Characterization of auxiliary membrane proteins in the chloroplast of Arabidopsis thaliana

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Akademisk avhandling


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Abstract
In nature, sessile plants have to adapt to their environment and to the never ending changes they are exposed to. They do so mainly by proteomic and metabolomic changes. In all cells, there are complex networks of auxiliary proteins that are responsible for quality control of all the cell's proteins. The auxiliary proteins are divided into chaperones and proteases, and these are further separated into different groups. Chaperones help other proteins in terms of stability and folding. In order for a protein to achieve its function, the three-dimensional structure has to be precise. A protease is a helper protein that is able to break peptide bonds in a process termed proteolysis. Chaperones and proteases can work independently, but sometimes the chaperone unfolds the substrate of the protease to ensure full degradation of the protein. In some cases, the chaperone and the protease functions are combined in one protein.

All proteins studied within this thesis are localized in the chloroplast, the organelle that originated from cyanobacteria, in which plants and algae convert the energy from sunlight into carbohydrates in the process called photosynthesis. Molecular oxygen is released as a by-product, and carbon dioxide is consumed. Photosystem II (PSII), one of the major protein complexes involved in photosynthesis, consists of more than 30 protein subunits, where around half of them are termed low molecular weight (LMW) proteins with a molecular size less than 10 kDa. In this thesis, data identifying one PSII LMW protein, PsbY, as a chaperone for the PSII subcomplex Cytochrome $b_{559}$ are presented. In the absence of PsbY, Arabidopsis plants were more sensitive to photoinhibition, and the protective circular electron transport around PSII is completely blocked.

Data on members of the Filamentation temperature sensitive protein H (FtsH) protease family are also discussed, with a focus on FtsH11 and FtsHi1-i5. Members of the FtsH protease family carry a protease domain and a chaperone domain. Our data show that FtsH11 has an influence on the structure and function of chloroplasts of Arabidopsis plants grown under continuous light along with protein import into the same. FtsHi1-5 are five members with mutations within the proteolytic motif, most probably rendering them proteolytically inactive, hence they are referred to as "inactive FtsH proteases". Knock-out plants of the inactive members are embryo lethal, and knock-down plants grow slower than wild type, probably because of an affected level of plastid proteins at the translational level.

Keywords
Arabidopsis thaliana, chaperone, chloroplast, Cytochrome $b_{559}$, FtsH, membrane proteins, photosynthesis, Photosystem II, protease, PsbY.