

DESCRIPTION FOR THE GENERAL PUBLIC

In every natural, though somewhat humid environment, under a rotting autumn leaf, in a puddle, a lake, live invisible to the human eye, almost transparent unicellular, eukaryotic organisms called ciliates. It may seem that these are primitive and unimportant organisms, but they have a recipe for immortality. The model organism *Paramecium tetraurelia*, like other Eukaryotes', has two types of nuclei within the same cytoplasm, somatic macronucleus and generative micronucleus. They represent physically separated lines: somatic and germline. Each time during the sexual cycle, the macronucleus is degraded, and a new is developed from micronucleus. Due to the fact that these nuclei do not contain identical genetic information, the process of creating a new somatic nucleus is preceded by a programmed reconstruction of micronuclear DNA. The rearrangement pattern is transferred from the old macronucleus to the new one with the participation of epigenetic factors. At the top of the avalanche of epigenetic processes, that trigger the rearrangement of the *Paramecium tetraurelia* micronuclear genome, are short and long non-coding RNAs. Short RNAs are the image of the entire genome contained in the micronucleus and have the ability to move between the nuclei in the *P. tetraurelia* cell. On the principle of scanning and selection by pairing with longer transcripts, only short RNAs matching exclusively micronuclear sequences reach the new macronucleus and mark the DNA sequences for elimination.

The nature of epigenetic information is one of the most intensively studied areas of modern science, because it ensures the change of the phenotype without changing the DNA sequence, and also enables the phenotype to be preserved in subsequent generations. It also allows, at the level of expression, to react dynamically to changing environmental conditions. One of the key epigenetic effectors in all eukaryotic organisms is short non-coding RNA.

The aim of the project is to identify the factors responsible for the transport of short non-coding RNAs between the germline (micronucleus) and somatic (macronucleus) line to build a simplified model of the processes occurring in higher eukaryotes. It is planned to understand which proteins are responsible for transport of key ribonucleoprotein complex. It will also be shown that the transport of these short RNAs is not based on genomic comparison, but on the communication of two independent transcription machineries.