Description for the general public

Regulation of gene expression is a complicated process, based on the coordination of many different pathways, including epigenetic control of chromatin state, transcription, RNA processing (5' cap formation, splicing, polyadenylation), the export of mature transcripts to the cytoplasm, and translation into proteins. In recent years, the development of high-throughput sequencing techniques, and the increasing number of identified RNA modifications have added another layer to this regulatory landscape.

So far, more than 150 different types of RNA modifications have been found. Most of the RNA modifications, such as N6-methyladenosine (m6A) and pseudouridine (Ψ), were originally identified in highly abundant structural RNA like rRNAs (ribosomal RNAs), tRNAs (transfer RNAs), and snRNAs (small nuclear RNAs). Current methods provide the opportunity to identify new types of modifications and to precisely localize them not only in highly expressed RNAs but also in mRNA and small RNA (18-30 nt) molecules. According to our data pseudouridine is present in small RNAs and their precursors, in plant and mammalian cells. Moreover, m6A is present in miRNA precursors. The presence of many other modifications in small RNAs has not been confirmed yet. It is not clear what is the role of particular modification in small RNAs

We hypothesize that small RNA modifications are important for their transport between cell compartments or even outside the cell. We speculate, that depending on the presence and/or type of modification miRNA may have different pathways of action.

We are going to use high-throughput sequencing methods to get a broad view of small RNA modification patterns as well as precise and sophisticated methods to identify factors involved in this process.

The results of these studies will significantly increase our current knowledge about the biogenesis and functioning of small RNAs in Arabidopsis but also in liverworts and monocots.