Lectures

L.6.1

Novel regulators of photosynthesis

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Photosynthetic processes in the chloroplast demand a tight coordination of gene expression in two genetic compartments, and the proper assembly and function of genetically-chimeric multi-protein complexes. The evolution of photosynthetic eukaryotes created novel nuclear encoded proteins to sustain a stable fusion of the two organisms. Concomitantly, nuclear encoded proteins evolved with functions in the regulation of photosynthesis allowing the adaptation of photosynthetic eukaryotes to multiple environmental conditions and acclimation to changes within. We employ different approaches for identifying novel photosynthesis-associated proteins. This includes the guilt-by-association approach that is based on the fact that nuclear genes for proteins with photosynthesis-associated functions exhibit similar transcript profiles. Employing this approach as a starting point we identified and characterised PGRL1, the FQR enzyme in cyclic electron flow; CSP41, a protein that binds and stabilises distinct plastid transcripts; and a novel thylakoid protein which controls thylakoid architecture. Additionally, we study the effect of phosphorylation events on the regulation of photosynthesis in response to changes in incident light.

L6.2

Redox control of photosynthetic acclimation in plants

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Photosynthesis is a very dynamic process that needs to deal with multiple environmental fluctuations which affect photosynthetic efficiency. Photosynthetic organisms, therefore, developed a number of acclimation mechanisms during evolution which help them to maintain photosynthetic efficiency even under adverse conditions. It is known that in forests or crop fields strong light gradients occur which require a structural and functional acclimation of the photosynthetic apparatus. In a short-term this is achieved by phosphorylation-dependent modification of the antenna structure of the photosystems or its super-complex assembly. In the long-term photosystem stoichiometry is adjusted by redox-controlled changes in the expression of nuclear and chloroplast genes encoding the photosynthetic apparatus. In addition, photosynthetic acclimation appears to redirect the metabolic state of plant cells being an interesting target for bioenergy applications. Our research aims to understand these regulation networks by identifying and analysing decisive regulatory factors such as novel structural components, kinases or transcription factors. This will help to engineer more stress-resistent crops for food and biofuel production.

Oral presentations

O6.1

A new role for thioredoxin z in modulating the redox regulation activity of other thioredoxins in chloroplasts

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One of the main factors involved in regulation of the cellular redox state, which allow plant adaptation to environmental stress conditions, is a multigenic family of small ubiquitous oxidoreductases named thioredoxins (TRX). *Arabidopsis* genome encodes *ca.* twenty canonical TRX, including ten plastidial isoforms (2f-, 4m-, x-, 2y- and z-TRX types). TRXf and m were found to mainly redox regulate the activity of enzymes involved in the primary metabolism whereas TRXx and y serve as reducing substrates for antioxidant enzymes. TRXz was more recently identified as an essential subunit of the plastid-encoded RNA polymerase complex. The reduction of TRXm and f in chloroplasts is performed in the light by ferredoxin:thioredoxin reductase (FTR) that uses photosynthetically reduced ferredoxin (Fd) as a reductant. Recently, we demonstrated that FTR can reduce the x and y isoforms but not TRXz (Bohrer et al., 2012). Our data also revealed that TRXf and m can reduce efficiently TRXz. Here, we revealed that TRXz can also interfere with the redox regulation activity of TRXf and m on their specific targets. These data suggest a new important role for TRXz in modulating the redox regulation of metabolic enzymes in the chloroplast.

O6.2

A trade off between PSI and PSII photoprotection under high light by the NPQ-related protein PsbS

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Light harvesting complexes enhance light adsorption, but excess excitation can lead to singlet oxygen ($^1O_2$) production and photoinhibition. In higher plants, PsbS is a thylakoid membrane protein that dissipates excess light energy via its participation in non-photochemical quenching. Therefore, PsbS may protect against $^1O_2$-mediated photoinhibition at excess light intensities. This hypothesis was tested in PsbS deficient *Arabidopsis* (*npq4*) and in a mutant over-expressing PsbS (*oePsbS*). Chloroplasts from *npq4* generated more $^1O_2$, as measured by spin-trapping EPR, than those from *oePsbS*. Moreover, enhanced $^1O_2$ production by *npq4* accompanied a greater extent of PSII photoinhibition. In contrast, *oePsbS* was damaged by high light at the level of PSI. In *oePsbS*, the plastoquinone pool was more oxidised and the amount of photo-oxidisable P700 level was higher. Taken together, this indicates that the level of PsbS also has a novel regulatory role in cyclic electron flow. Overall, the PSII of *oePsbS* plants were better protected from $^1O_2$, whereas a lack of cyclic electron flow rendered them susceptible to damage at PSI. Therefore, cyclic electron flow is concluded to be essential for protecting PSI from high light stress.

O6.3

Fluorescence dynamics in *Arabidopsis thaliana* studied by time-correlated single photon counting

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Energy absorbed by plants is divided into photochemistry, heat, and fluorescence. Any changes in the distribution ratio induced by changing conditions influence the fluorescence decay (FD) of the PS II fluorescence. Here, we study the effect of excess light treatment upon the FDs of *Arabidopsis* and recessive null mutant *npq4-1* by time-correlated single photon counting (TCSPC) technique. This technique uses picosecond lasers and fast avalanche photodiode coupled to a TCSPC card. The experiments are carried out in a confocal microscope geometry, and FDs are measured from PS II *in vivo* from single chloroplasts. Analysis of FDs from the PS II of *Arabidopsis* and its mutant allows to determine dominant channels of energy dissipation. We find that irrespective of the genotype or treatment the FD of PS II can be described by a combination of three decay times with varied amplitude. These decay times can be attributed to processes responsible for excess energy dissipation. This work was supported by the Welcome/2008/1 and Welcome/2008/2 Programs awarded by the Foundation for Polish Science.

O6.4

NADPH-dependent alkenal/one oxidoreductase (AOR) supported the growth and the acclimation to the high light in *Arabidopsis thaliana*

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We characterized *Arabidopsis thaliana* RNAi plants which were deficient in NADPH-dependent alkenal/one oxidoreductase (AOR) to elucidate the relationship between the detoxification of reactive carbonyls (RCs) and sugar metabolism, especially photosynthesis. Compared to wildtype plants (WT), the growth of RNAi plants was retarded and the photosynthetic capacity was lowered under low light condition. Enzymatic activities of acrolein, methylglyoxal (MG) and Glyoxal (GLY) reduction were decreased in RNAi plants compared to the wild type. Under high light, the accumulation of acrolein was stimulated in both the wild-type and RNAi plants, and the extent to which its stimulation was larger in RNAi plants. The accumulation of advanced glycation endoproducts (AGEs) was enhanced under high light conditions, especially in RNAi plants. Under high light, the rate of photosynthesis did not increase as much in RNAi plants as in the wild type. These results indicated that AOR contributed to the acclimation to the high-light condition, where CO_2 fixation is enhanced and the production rate of sugar-derived RCs is increased.