DESCRIPTION FOR THE GENERAL PUBLIC (IN ENGLISH):

All eukaryotic RNA Polymerase II mature RNAs are produced from primary transcripts as a result of extensive processing, including addition of the cap structure at the 5' end, removal of introns and ligation of exons (splicing), and addition of a poly(A) tail at the 3'end during the cleavage and polyadenylation process. The excision of introns from primary transcripts is catalyzed by a highly dynamic and large ribonucleoprotein complex called the spliceosome, composed of U1, U2, U4, U6 and U5 snRNPs, as well as other spliceosomal proteins. Recently, it has been shown that in addition to its crucial role in splicing, U1 snRNP is also involved in the protection of newly synthesized precursory mRNAs form premature termination caused by cleavage and polyadenylation at so called cryptic polyadenylation site. In our laboratory, we have also discovered the influence of U1 snRNP on polyadenylation of miRNA primary transcript. Thus, both in mammals and plants, U1 snRNP seems to control polyadenylation, however, the mechanism of this phenomenon has not been described yet. We propose a model of the mechanism of U1 snRNP-mediated inhibition of premature cleavage and polyadenylation of RNA Polymerase II primary transcripts.

In our model, the direct interactions between U1 snRNP and proteins of CstF and PCFS complexes, which are both parts of the cleavage and polyadenylation machinery, are crucial for the regulation of polyadenylation site selection. The main aim of this project is to uncover and understand the molecular mechanism of this U1-medaited suppression of polyadenylation.

Our studies, although concern the model plant *Arabidopsis thaliana*, will also be helpful for researchers working on human and yeast cells, since we study for a very general mechanism of the crosstalk between the spliceosome and the polyadenylation machinery.