The observed huge diversity of the living world is the reflection of the diversity of genetic information encoded in our DNA. This is where all the instructions needed to change a single cell into a complex organism are contained. With just a few exceptions, the DNA contained in each cell of the same organism has exactly the same sequence. So how do genetically identical groups of cells arise in different ways? The key to understanding the answer to this question is to realize that the DNA contained in a cell is not freely distributed there. Each human cell contains about 2 meters of DNA. In contrast, the nucleus, a structure in which the DNA is located, has a diameter of about 0.00001 meters. This can be compared to a rope 20 kilometers long closed in football. Placing in such a small volume, such a long thread requires an extremely tight and organized packaging. The DNA of all nuclear organisms is wrapped around protein complexes called nucleosomes, forming a structure resembling beads on the string, which biologists call chromatin. In order to read the information contained in the genes and convert it into a functional product, special proteins, responsible for their activation, must first be attached to the desired gene. However, this task is difficult due to the strict packaging of chromatin.

Since chromatin packaging is necessary but it also hinders access to proteins that are responsible for gene reading, there must exist mechanisms, which allow for specific relaxation of the chromatin structure only at a specific location and time. This role is executed by the specialized chromatin remodeling protein complexes. There are several types of such complexes, but the best known and, playing one of the most important role in gene reading are SWI/SNF complexes. These complexes consist of several proteins, some of which compose the core of the complex while others are attached and disconnected depending on the time and location of the complex action. One of the core proteins retained by evolution in all described SWI/SNF complexes is the SNF5 protein. In yeast, the absence of this protein affects the structure of the complex and makes it improperly functioning. In humans, the lack of SNF5 results in the development of extremely aggressive cancers which are difficult to treat.

The above data suggest that this protein plays an extremely important role in all organisms. However, in our lab, we identified plants (*Arabidopsis thaliana*) with a inactivated gene coding for this protein, which means that it cannot be produced. These plants did not show significant changes in appearance and developmental cycle. This is an unexpected result and gives us a unique opportunity to better understand the function of SNF5 protein (called BSH in Arabidopsis) in plants, because by having plants lacking this protein, we can test how it affects the cellular processes of the plant and on that basis we can conclude its function. In this project we want to cross mutants in the SNF5 encoding gene with mutants in genes encoding other components of the SWI/SNF complex so that we can understand the mutual functional relationships between these proteins. We will also check reading of which genes is influenced by SNF5, where the SNF5 attaches DNA to regulate them directly and how ultimately it all affects the chemical composition of plant cells.