Transcriptomics and Proteomics of a Secondary Green Alga

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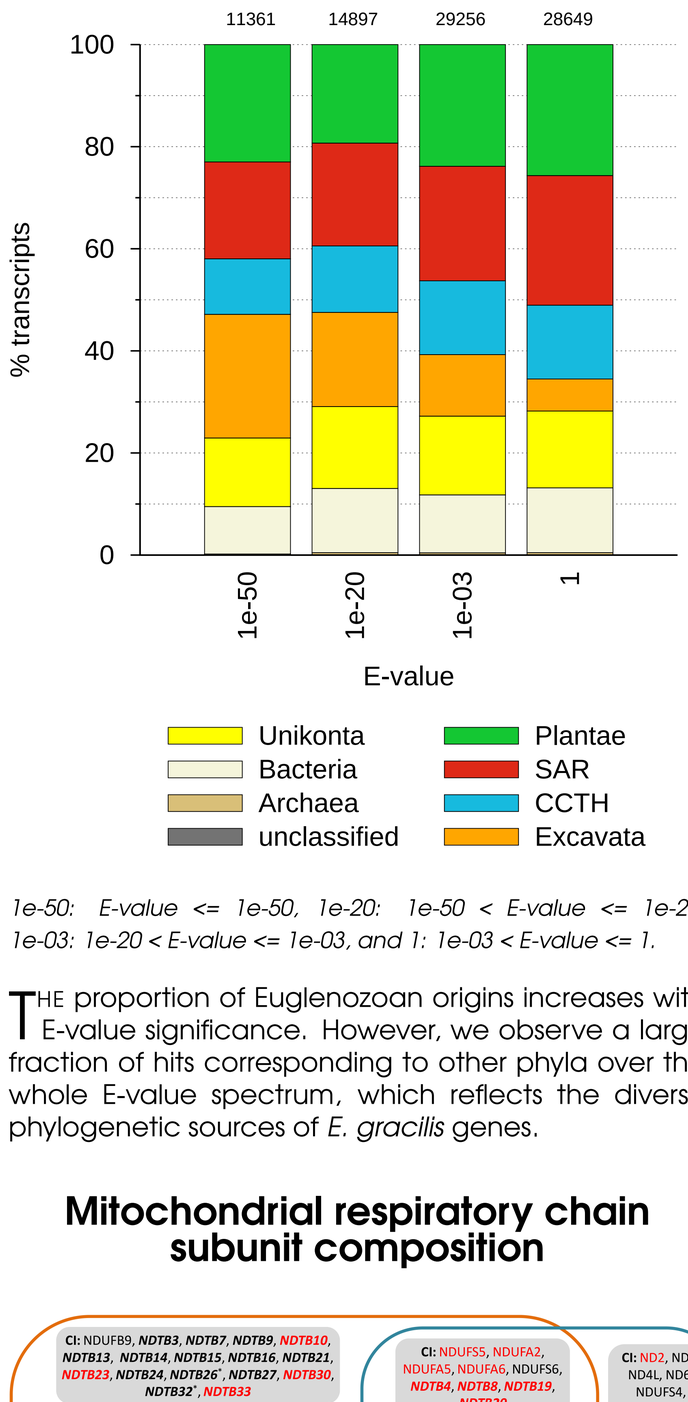
Abstract

Euglena gracilis is a secondary green alga related to Trypanosomatidae. It derives from a secondary endosymbiosis between a phagotrophic ancestor and a prasinophycean green alga. Our general objective is to study the interactions established between the chloroplast and the mitochondrion following the endosymbiotic event and to determine the phylogenetic origins of the genes encoding the proteins involved in these interactions. We sequenced the complete transcriptome of E. gracilis, assembled the transcripts and predicted the corresponding proteins. We analysed the mitochrondrial respiratory chain composition of E. gracilis and assessed its similitude with the chain described in Trypanosomatidae. Finally, we performed a high-throughput analysis of the mitochondrial proteome of E. gracilis.

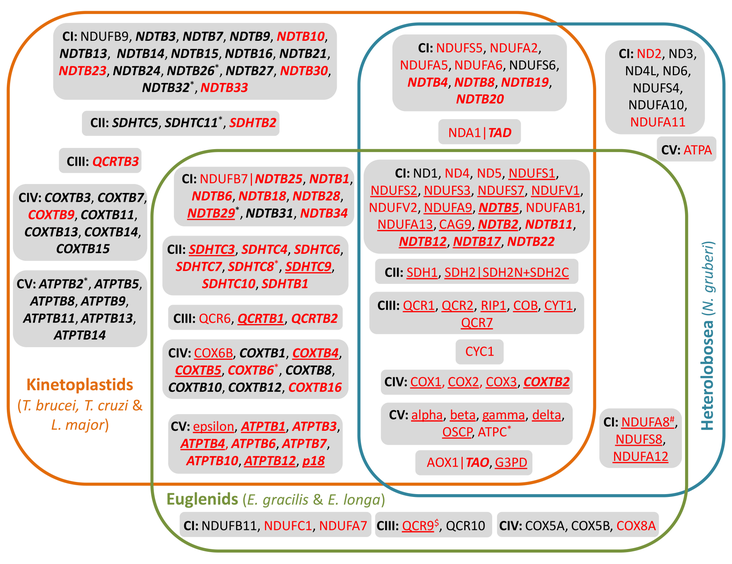
Taxonomic affiliation of *Euglena gracilis* transcripts



1e-50: E-value <= 1e-50, 1e-20: 1e-50 < E-value <= 1e-20, 1e-03: 1e-20 < E-value <= 1e-03, and 1: 1e-03 < E-value <= 1.

The proportion of Euglenozoan origins increases with E-value significance. However, we observe a large fraction of hits corresponding to other phyla over the whole E-value spectrum, which reflects the diverse phylogenetic sources of *E. gracilis* genes.

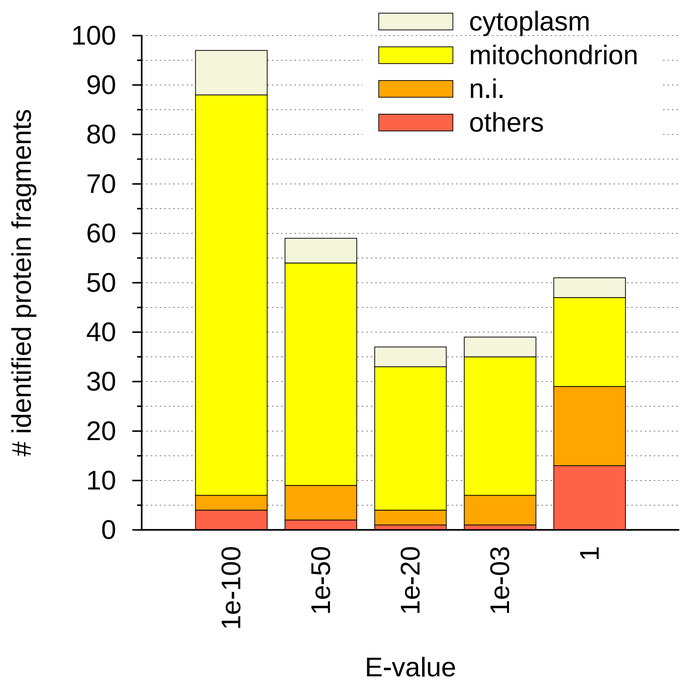
Mitochondrial respiratory chain subunit composition



*#,$: Not identified in bioinformatic analyses. Underlined: Found in proteomic analyses. Bold and italics: Specific to Euglenozoa. *: Found in diplonemids (D. papillatum). $: Not homologous to the canonical QCR9. Red: Found in E. gracilis complete transcriptome.*

We demonstrate that the secondary green alga shares many additional subunits with Trypanosomatidae. In addition, our transcriptome allows us to identify 30% more proteins than public ESTs (missing proteins were identified using genomic reads).

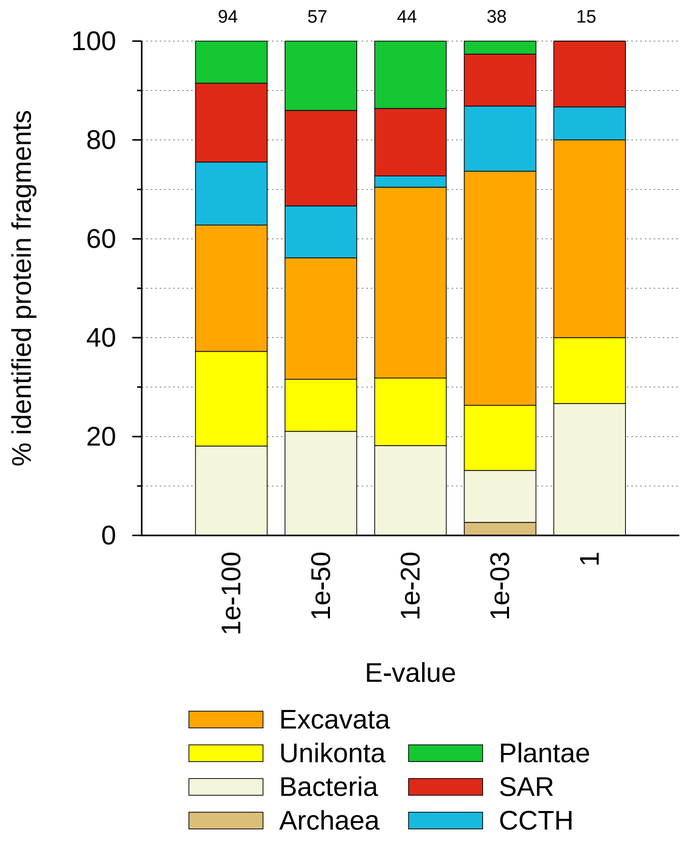
Subcellular localization of protein fragments



1e-100: E-value <= 1e-100, 1e-50: 1e-100 <= E-value <= 1e-50, 1e-20: 1e-50 < E-value <= 1e-20, 1e-03: 1e-20 < E-value <= 1e-03, and 1: 1e-03 < E-value <= 1.

The subcellular localization of the protein fragments is mainly the mitochondrion. It indicates that our mitochondrial extracts are relatively pure.

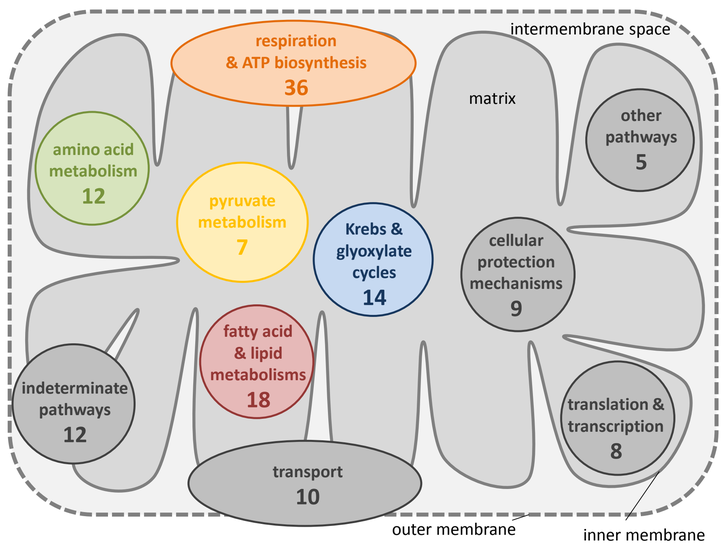
Taxonomic affiliation of protein fragments



1e-100: E-value <= 1e-100, 1e-50: 1e-100 <= E-value <= 1e-50, 1e-20: 1e-50 < E-value <= 1e-20, 1e-03: 1e-20 < E-value <= 1e-03, and 1: 1e-03 < E-value <= 1.

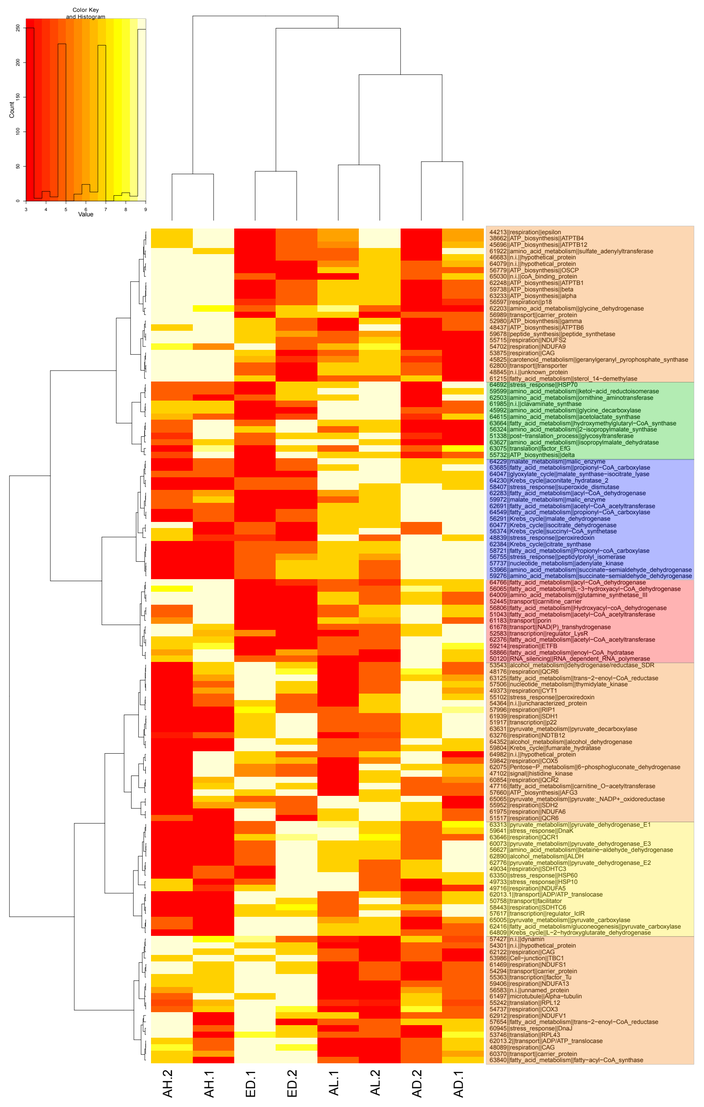
The results are inconclusive, probably due to the reduced set of proteins examined (248 mitochondrial proteins *vs.* 84,163 transcripts). However, the diverse origins of *E. gracilis* mitochondrial proteins is obvious.

Coverage of the mitochondrial metabolic pathways



We identify a total of 131 mitochondrial proteins involved in about 10 different metabolic pathways, including energy producing pathways.

Relative abundance of mitochondrial proteins across different conditions



AD: Acetate 60mM Dark, AL: Acetate 60mM Low Light, AH: Acetate 60mM High Light, and ED: Ethanol 1% Dark.

Some patterns can be observed. Components of Krebs and glyoxylate cycles are more abundant in AH and ED conditions, components of fatty acid/lipid metabolisms in ED and AL conditions, and components of the amino acid metabolism in ED, AD and AH conditions. Finally, components of the respiration/ATP synthesis are more abundant in AD condition, while one half (ATP synthesis) is more abundant in ED condition and the other half (respiration) in AL condition.

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