

Stable yielding of native legumes and obtaining proteins with optimal nutritional amino acid composition is a considerable challenge in modern agriculture. This is particularly important given the significant dependence of the feed market on the import of soy meal and its use as a rich source of vegetable protein. The agrotechnical measures applied so far and the continual selection of new varieties, especially lupins and peas, seem to be insufficient to meet the challenges. That is why new solutions are sought, including those which make use of the tools of molecular biology, in order to study and learn the basics of selected physiological processes. Describing the mechanisms through initially conducted basic research in many cases results in the discovery of application possibilities used in agriculture. This can be seen, for instance, in the case of research on the role of phytohormones. Several years after the first reports on the mechanisms of operation of these compounds in plants and their participation in the control of numerous physiological processes, a considerable increase in the use of biostimulant preparations containing gibberellins, cytokinins and other types of hormones have been noticed.

Homeostasis between these compounds plays a very important role in almost every growth and development process in plants. It is no different in the case of accumulating storage proteins, one of the stages of seed development. The synthesis of the results of research conducted on various plant species showed that the cooperation of abscisic acid (ABA) and gibberellins (GA) and several regulatory proteins determines the activation of the expression of genes coding seed storage proteins (SSP). Among the regulatory proteins that control these transformations one can notice transcription factors LEC1/2 (LEAFY COTYLEDON1/2), ABI3 (ABSCISIC ACID-INSENSITIVE3) and FUS3 (FUSCA3) as well as peptides involved in the chromatin remodeling process PKL (PICKLE). In the end, there is a noticeable increase in the expression of genes encoding storage proteins. In lupins, conglutins serve such a function – as storage material. In previously conducted studies, four classes of such peptides were described in various species (α , β , γ and δ conglutin).

One of the lupine species that accumulates a large number of storage proteins and which could successfully become an alternative to soy is yellow lupine (*Lupinus luteus* L.). Its advantage is also the symbiosis with *Rhizobium* bacteria, so that it does not require additional nitrogen fertilization. However, the growing area of yellow lupine is so small that the production of lupine-based feed is unprofitable. There is little interest among the farmers in lupins, mainly attributed to the instability of yield, which results in low profitability of crops. The reason for this phenomenon is the abscission of flowers and pods at the early stages of their development or the production of seeds that are not fully developed, low in weight and protein content.

The results of our research carried out in the last two years have identified the coding sequences for *LIPKL*, *LIABI3*, and encoding β and δ conglutin in yellow lupine. In preliminary experiments, their transcriptional activity was established in developing seeds. These studies confirmed the existence of dependencies between these genes. It has been shown that drastic increase in conglutin expression occurs on the 25th day of seed development, when the transcription factors responsible for the seed filling process are unblocked.

In the proposed project, we suggest extending these preliminary studies in order to determine the expression of the genes in the later stages of the development of yellow lupine seeds. The obtained results will allow to determine a pattern of changes in the process of accumulation of storage proteins at the level of transcriptional activity of key genes. The identification and determination of the level of synthesis of proteins encoded by the tested genes in subsequent stages of development of yellow lupine seeds will serve as confirmation of the research. Combining these results will outline the mechanism on the transcriptional and translational level. Research aimed at establishing the endogenous levels of ABA and GA in growing seeds will complement the scheme. The comparison of the obtained results will give a full picture of the dependencies within the studied genes, proteins encoded by them and a selected pair of phytohormones, which occur during the process of seed filling. Our previous studies have shown how exogenously applied hormones can affect the modulation of the expression of numerous genes. With the use of sprayings, we want to examine whether ABA and GA applied in this form also affect the expression of the examined genes and whether they change the amount of proteins and their endogenous counterparts during the development of seeds in lupine.

The experiments planned as part of the project will enable the formulation of a model of multi-level regulation of mechanisms for accumulation of storage proteins in the yellow lupine seeds, Taper variety. The answer to the question how the amounts of phytohormones, proteins and gene expression change relative to one another, will enable the identification of critical points in the development of seeds. Through the use of exogenous phytohormones, their sensitivity to these factors can be demonstrated, and new ways of optimizing the process of storage proteins accumulation in the studied species may be found.