Energetical metabolismus of heterotrophic euglenoid *Rhabdomonas costata*

P. Soukal[1], Š. Hrdá[1], A. Karnkowska[2], R. Milanowski[3], J. Szabová[1], M. Hroudová[4], H. Strnad[4], Č. Vlček[4], I. Čepička[5,] and V. Hampl[1]

1. Department of Parasitology, Charles University, Faculty of Science, Prague, Czech Republic.

2. Department of Plant Systematics & Geography, University of Warsaw, Faculty of Biology, Warsaw, Poland.

3. Department of Molecular Phylogenetics and Evolution, University of Warsaw, Faculty of Biology, Warsaw, Poland.

4. Institute of Molecular Genetics, Academy of Sciences of the Czech Republic, Prague, Czech Republic.

5. Department of Zoology, Charles University, Faculty of Science, Prague, Czech Republic.

Euglenoids represent a group of protists with diverse modes of feeding including phagotrophy, osmotrophy, phototrophy and mixotrophy. We have prepared genomic and transcriptomic drafts of primary osmotroph *Rhabdomonas costata*. The comparison of transcriptomic and genomic data allowed us to estimate features of its introns. In total we have detected 10,081 introns with canonical boundaries GT/C-AG as well as 4 noncanonical introns with secondary structure similar to those in Euglena gracilis nuclear DNA. The set of 39,585 putative *Rhabdomonas* proteins was predicted from the decontaminated transcriptome. Only 26,052 predicted proteins have any homologue in NCBI. Annotation of the mitochondrial backbone metabolism provides the first data on *Rhabdomonas* mitochondrion, which is consistent with our knowledge on the mitochondrion of *Euglena gracilis*. Almost all enzymes of classical Krebs cycle and respiration chain were found. Of the three alternative enzymes α-ketoglutarate decarboxylase, succinate semialdehyde dehydrogenase (SSDH) and alternative oxidase known from *E. gracilis* only SSDH is present. Although *R. costata* is unable to grow under strictly anaerobic conditions, almost all enzymes of wax ester fermentation known from *E. gracilis* are present. The presence of rhodoquinone (RQ) is inferred from the presence of rhodoquinone biosynthesis methyltransferase.