The yeast *Saccharomyces cerevisiae* mitochondria are slightly peculiar since they do not exhibit a complex I but have a number of external and internal dehydrogenases in the inner mitochondrial membrane. These dehydrogenases give their electrons to the quinone pool. On the outer side of the inner membrane, two dehydrogenases activities are localized: the NADH dehydrogenase and the glycerol-3-phosphate dehydrogenase. On the matrix side of the inner membrane, one can find NADH dehydrogenase and succinodehydrogenase. We have previously shown that in mitochondria isolated from *S. cerevisiae*, electrons coming from certain dehydrogenases have the right of way on electrons coming from others. Typically, electrons coming from the external NADH dehydrogenases, have the right of way on other dehydrogenases. In order to understand the possible relationship between this process and the supramolecular organization of the respiratory chain, we undertook a functional and structural study of yeast mutants that do or do not exhibit a supramolecular organization. We have thus studied the electrons competition process in a cardiolipin delta mutant known to possess an altered respiratory chain supramolecular organization. We also studied the organisation of the respiratory chain by BN-PAGE method in a mutant that exhibit an altered electron competition process. Results pertaining to this study will be presented.

doi:10.1016/j.bbabio.2008.05.354

S13.11 Towards crystallizing co-complexes of newly identified inhibitors with the QFR from *Wolinella succinogenes* and with other members of the superfamily of succinate:quinone oxidoreductases

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The members of the superfamily of succinate:quinone oxidoreductases exhibit a high degree of variability with respect to the sensitivity of their quinone sites to various inhibitors. The goal of the project is the identification of potent inhibitors of the diheme-containing membrane protein complex quinol:fumarate reductase (QFR) from *Wolinella succinogenes* and a comparison of these newly identified inhibitors to those of other members of the superfamily, e.g. 2-heptylquinoline-*N*-oxide (HQNO). We shall present first results which are a prerequisite for the co-crystallization of these inhibitors with the respective membrane protein complexes.

doi:10.1016/j.bbabio.2008.05.355

S13.12 Hybrid protein-semiconductor photonic structures using bacteriorhodopsin and glucose oxidase

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The aim of this work is to characterize porous silicon (PSi) photonic structures impregnated with glucose oxidase (GOX) or solubilized bacteriorhodopsin (BR) as a first step in developing hybrid matrices for future biophotonic applications. PSi Bragg mirrors and microcavities are multilayered structures of periodic refractive index with layer thicknesses in the order of visible light wavelength. The pore size of PSi can be tuned to accommodate biomacromolecules, and the silicon surface can be functionalized for covalent protein attachment. Both proteins have previously been shown to possess nonlinear optical properties. We have used atomic force microscopy and multi-photon microscopy to characterise the surface and in depth, respectively, the GOX or BR impregnated PSi structures. Two photon fluorescence emission and second harmonic generation of the BR-PSi and the GOX-PSi systems were observed at some particular pores of PSi and subsequent enhancement of the signal arising from the proteins adsorbed within the pores was detected. The results constitute the first steps in an innovative biomimetic approach for the future design and development of protein based integrated optical devices.

doi:10.1016/j.bbabio.2008.05.356

S13.13 Multiheme periplasmic cytochromes of *Geobacter sulfurreducens*: Optimized cellular devices to face extracellular electron acceptors?

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Multiheme cytochromes are key proteins in the reduction of extracellular metal ions as Fe(III) and U(VI) in *Geobacter sulfurreducens* (Gs). In contrast with cytoplasmic acceptors, theoretical studies showed that reduction of extracellular acceptors leaded to the dissipation of the membrane potential due to cytoplasm acidification. To counteract this, additional energy transduction steps are needed to generate energy. PpcA, a small periplasmic triheme cytochrome, was proposed to contribute to the energy transduction cycle that leads to ATP synthesis in Gs. Four homologs of PpcA were identified in Gs genome, being PpcB the most closely related, with 77% sequence identity. In this study the redox centers of PpcB were characterized using NMR and visible spectroscopy techniques. Despite being sequence and structurally homologous, the functional redox properties of PpcB and PpcA are quite distinct. This correlates with the results of phenotypic studies that showed that knock-out of PpcA gene disrupts electron transfer to extracellular Fe(III), while the effect of PpcB gene deletion is notorious on the U(VI) reduction activity. This suggests that each protein uniquely modulates the properties of their co-factors to assure effectiveness in the metabolic pathways they participate.

doi:10.1016/j.bbabio.2008.05.357

S13.14 Spectroscopic and structural studies of the alternative oxidase

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