Plants produce many complex compounds called secondary metabolites, which are valuable to us due to their pharmacological properties. Some of these compounds have antibacterial, antifungal or anti-inflammatory activity. Some might have the potential to be used in anti-cancer therapy because they exhibit cytotoxic properties. Many secondary metabolites that have potential medical use belong to the group of sesquiterpene lactones and are produced by plants belonging to the *Asteraceae* family. Knowing how a plant produces secondary metabolites is very important to us. Scientific research conducted at the molecular level allows us to understand how a plant, step by step in a complex, multi-stage biosynthetic pathways, transforms some compounds into others - those that it needs at a given moment. What's more, we can also observe how the production of secondary metabolites is controlled, learning about the complex regulatory mechanisms that occur at various levels (for example, at the transcriptome or proteome level). So far, scientists have been able to characterize the biosynthetic pathways of such sesquiterpene lactones as artemisinin produced in *Artemisia annua* tissues, costunolide produced by *Saussurea lappa* or parthenolide produced by *Tanacetum parthenium*. However, there is no information on the molecular basis of the biosynthesis of sesquiterpene lactones in species belonging to the genus *Arnica*. Mountain arnica (*Arnica montana*) is a plant that is commonly used as a medicinal raw material. It is a source of valuable secondary metabolites which reduce swelling and inflammation. However, it is under strict species protection and is difficult to cultivate. Chamisso arnica (*Arnica chamissonis*), on the other hand, is not a protected species, is easier to grow and can be considered a substitute for mountain arnica.

The completed project focused on the final stages of biosynthesis of sesquiterpene lactones in Chamisso arnica. The changes in the expression of the *FDS*, *GAO* and *GAS* genes, which encode the enzymes involved in the biosynthesis of these secondary metabolites, were studied. The level of expression of the indicated genes was analyzed in the leaves and in the flower heads, as these are the main parts of the plant where the listed metabolites occur. Moreover, the research was carried out on flower heads at different stages of development to be able to observe what changes occur at the molecular level during the flowering. For example, expression levels of the *FDS* gene have been observed to be similar in arnica leaves and flowers at the yellow bud stage and early flowering stage. This means that the demand of the mentioned parts of the plant for the enzyme encoded by this gene is similar. When the flowers enter the full flowering phase, the level of *FDS* transcripts decreases (the enzyme encoded by this gene is no longer needed so much). The expression of the other two genes, *GAO* and *GAS*, is highest at the yellow bud stage. It has been shown that as the flowers develop, the expression of both genes is significantly downregulated. Moreover, the level of expression of the *GAS* gene observed in the leaves is residual (more than 2500 times lower compared to the buds).

The conducted research helps to broaden our knowledge on the biosynthesis of valuable secondary metabolites in materials of plant origin. Research aimed at characterizing the biosynthesis of secondary metabolites in plants has not only cognitive significance but also great practical potential. This knowledge can be used to select plants with highest level of biosynthesis of given compounds. In addition, by understanding the biosynthetic pathway well, scientists can try to influence it in order to increase the production of valuable metabolites. Another perspective is the use of metabolic engineering to increase the production of valuable secondary metabolites in plant cells using genetic engineering techniques.