Study of the mechanisms involved in synthesis of non-coding transcripts

*Paramecium tetraurelia* is a unicellular model organism that harbors two types of nuclei within the same cell. Somatic macronucleus that is responsible for the gene expression, and germline micronuclei that are used for sexual exchange of genetic material.

At each sexual cycle, maternal macronucleus degenerates and new nucleus is formed from the micronucleus. During this process micronuclear DNA is extensively rearranged and some sequences are eliminated. It was previously showed, that rearrangement patterns are maternally inherited between the old and the new macronucleus and this process is not only DNA-dependent but involves other, DNA-independent factors. It is an example of epigenetic inheritance. Epigenetic processes regulate several important organism functions – from inheritance and development to regulation of gene expression.

Several classes of non-protein-coding RNAs (ncRNAs) is involved in development of the new macronucleus in *Paramecium*. Non-coding RNAs are intensively studied recently, as they play important, not totally established role in cells and organisms. Thanks to high diversity of ncRNAs in Paramecium, this organism is a perfect model for studies of ncRNAs production and function.

The aim of our project is to verify if selected factors, that are known to be involved in RNA synthesis (transcription) that lead to protein production, play as well an important role in ncRNA synthesis. We are going to provide description of these ncRNAs – including their genomic origin and their possible interactions with other RNAs and proteins. The project may have a greater impact as it was shown recently that mutation in the transcription factors and cofactors can cause many different diseases and syndromes, including cancer, neurological disorders, obesity and diabetes.We believe that our project will allow us to unravel the mechanisms involved in non-coding transcription not only in the ciliate *P. tetraurelia*, but also in other eukaryotes.