ABSTRACT

Endosymbiotic gain and transfer of plastids is a widespread evolutionary phenomenon and a major driving force of eukaryotic evolution. The integration of a new organelle is accompanied by changes in its structure, gene content, molecular mechanisms for biogenesis and transport, and re-wiring of the host and organelle metabolic pathways. To understand the course and underlying mechanisms of plastid evolution, it is important to study these processes in variety of secondary algae and notice their differences and similarities.

Euglenophytes gained their plastids from green eukaryotic algae after a long history of heterotrophic lifestyle. In my thesis, I participated in analyses of newly generated sequence datasets: transcriptomes of *Euglena gracilis* and *Euglena longa* and mass spectrometry-determined proteome of *E. gracilis* plastid with especial regard to the potential novelties associated with plastid gain and incorporation. In the resulting publications we particularly focus on plastid protein import machinery and targeting signals and report extremely reduced TIC and completely absent TOC in euglenophyte plastid. Using the proteomic dataset, we predict potential novel plastid protein translocases recruited from ER/Golgi and re-analyze plastid signal domains, characterizing previously overlooked features. Protein inventory of *E. gracilis* plastid suggests complex, in some cases redundant metabolic capacity. Chlorophyll recycling is one of the sources of phytol for reactions not connected to MEP/DOXP pathway. Plastid contribution to amino acid metabolism is very low, if any. We screen the proteome for proteins of other than green algal phylogenetic affiliation and report substantial contribution from "chromists" as well as several cases of LGT from bacteria, including an acquisition of additional SUF pathway.

In summary, the work presented in this thesis provides a solid contribution to plastid proteomics, resource for both basic and applied *Euglena* research and potential foundation for various follow-up studies.