

Abstract

The development of seeds is a process of particular importance both for the plant itself – it assures the survival of the species, and for the human population – for nutritional and economic reasons. Controlling this process requires a strict coordination of many factors at different levels of cellular organization and complexity of regulatory mechanisms, the most important of which are gene transcriptional activity and hormonal homeostasis. From the nutritional point of view, the key to seed development is the ability of seeds to accumulate large amounts of proteins with different structures and properties. The world's food deficit is mainly related to shortages of protein and taking into consideration the environmental changes occurring on Earth, it is becoming necessary to search for a way to obtain large amounts of plant-derived protein, while maintaining the diversity of its origin. Yellow lupine is one of the native plant species that accumulate large amounts of this nutrient in their seeds. Using modern molecular biology techniques, including RNA-seq, chromatographic techniques and quantitative PCR analysis, key changes in developing yellow lupine seeds of the Taper variety were determined.

The aim of this study was to identify and determine the expression of genes involved in the process of accumulating storage proteins, to investigate the effect of the application of exogenous phytohormones and drought on the transcriptional activity of selected genes, the amount of accumulated proteins and the endogenous level of phytohormones at various stages of development of yellow lupine seeds of the Taper variety.

The conducted research showed the functioning of the following genes in the process of yellow lupine seed maturation: *LIPKL*, *LILEC2*, *LIAB13*, *LIFUS3*, *LIVAL1*. The identified genes show a high degree of similarity to their counterparts found in other legume species, including *L. angustifolius*, *L. albus*, *Glycine max*. As a result of their activity, there is an accumulation of reserve proteins (conglutins), which is also determined by a decrease in the amount of endogenous ABA as well as bioactive GA₁ and GA₃ in the following days of seed development, and an increase in the level of GA₄ and GA₇ accumulation. It can be suggested that these two classes of gibberellins play a different role in regulating the processes related to seed development. Exogenous application of GA₃ and ABA phytohormones in natural conditions does not bring the expected changes in the level of transcription or accumulation of storage proteins, except for the use of GA₃ and the level of conglutin expression in the oldest seeds. It was also shown that a prolonged period of drought causes a decrease in the expression level of all tested genes in comparison to

the control variants. In the context of changing climatic conditions and the increasing nutritional deficit, the fact that this decrease applies to reserve proteins is particularly concerning. The research carried out with the use of various research methodologies allowed, for the first time, to study the expression of genes, endogenous levels of phytohormones and the influence of drought and exogenous application of ABA and GA in developing seeds of yellow lupine. The study also shows many factors and variables which determine the correct course of seed maturation processes, and at the same time indicates the need to continue the research and cover many aspects discussed in this paper in more detail.

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