DESCRIPTION FOR THE GENERAL PUBLIC

A single-celled model organism belonging to the ciliate phylum, *Paramecium tetraurelia* is a very large eukaryotic cell 120 micrometres long, generously covered with vibrating cilia. Its simple external structure covers complexity of its life processes, which is why it has served for many years as a model for genetic studies of the processes exerting in multicellular eukaryotes. *Paramecium* have the fascinating property of having separate germ and somatic lineages within the same cytoplasm, which is reflected in having two different nuclei. The generative nucleus (micronucleus, **MIC**) is responsible for transmitting genetic information through sexual processes, while the second somatic nucleus (macronucleus, **MAC**) ensures the expression of this information. Each time during the sexual process, the macronucleus is degraded and a new one is formed from the micronucleus by programmed rearrangements of the entire genome with significant involvement of epigenetic factors, that is, those that are not directly derived from the DNA sequence. Both *Paramecium* nuclei present in the same cytoplasm do not share the same genetic information. The micronucleus contains active transposons, mobile genetic elements that can change position in the genome and multiply in an uncontrolled manner, leading to, among other things, cell death. *Paramecium* copes with this potential threat by transferring the rearrangement pattern of the somatic nucleus from one generation to the next using micro-nuclear transposon sequences as a specific anti-transposon vaccine. During the sexual process, the entire genetic information of the MIC is transcribed into RNA and cut into a 25-nucleotide fragments (scnRNA), loaded onto a Piwi-type protein and travel to the somatic MAC. Based on comparison of complementary sequences, those that should not be there are selected and moved to the new MAC marking transposons for definitive elimination by physical excision.

Our recent findings described the role of the Gtsf1 protein in the genome rearrangement process of *Paramecium* as a factor directly involved in the selection and degradation of scnRNAs and Piwi in the somatic nucleus and indirectly by determining the boundaries of rearrangement in the new MAC genome. The absence of Gtsf1 during the sexual process results in transposon activation and cell death. Gtsf1 is present in analogous processes in all animals and is thought to be an important factor fulfilling the control of transposon element silencing and fertility.

The research proposed in the project aims to investigate the selection phenomenon and the associated degradation of scnRNA and Piwi protein in depth. We will study the interactions between different RNA molecules, search for the enzyme directly responsible for RNA degradation and study the properties of the Gtsf1 and Piwi proteins. We will also look at the modifications of the above-mentioned proteins and check whether non-coding RNA molecules are also modified.

Discoveries in this field could inspire many biological fields concerning the evolution of transposon sequences, the cellular control of their expression as well as epigenetics, mechanisms leading to the establishment of silent chromatin regions and reproductive biology.