Investigating the protein composition of plastid envelope membranes and plastid protein targeting and import in *Euglena gracilis*.

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Euglena gracilis is a facultatively phototrophic flagellate belonging to Euglenozoa within the Excavata paraphylum. It used to be a very popular model organism in the past and it is gaining relevance again today as its capacity to synthesize various chemical compounds usable in biofuel industry or pharmacology is being investigated.

Phototrophic euglenids are endowed with secondary plastids derived from those of a *Pyramimonas*-related endosymbiont. These organelles are enveloped by three membranes, as opposed to most other secondary plastids which are generally equipped with four membranes: two of these inherited from the cyanobacteria, one from endosymbiotic primary alga, and one from the endomembraneous system of the final host. Which one of these membranes is the one missing in euglenid plastid was not confirmed yet, neither was the protein composition or transport system of the remaining three investigated very thoroughly.

Several potential translocation-associated proteins have been identified in the transcriptomic and proteomic sequence data. In this study, thorough homology detection and other *in silico* analyses as well as gene silencing via RNA interference were used to obtain more hints regarding the functions of these candidates and their roles in plastid protein import. A set of protein sequences with highly credible plastidal localization determined by mass spectrometry was used for the analysis of plastid-targeting signals which might be both sequence- and structure-coded, and for the optimization of the methods for their prediction.

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