MODIFICATION AND ACTION OF NON-CODING RNA

The goal of the project|

The aim of our project is to verify if selected factors, that are known to be involved in RNA modification of transcripts playing a role in protein production, differ from the ones that are important during ncRNA synthesis.

Description of the research, reasons why this research topic was taken

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.

During our research, we will analyze the function of selected proteins involved in RNA modification. We will learn about their role in cell growth and sexual processes. We will examine their intracellular localization, examine non-coding RNA arising in sexual processes and how the genome rearrangements occur while their expression is silenced.

The most important expected results

We will discover a role of RNA modifiers in genome rearrangements in *Paramecium*, we will find their protein regulatory partners as well as RNA molecules that are produced due to their activity. The project may have a greater impact as it was shown recently that mutation in the these 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.