period of regular exercise. This is a result of an exercise-induced augmentation in the expression of protein import machinery components. During the aging process, mitochondrial content in muscle declines, and this is reflected in a reduced endurance performance. The decrease in mitochondrial content does not appear to be due to altered post-translational import mechanisms, but may be transcriptionally-related, since PGC-1α levels are markedly reduced, particularly in slow-twitch muscle fibers. In addition, in response to a standardized acute contractile activity paradigm, signaling kinase activation is increased to a lesser degree than in muscle from young animals, which could lead to a reduced transcriptional activation with age. This likely contributes to the reduced adaptation of aged muscle to regular exercise, consisting of attenuated increases in the expression of biogenesis regulatory proteins of transcription and protein import, reduced increases in mitochondrial enzymes, and lesser improvements in endurance performance. These data suggest that the exercise-induced activation of mitochondrial biogenesis is down-regulated with age. Despite this, adaptive responses to exercise can still occur in aging muscle, leading to reduced fatiguability and improved quality of life.

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13L.4 ATP-dependent proteases in biogenesis and maintenance of *Arabidopsis* mitochondria

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It is now widely accepted that tissue- and time-specific control of the quantity and quality of mitochondrial proteins is essential to cope with the challenges of changing developmental and environmental conditions. Recent studies indicate that in plant mitochondria, like in the yeast and animal ones, ATP-dependent proteases are the key components of such control. One of the best characterized plant mitochondrial ATP-dependent protease is FtsH4 from *Arabidopsis*. I will present results which imply that AtFtsH4 is involved in maintaining mitochondrial homeostasis late in rosette development under short-day photoperiod and in plant thermo-tolerance after prolonged exposure to moderately elevated temperature. I will then present some new data on the role of ATP-dependent proteases including AtFtsH4 in coordination of nuclear and mitochondrial genome expression in *Arabidopsis* mutant with impaired mitochondrial translation due to silencing of ribosomal RPS10 gene expression.

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13L.5 RNA turnover in human mitochondria

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Perturbations in functioning of mitochondrial (mt) gene expression have been linked to many human conditions including cancer, aging and neurodegenerative diseases. Therefore research on mechanisms of mt gene expression is of great importance. RNA degradation plays a very important role as it controls three major aspects of RNA metabolism: it determines the half-life of a given RNA species, it destroys the aberrant RNAs that might interfere with replication, transcription or translation in mitochondria, and finally it degrades processing intermediates. In our laboratory we are studying the human nuclear-encoded proteins: SUV3 helicase, polynucleotide phosphorylase (PNPase) and poly(A) polymerase. A model will be presented which describes this interplay of the proteins in ensuring transcript stability and surveillance in mitochondria. In addition we shall discuss data on their participation in molecular events outside mitochondria: cell cycle control and nuclear chromatin maintenance.

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Posters

13P.1 Transfer of disulfide bonds in biogenesis of mitochondrial intermembrane space proteins

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Mitochondria play a critical role in cellular metabolism and are involved in apoptosis, ageing and a number of diseases. Biogenesis of mitochondrial proteins involves several steps including targeting to mitochondria, transport across the mitochondrial membranes, maturation and associations with partner proteins to form functional complexes ([3]). The novel MIA (Mitochondrial Intermembrane Space Assembly) pathway is essential for the biogenesis of intermembrane space proteins in the entire eukaryotic kingdom ([1,2]). A hallmark of this pathway is the regulated transfer of disulfide bonds, a process that had not been previously described in mitochondria ([1,4]). The MIA pathway represents a novel disulfide-transferring system to control the vectorial translocation of proteins into mitochondria ([7]). Mia40, one of the essential components of this pathway, acts in a receptor-like manner ([5]). It dictates precursor entry into the intermembrane space specifically selecting the proteins that possess a cysteine-containing signal MISS (Mitochondrial Intermembrane Space Signal) ([6]). Furthermore, a mode of the cooperation between Mia40 and the sulfhydryl oxidase Erv1 is unique. We propose that the simultaneous association of Mia40, Erv1 and a substrate protein in the ternary complex allows the efficient transfer of multiple disulfide bonds into substrate proteins ([8]). Our findings have important implications for the biogenesis of mitochondria, generation and transfer of disulfide bonds and their impact on protein compartmentalization and organelle functioning.

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13P.2 Biogenesis of the bacterial cbb_3 oxidase of *Rubrivivax gelatinosus:* Evidence for an active core-complex, composed of the catalytic subunit CcoN and the monoheme cytochrome CcoO

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The purple b-proteobacterium *Rubrivivax* (*R.*) *gelatinosus* expresses high amounts of active cbb_3 cytochrome *c* oxidase when grown under micro-aerobic conditions (Khalfaoui-Hassani *et al., J. Biol. Chem.*, 2010). Cytochrome *c* oxidases are the terminal members of the electron transport chains in mitochondria (aa_3 oxidase) and many bacteria (cbb_3, caa_3 and aa_3 oxidases). They belong to the heme-copper oxidase superfamily. The four genes coding for the cbb_3 oxidase (*ccoNOQP*) were identified and cloned; they encode respectively for four subunits: the membrane-integral catalytic subunit CcoN containing heme *b* and heme b_3-Cu_B binuclear centre, the monoheme cytochrome CcoO, a short cofactor-less subunit CcoQ and the diheme cytochrome CcoP. The major features of this enzyme are the lack of Cu_A-containing subunit and the presence of three *c*-type hemes in CcoP and CcoO. Here we report the importance of each subunit for the stability of the cbb_3 oxidase in the membrane, for the oxidase activity and for micro-aerobic growth of *R. gelatinosus*. Individual mutants of each subunit were constructed. They were all analysed for the O_2 consumption under micro-aerobic growth, for the oxidase activity of solubilised membranes on BN-PAGE, for the presence of cytochrome *c* and subunits identified respectively by gel detection with TMBZ and western blots. Our data revealed the importance of both CcoN and CcoO subunits for activity and stability of the complex in the membrane. However in the absence of CcoP or CcoQ, active complexes were produced but displaying lower activities compared to the wild type. Altogether these data allowed us to conclude that CcoN and CcoO can assemble in the absence of CcoP or CcoQ and produce a partially active and functional core-complex.

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13P.3 Coordination of mitochondrial and nuclear genes expression in *Arabidopsis* mutant with impaired mitochondrial translation

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In *Arabidopsis thaliana* the *Rps10* gene encodes the S10 protein, which is part of the small subunit of mitochondrial ribosomes. Transgenic lines obtained by RNA-i mediated silencing of *Rps10* gene expression were utilized to investigate how impaired mitochondrial translation influences biogenesis of mitochondria. It is well known that subunits of oxidative phosphorylation complexes are encoded by both nuclear and mitochondrial genomes and synthesized in cytosol and mitochondria, respectively. Therefore, first we have focused on changes in expression of oxidative phosphorylation genes in *Rps10* mutants. All of mitochondrial encoded transcripts increased approximately four-fold, whereas the abundance of nuclear-encoded transcripts were constant or altered in less degree. Analysis at the protein level revealed that both mitochondrial- and nuclear-encoded subunits of oxidative phosphorylation complexes were at much lower level in *Rps10* mutants compared to wild type plants. Thus, silencing of *Rps10* gene altered expression of mitochondrial genes at the transcript and protein levels, while for nuclear genes, significant changes in expression were observed only at the protein level. These results suggest that mitochondria try to compensate the lower amount of mitochondrial proteins by the increase in abundance of mitochondrial encoded transcripts, but the level of nuclear-encoded transcripts is insensitive to impaired mitochondrial translation. Furthermore, differential abundance in transcripts of genes encoding mitochondrial and nuclear proteins from the same oxidative phosphorylation complex indicates that coordination of expression between mitochondrial and nuclear genes in the *Rps10* mutants occurs at the posttranscriptional level. Now, we are checking the hypothesis that biogenesis of oxidative phosphorylation complexes in the *Rps10* mutants is limited by the abundance of mitochondrial encoded subunits and the excess of nuclear-encoded proteins are degraded by mitochondrial ATP-dependent proteases.

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13P.4 Assembly of cytochrome cbb_3 oxidase

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Cbb_3-type cytochrome oxidases (cbb_3-Cox) represent a subfamily of the heme-copper oxidase superfamily. Due to their high oxygen affinity, they are considered to be important factors for the bacterial adaptation to different oxygen concentrations. In particular, many pathogenic bacteria like *Vibrio cholerae*, *Helicobacter pylori*, *Bordetella pertussis*, *Campylobacter jejuni* or *Neisseria meningitidis* seem to depend on the cbb_3-Cox for colonizing the human host. In contrast to well studied aa_3-type cytochrome oxidase, only little is known about the assembly of cbb_3-Cox. By combining Blue–Native–Page analyses with *in vitro* transcription/translation assays and chemical cross-linking, we have been able to determine a first model for cbb_3-Cox assembly in the model organism *Rhodobacter capsulatus*. Our data reveal that the functional assembly is initiated by the formation of two independent subcomplexes. The catalytic subunit CcoN first assembles with the mono-heme cytochrome CcoO subunit to form a 200 kDa complex. To this complex, a 40 kDa complex containing the di-heme cytochrome subunit CcoP and the small CcoQ subunit is recruited to form the active 230 kDa cbb_3-complex [1]. Further analyses of this process led to the identification of several assembly proteins which are essential for cbb_3-Cox assembly. One is CcoH, a small integral membrane protein, which is essential for cbb_3-Cox biogenesis and appears to be required for the recruitment of the CcoPQ complex into the CcoNO complex. In agreement with this, we show by cross-linking that CcoH is able to interact directly with CcoP and CcoN subunits. In addition, CcoH appears to form a stable complex with both the CcoNO and the CcoQP subassemblies as well as with fully assembled 230 kDa complex on BN-PAGE. It suggests that CcoH serves as an adapter protein that by dimerization assembles both sub-complexes into a functional unit and is a permanent component of an active form of cbb_3-type oxidase.

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13P.5 Developmental changes of mitochondrial DNA content and expression of genes involved in mtDNA transcription and maintenance in human fetal liver and muscle tissues

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