

Abstract

Algae form a diverse group of simple photosynthetic eukaryotes of polyphyletic origin. Algae with a primary plastid (Archaeplastida) acquired it by ingesting cyanobacterium, a prokaryote; algae with a complex plastid acquired their plastid by ingesting another eukaryote with a primary or already complex plastid. Algae with a complex plastid are chimeras containing genes derived from the host genome, as well as genes derived from the genome of the endosymbiont, and also genetic material derived from genomes of their previous stable or transient endosymbionts. One of the groups with plastid derived from green algae are euglenophytes. This thesis deals with the genomes of three organisms that represent individual actors in the endosymbiotic process in euglenophytes. These are a heterotrophic host from the class Euglenida, a phototrophic endosymbiont from the class of green algae Prasinophyceae and the resulting phototrophic euglenid from the group Euglenophyceae. Knowledge of their genomes should illuminate the course of endosymbiotic gene transfer (EGT) in the formation of algae with a complex plastid.

We annotated the plastid genome of a phototrophic euglenid *Eutreptiella gymnastica* and published it as the third plastome of Euglenophytes after the iconic and economically important *Euglena gracilis* and its secondarily non-photosynthetic relative *E. longa*. We have shown that the content of genes in the plastid genomes of Euglenophytes is almost the same and that the reduction of plastid gene content by about 20 % has already occurred in the common ancestor of all euglenophytes. We further found that the plastome of the basal euglenophyte *Etl. gymnastica* has only few introns and therefore the extremely high number of introns in *E. gracilis* plastome is not a common feature of the whole group but a species-specific feature. Last but not least, we confirmed that the green alga *Pyramimonas parkeae* is related to the ancestor of euglenophytes' endosymbiont. The plastid genome of this alga was already known, and we complemented it by the mitochondrial genome with relatively high gene content. None of these genes is probably present in current euglenophytes' genomes, and the entire mitochondrial gene pool of the endosymbiont has been lost during endosymbiosis. The last organism examined in this study is the osmotrophic euglenid *Rhabdomonas costata* whose partial nuclear genome and almost complete transcriptome were compared with the currently available genome, transcriptome and mitochondrial proteome of *E. gracilis*. We found unconventional introns typical for euglenids in *R. costata* nuclear genome. Its transcriptome contains a very low portion of genes related to the genes of photosynthetic organisms and lacks some genes obtained by *E. gracilis* via EGT which disproves the hypothesis of early plastid acquisition in Euglenozoa.

These individual findings undoubtedly contributed to the understanding of the evolution of Euglenida and the collected data will be used in further studies.