhibits light-induced synthesis and stimulates ATP hydrolysis suggesting participation of carbonic anhydrase activity in transmembrane proton transfer coupled with ATPsynthesis/hydrolysis in thylakoid membrane of chloroplasts.