

Almost all cells in one living organism contain the same set of DNA information. However, the cells might look completely different and have many different functions e.g. in mammalian neuronal and hepatic cell, in plant meristematic and phloem cells. One of the reasons of this phenomenon is differential gene regulation. The set of genes expressed (activated) in two different cells might be completely diverse which will lead to unique properties (e.g. shape or function) for each of them. This demonstrates that precise and tight regulation of the gene expression is extremely important. In eukaryotic cells, this regulation, can be controlled at various stages, from chromatin accessibility, transcription, RNA processing to translation and protein activity. One of fundamental, sequence-specific gene expression regulatory elements are microRNAs. MicroRNA biogenesis is a multistep process and many proteins are involved in this pathway. One of them, HYL1 protein, binds double stranded RNAs and interacts with DCL1, the main RNase which releases mature microRNAs from their precursors. In cell HYL1 protein can exist in two isoforms – phosphorylated and unphosphorylated. Experiments suggest, that unphosphorylated HYL1 plays important role in microRNA biogenesis and phosphorylated serves as a reserve (inactive) pool of HYL.

In the previous studies we have identified a new unknown role of the HYL1. We also established that, apart from the involvement of microRNA precursors processing, HYL1 is also involved in early steps of microRNA biogenesis – in transcription. Nevertheless, more work is needed to propose a detailed mechanism of how HYL1 affects gene regulation via transcription. In this project we will perform experiments to discover and describe this mechanism. We hypothesize that phosphorylated HYL1 (currently assumed as inactive pool of HYL1) is mainly involved in transcriptional gene regulation. Moreover, our initial experiments suggest that mostly genes which are important for light dependent development of plants are affected. To test our hypothesis we will apply modern methods currently used in molecular biology research i.e. Next Generation Sequencing and fluorescence imaging using confocal microscopy. The results of the project will extend our knowledge about gene regulation processes, so our understanding of one of the fundamental and critical processes in eukaryotic cells.