DESCRIPTION FOR THE GENERAL PUBLIC

The aim of our project is to investigate the role of low-molecular regulatory RNAs and their target genes in the development of generative organs in yellow lupine.

Yellow lupine (*Lupinus luteus* L.), like the other members of the family *Fabaceae* (*Fabaceae* L.), has enormous practical importance. The plant possesses a high content of storage proteins in seeds, which are used as a source of feed and thanks to symbiosis with bacteria that enable atmospheric nitrogen fixation and its use for the growth and development of plants, are a natural source of enriching the soil with nitrogen. The formation and development of flowers and seeds of lupines are crucial for the productivity of the plants. This stage of development is, however, associated with an undesirable phenomenon, which is the flowers' abscission.

Little is known about the molecular mechanisms of both the development of and the reasons for drop generative organs of lupine. In addition, there is a lack of research on the involvement of such important regulatory molecules which are undoubtedly short ~ 21 nt non-coding sRNA, namely miRNAs and siRNA, involved in post-transcriptional control of the activity of their target genes. sRNA are involved in gene silencing, which occurs by binding a complementary specific mRNA molecule encoding a protein of interest, and conducting cleavage within the associated sequence, or inhibiting translation ie protein synthesis.

Studies in various plant species indicate that a number of genes essential for the development of flowers and fruit are regulated by the miRNA. MicroRNAs are also involved (with siRNA) in the regulation of the auxin signal transduction pathway, a phytohormone crucial among others for the development of the generative organs, and for the functioning of the abscission layer.

A summary of literature data and the results of our preliminary research allow us to hypothesize that sRNAs may play a considerable role in the regulation of hormonal balance and response to environmental changes. In turn, these factors may affect the efficient process of generative growth of yellow lupine. To achieve the designated goal of the proposed project it is necessary to identify micro and siRNAs and their target genes specific to particular stages of development and maintained and rejected flowers of lupine. Then, the changes in their expression in developing generative organs and under the influence of various factors such as growing conditions and the application of phytohormones should be determined.

To conduct the project we propose the use of a range of the newest molecular biology techniques. We plan to make use of next-generation sequencing (NGS) libraries of low-molecular-weight RNAs and transcriptomes. The use of this technique allows for analyzing comprehensive changes in the accumulation of miRNAs and transcripts and, by running a comparison, describing specific miRNAs and their target genes for the process and species investigated.

The results of the studies proposed in this project will be important to broaden the understanding of the biology of lupine and deepen our understanding of the evolutionary preservation of relevant mechanisms regulating plant development. They will also enable us to answer the question of whether there is a correlation between the accumulation of miRNA, transcript of the target gene, and efficient development of generative organs. The innovation, not yet undertaken in research, is the planned identification of sRNAs associated with the process of abscission of the generative organs. Extremely important, from the point of view of present interest of the world's researchers in sRNA interactions with the action of plant hormones and stress responses, is the determination of the impact of exogenous factors on the transcriptional activity of the tested genes. Implementation of the proposed project will enable better understanding of the involvement of low-molecular regulatory RNAs in the regulation of plant growth.