Signaling from the mitochondria under a stress condition to nucleus (also known as retrograde signaling) affects expression of nuclear genes allowing for cell adaptation to impairment of mitochondrial functions. These adaptive changes can lead to an enhancement of mitochondrial mass and expression of a number of mitochondrial and nuclear genes encoding for mitochondrial proteins. Mitochondria-to-nucleus signaling can be mediated by a number of molecules and one of them are reactive oxygen species (ROS). The mitochondrial stress affects production of ROS. On the other hand, increased ROS level has been shown to be a causative factor of diseases associated with mitochondrial dysfunction. In the lecture the current understanding of mitochondrial stress mechanism will be presented.

References

[1] Lebiedzinska M. *et al.,* (2009) *Int. J Biochem. Cell. Biol.* **41:** 1805–1816.
[2] Lebiedzinska M. *et al.,* (2009) *Arch. Biochem. Biophys.* **486** 73–80.
[3] Koziel K. *et al* (2009) *Int. J. Biochem. Cell. Biol.* **41:** 2440–2449.
[4] Wieckowski M.R *et al.,* (2009) *Nat. Protoc.* **4:** 1582–1590.
[5] Czyz A *et-al.,* (2009) *Biochem. Biophys. Res. Commun.* **381:** 176–180.
[6] Wojewoda M *et al.,* (2010) *Bioch. Biophys. Acta - Bioenergetics,* accepted.
[7] Lebiedzinska M *et al.,* (2010) *Bioch. Biophys. Acta - Bioenergetics,* accepted.
[8] Suski J *et al.,.* (2010) *Curr. Drug Targets,* accepted.
[9] Koziel R *et al.,* (2010) *J. Physiol. Pharm.* accepted.

PL. 4

The family of proton-pumping heme–copper respiratory oxidases
Robert B. Gennis
Department of Biochemistry, University of Illinois, Urbana, IL 61801 USA
E-mail: rennis@illinois.edu

The respiratory chains of nearly all aerobic organisms contain at least one member of the heme-copper superfamily of oxygen reductases to catalyze the 4-electron reduction of dioxygen to water. Genomic and metagenomic studies have revealed that there is a remarkable diversity to these enzymes, but that they have a single evolutionary origin. The superfamily includes not only the respiratory oxygen reductases, but also several families of NO reductases. The superfamily is defined by homology within a single transmembrane subunit which, in all cases, have three histidines which are the axial ligands to one low spin heme and to one high spin heme. In addition, there are three additional histidines which ligate to a copper ion located at the active site of the oxygen reductases, or to an iron in the case of the NO reductases. More than 99% of the respiratory oxidases can be grouped into three families (A-, B- and C-families). Members of each of these families have been examined and shown to pump protons across the membrane. The stoichiometry of proton pumping for the A-family enzymes, which includes the mitochondrial cytochrome *c* oxidase, is 1 proton per electron. However, the stoichiometry of proton pumping appears to be about half (0.5 proton per electron) for members of the B-family and the C-family. This might be the result of an adaptation to life at very low dissolved oxygen concentrations.

PL. 5

How plants regulate the photosynthetic activity: Linear versus cyclic electron flow and non-photochemical quenching
Pierre Joliot, Anne Joliot
CNRS UMR 7141 Institut de Biologie Physico-Chimique, 13 rue Pierre et Marie Curie 75005 Paris, France
E-mail: pjoliot@ibpc.fr

Plants have developed different strategies to adapt photosynthetic activity to the highly variable light intensity in their environment. The ATP concentration within the chloroplast is one of the key parameters that control the rate of CO_2 assimilation *via* the Benson–Calvin cycle. It can be estimated by the measurement of the electrochemical proton gradient [1]. At the onset of illumination, the photosynthetic process mainly operates according to the cyclic process that induces a fast increase in the ATP concentration. Under weak illumination, a tight correlation is observed between an increase in the rate of linear electron flow, which reflects the activation of the Benson–Calvin cycle and the decrease in the rate of cyclic electron flow [2]. After a few-minute illumination sufficient to induce steady state conditions, ATP generated by the linear electron transfer chain is sufficient to sustain the ATP consumption through the Benson–Calvin cycle and the rate of the cyclic electron flow is negligible. The rate of the cyclic flow increases as a function of the light intensity while the ATP concentration in the chloroplast has reached its maximum value. Thus, under strong light excitation, the cyclic flow exclusively promotes a large proton gradient. The acidification of the lumen induces: 1) the formation of non photochemical quenchers (NPQ) in the vicinity of PS (photosystem) II reaction centers. NPQ protects PSII from the photodestruction induced by the excess of light; 2) a slowdown of the cytochrome $b6/f$ turnover that leads to the partial oxidation of the PSI primary donor P_{700}. Oxidation of P_{700} protects PSI by preventing the occurrence of back reactions that would induce photodamages. The inhibition of NPQ formation and of P_{700} oxidation is observed in the presence of low nigericin concentration $(0.4\,\mu M)$ that partially collapses the proton gradient. In these conditions, the illumination $(>1\,h)$ induces partial photodestruction of both PSI and PSII reaction centers. Thus, the acidification of the lumen associated with the activation of the cyclic electron flow protects both photosystems against photodamages induced by an excess of light.

References

[1] Joliot P, Joliot A (2008) *Biochim. Biophys. Acta* **1777:** 676–683.
[2] Joliot P, Joliot A (2006) *Biochim. Biophys. Acta* **1757:** 2006 362–368.

PL. 6

Biogenesis of the membranes of mitochondria
Walter Neupert
Institute for Biochemistry, University of Munich and Max Planck Institute for Biochemistry, Martinsried, Germany
E-mail: neupert@med.uniuenchen.de

Mitochondria, unlike most cellular organelles, have an architecture that is quite unique, elaborate and highly variable between different organisms and tissues. The membranous elements of mitochondrial structure are the outer membrane and the inner membrane. The inner membrane is divided in a complex manner into subdomains: the inner boundary membrane (IBM) which together with the tightly linked outer membrane forms a kind of double