

Elongation factors in synthesis of developmentally controlled 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 transcript elongation during RNA synthesis that lead to protein production, diverge from the ones that are important during ncRNA synthesis. We will check if the composition of the transcription machinery differs between macro- and micronucleus. We will analyze as well the epigenetic landscape that allow for expression of the somatic and germline genome.

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 (somatic function), and germline micronuclei that are used for sexual exchange of genetic material (generative function).

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. 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*. Thanks to high diversity of these ncRNAs in *Paramecium*, this organism is a convenient model for studies of ncRNAs production and function. The *Paramecium* transcription machinery seems to be perfect to study differential RNA polymerase activity: as we have predominantly mRNA synthesis necessary for protein production in vegetatively growing cells, while during sexual processes genome wide transcription of the germline micronucleus takes place.

The most important expected results

We will discover a role of elongation factors and RNA polymerase itself in generation of non-coding RNAs, we will find their protein regulatory. We will examine the differences between the somatic and generative genomes at the epigenetic level. 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.