

## **CHARACTERISTICS OF NONCONVENTIONAL INTRONS IN NUCLEAR GENES OF EUGLENIDS**

Nuclear genomes contain introns excised by the ribonucleoprotein complex – spliceosome. The vast majority of spliceosomal introns are characterized by the presence of conserved GT/C-AG ends. Conventional spliceosomal introns are also present in nuclear genes of euglenids (Euglenida, Euglenozoa, Excavata); however, they are not the only type of introns. Nuclear genes of euglenids contain also another type of introns called nonconventional ones. They have non-canonical borders and form a stable RNA secondary structure bringing together both ends. The mechanism of nonconventional introns removal is still unknown. The objective of the project is verification of preliminary research, which indicate that nonconventional introns are removed as linear or circular particles. Preliminary studies show also that nonconventional introns are removed later than conventional ones, which is contrary to the literature data.

In order to verify the preliminary results, which indicate that the nonconventional introns are removed as linear or circular particles, the series of Northern analyses of excised introns is planned. To verify the data suggesting that nonconventional introns are removed later than conventional ones the PCR analysis of the splicing intermediate products will be performed. To determine the cellular location of nonconventional splicing process, the analysis of intronic RNA in different cellular compartments and FISH analysis will be carried out.

Nonconventional introns of euglenids are the only type of introns for which mechanism of removal is not understood yet. Furthermore, as in the case of no other introns they are characteristic for a relatively small, well-defined group of eukaryotes. Accurate characterization of this type of introns takes us closer to answer such questions as: (1) what is the mechanism of their excision; (2) what was the point of their arising; (3) what is the meaning of their maintenance in the genomes. Planned research significantly expands our knowledge about mechanisms responsible for mRNA maturation, which are often distinct in different groups of organisms; these mechanisms remain very often unexplored due to the interest of researchers focused mostly on the model species which are extensively studied. The results would help us also to understand evolution and hidden functions of other types of introns so commonly found in eukaryotic genomes.