

Exception within exceptions – unusual organization of rRNA genes in *Euglena longa*

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Eukaryotic ribosomes are composed of a few dozen proteins and usually four RNA molecules. Genes coding three of them, 18S (SSU), 5.8S and 28S rRNA (LSU) are clustered in a single operon (rDNA) and transcribed together. In majority of known eukaryotes, rDNA occurs in several hundred copies, usually in tandem repeats. Several exceptions from standard are known, one of them is observed in euglenids.

The most known representatives of Euglenida (Euglenozoa, Excavata) are green euglenids and among them the euglenid model species – *Euglena gracilis*. It was revealed that all detectable copies of *E. gracilis* rDNA are located on thousands of extrachromosomal circular DNA molecules, each of them containing single rDNA copy. We analysed genomic sequences of *E. gracilis* and found continuous rDNA operon, in accordance with previous results. Similar picture was found in other euglenids, however organization of rDNA seems to be different in secondary osmotroph *Euglena longa*, sister species of *E. gracilis*. During analysis of its genome, we found two separate sequences containing the SSU and LSU rDNA respectively. The reason for this is the presence of a several hundred nucleotides long repeated sequence in both the internal transcribed spacer 1 (ITS-1) and the intergenic spacer (IGS). Based on this information, we predicted two possible structures of rDNA: the typical one with the SSU and LSU rDNA organised together, and the second with the SSU and the LSU rDNA separately. Data from long reads sequencing of *E. longa* genome and molecular analyses indicate that both structures are present in the cells of *E. longa* – a combination not known before in eukaryotes.