Homeostatic control of plastid transcription and consequences for development and stress responses

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Project Description

Chloroplasts and other plastid types, the biosynthetic centers of plant cells, are hybrid organelles, i.e. their machineries for photosynthesis and gene expression contain mixed ensembles of plastid- vs. nuclear-coded proteins. This is evident e.g. for the multi-subunit organellar RNA polymerase - a key enzyme for the transcription of most plastid genes: Its catalytic core is made up of (plastid-coded) subunits very similar to those of bacteria, and these core proteins act in concert with multiple regulatory sigma factors. The latter, however, are nuclear-coded and have acquired eukaryotic features, including phosphorylation control by specialized protein kinase(s). Previous work has provided a general picture of plastid sigma factors in organellar gene transcription by defining functional determinants of individual members of this protein family. We now proceed by addressing questions of how the entire sigma factor network is balanced during normal development, or is disrupted and re-shaped following genetic manipulation and in stress-related situations. Molecular genetic strategies resulting in (conditional or permanent) imbalance of the network will be applied using Arabidopsis thaliana. Biochemical and physiological analyses will allow insights into the mechanisms underlying homeostatic vs. transitory states in plastid gene expression.

DFG Programme Individual Grants

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