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 in plant and mammalian cells. However, it is not clear how and when this modification is deposited as well as what is the function of pseudouridine in small RNAs. We hypothesize that uridine to pseudouridine conversion may occur co-transcriptionally, at least for some small RNA precursors in plants, and this mark is important for small RNA transport, especially in germlines. We are going to use high-throughput sequencing methods to get a broad view of pseudouridylation pattern in Arabidopsis and 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 and the mechanism responsible for epigenetic inheritance in plants.