Precise timing of flowering is essential for the reproductive success of a plant. To match flowering time with seasonal changes in weather patterns, plants are continuously monitoring day length and temperature. Information about variability of environmental conditions is transferred in such a way, that particular proteins are activating target genes which are subsequently launching production of another proteins which may activate or de-activate genes directly controlling production of a mobile "florigen" signal, a protein encoded by the *Flowering locus T* gene. Moreover, there is also additional level of regulation, related with modification of DNA or surrounding proteins (histones), which changes the accessibility of DNA for proteins and makes the gene inactive for some period of time. In this project we will study both regulatory levels acting on the *Flowering locus T* gene. *Flowering locus T* gene exists in a model plant *Arabidopsis thaliana* in a single copy, however, in legume plants several copies are present. These "additional" *Flowering locus T* copies appeared several million years ago during the evolution of legumes, when whole genetic information was duplicated. Such an event opened novel possibilities for de-regulation or gaining novel functions by these genes, because there was always some backup in the form of a gene duplicate performing basic required activity. This process provided a lot of flexibility for legumes, facilitating their adaptation to a large variety of environments.

In this project, a model of yellow lupin was selected for the study. Yellow lupin is a plant species that requires a period of low temperature during germination to induce flowering. This trait is known as high vernalization requirement. Moreover, yellow lupin prefers long days for flowering induction. Thus, under short days (8 hours of light) yellow lupin delays flowering induction by several weeks as compared to 16-hour day length. It is so-called photoperiod responsiveness. As both traits are very undesired for farmers, during domestication of lupins as crop plants, efforts were undertaken to select yellow lupin lines which are early flowering and independent to vernalization and photoperiod. Sequencing of genes from such plants revealed that they differ from late flowering lines by several mutations in *Flowering locus T* genes. In this project we will study both early and late flowering yellow lupin lines in various conditions of vernalization and photoperiod to determine molecular mechanisms involved in control of flowering initiation in response to these two factors. We will use new, high-throughput techniques to analyze differences in DNA sequences, induced genes and produced proteins. Moreover, large seed collection of yellow lupin, representing global diversity of the species, will be analyzed for flowering time and DNA sequence variability to find novel genes contributing to regulation of flowering induction. Populations developed from a cross between parents differing in flowering time and mutations in *Flowering locus T* genes will be used to find groups of genes which are co-regulated by the same proteins. Realization of the research scheduled in this project will constitute a significant step forward deciphering of complex molecular pathways conferring photoperiod and vernalization responsiveness in legume plants.