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Characterization of the ferredoxin/thioredoxin system and its targets in *Physcomitrella patens*

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Redox regulation is an ancient mechanism present in biological organisms and is involved in diverse cellular pathways. In particular in photosynthetic organisms it is responsible for fast adaption mechanisms to a constantly changing environment. In chloroplasts the ferredoxin/thioredoxin system represents the main redox regulatory cascade which links the activity of several plastid enzymes to the energy source, light. A central role in this system is played by the heterodimeric ferredoxin-thioredoxin reductase (FTR), which gains electrons from the photo-reduced ferredoxin and transfers those further on via reduction to plastidal thioredoxins. Those proteins in turn reduce their target enzymes and require therefore the availability of redox sensitive cysteine pairs whose reduction results in an inactivation/activation switch of the targets.

So far no viable plants could be obtained in complete absence of this redox regulation system. In this thesis single sections of the system were explored in the model plant *Physcomitrella patens*. Through gene manipulation the influence of the FTR enzyme on plant growth and development was analysed. In order to impact on the function of the reductase, firstly single nucleotide exchange of the catalytic cysteines was performed and later on the gene was completely deleted. Surprisingly, no significant effect could be observed on the viability and development of mutant lines compared to WT plants. Furthermore we found that *P. patens* possesses in contrast to seed plants additional thioredoxins which are functional for reduction of FTR target enzymes but are most likely not supplied with electrons by this reductase. Thus a possible rescue scenario independent of FTR could be assumed for *P. patens* and also by other redox regulation systems present in chloroplasts.

Two of the FTR target enzymes, fructose-1,6-bisphosphatase and sedoheptulose-1,7-bisphosphatase, are functional in the regeneration phase of the Calvin-Benson cycle and share similar characteristics in regulation and catalysis. By combining biochemical and structural approaches, a functional comparison of both phosphatases was conducted using cDNAs from *P. patens*. A stricter TRX-dependent regulation and catalytic cleavage ability for both substrates, FBP and SBP, could be observed for *Pp*SBPase, whereas *Pp*FBPase is only capable of cleaving FBP. By obtaining the oxidized X-ray structure of both enzymes these observations can be associated with the distinct positions of regulatory sites and the various sizes of the substrate binding pocket. In addition, the phylogenetic analysis revealed an independent prokaryotic origin for both phosphatases.

Furthermore we summarized in three review articles the amenability of *P. patens* as model plant for forest research, the general principles of redox regulation in respect of evolution and functional mechanisms in plants, and the current state of the art in forest redox regulation using poplar as exemplary model.